


```

Matches      20;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

QY      1  GAGCGGACGCCCCCTCTCCA  20
      1  GAGCGGACGCCCCCTCTCCA  20

Db

RESULT 2
LOCUS      AX286668
DEFINITION      Sequence 9 from Patent WO0181554.
ACCESSION      AX286668
VERSION      AX286668.1  GI:17048736
KEYWORDS
SOURCE      .
ORGANISM      synthetic construct
              other sequences; artificial sequences.
REFERENCE      1
AUTHORS      Conzelmann,K.K.
TITLE      Pneumovirus ns proteins antagonising the interferon (ifn) response
JOURNAL      Patent: WO 0181554-A 9 01-NOV-2001;
              Conzelmann, Karl-Klaus, Prof. Dr. (DE)
              Location/Qualifiers
FEATURES
  source
    1..57
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="Primer hns1-Nor15"

ORIGIN

Query Match
Best Local Similarity  77.0%;  Score 15.4;  DB 6;  Length 57;
Matches      16;  Conservative      0;  Mismatches      1;  Indels      0;  Gaps      0;

QY      2  AGCGGACGCCCCCTCTC  18
      6  AGCGGACGCCCCCTCTC  22

Db

RESULT 3
LOCUS      A00424/c
DEFINITION      Nucleotide sequence 11 from patent number WO8903877.
ACCESSION      A00424
VERSION      A00424.1  GI:14496
KEYWORDS
SOURCE      .
ORGANISM      unidentified
              unclassified sequences.
REFERENCE      1 (bases 1 to 60)
AUTHORS      Nigon,V.M.
TITLE      INTEGRATION AND EXPRESSION VIRAL VECTORS
JOURNAL      Patent: WO 8903877-A 11 05-MAY-1989;
              Institut de la Recherche Agromomique
              Location/Qualifiers
FEATURES
  source
    1..60
    /organism="unidentified"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32644"

ORIGIN

Query Match
Best Local Similarity  74.0%;  Score 14.8;  DB 6;  Length 60;
Matches      16;  Conservative      0;  Mismatches      2;  Indels      0;  Gaps      0;

QY      2  AGCGGACGCCCCCTCTCC  19
      22  AGCGGACGCCCCCTCTAC  5

Db

RESULT 4
LOCUS      CQ818714
      CQ818714      70 bp  DNA      linear  PAT 07-JUN-2004

```

```

DEFINITION      Sequence 144 from Patent WO2004039825.
ACCESSION      CQ818714
VERSION      CQ818714.1  GI:48427320
KEYWORDS
SOURCE      .
ORGANISM      synthetic construct
              synthetic construct
              other sequences; artificial sequences.
REFERENCE      1
AUTHORS      fresky Rd,P.O., Franch,T., Gouliayev,A.H., Lundorf,M.D., Felding,J.,
              Olsen,E.K., Holcman,A., Jakobsen,S.R., Sans,C., Glad,S.S.,
              Jensen,K.B. and Pedersen,H.
TITLE      Enzymatic encoding
JOURNAL      Patent: WO 2004039825-A 144 13-MAY-2004;
              Nuevolution A/S (DK)
              Location/Qualifiers
FEATURES
  source
    1..70
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="Artificially produced"
    46..50
    /note="n represents inosine (I)"

ORIGIN      misc_feature

Query Match
Best Local Similarity  74.0%;  Score 14.8;  DB 6;  Length 70;
Matches      16;  Conservative      0;  Mismatches      2;  Indels      0;  Gaps      0;

QY      1  GAGCGGACGCCCCCTCTC  18
      17  GAGCGGACGCCCCCGCTC  34

Db

RESULT 5
LOCUS      CHKER5LD/c
DEFINITION      Chicken RAV-O endogenous retrovirus, 5' leader region.
ACCESSION      M13372
VERSION      M13372.1  GI:211747
KEYWORDS      mutational analysis.
SOURCE      Gallus gallus (chicken)
ORGANISM      Gallus gallus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
              Phasianinae; Gallus.
REFERENCE      1 (bases 1 to 80)
AUTHORS      Katz,R.A., Terry,R.W. and Skalka,A.M.
TITLE      A conserved cis-acting sequence in the 5' leader of avian sarcoma
              virus RNA is required for packaging
JOURNAL      J. Virol. 59 (1), 163-167 (1986)
PUBMED      3012114
COMMENT      Original source text: Chicken DNA, clone pUD62.
              Draft entry and clean copy of sequence for [1] kindly provided by
              R.A.Katz, 10-Oct-1986.
              The 5' leader of the RAV-O endogenous retrovirus was inserted into
              Rous sarcoma virus (SR-B). Deletions (positions 17-47) in the 5'
              leader region of the insert resulted in loss of infectivity of
              SR-B, although the envelope gene was expressed normally. The
              amount of mutant viral RNA encapsidated into virions was severely
              reduced, despite the presence of helper-virus. The deleted DNA is
              probably an essential cis-acting packaging signal in SR-B.
              Location/Qualifiers
FEATURES
  source
    1..80
    /organism="Gallus gallus"
    /mol_type="genomic DNA"
    /db_xref="taxon:9031"
    <1..>80
    /product="env mRNA"

ORIGIN      59 bp upstream of SacI site.

Query Match
Best Local Similarity  74.0%;  Score 14.8;  DB 5;  Length 80;
Matches      16;  Conservative      0;  Mismatches      2;  Indels      0;  Gaps      0;

```

QY 2 AGCGGACGCCCTCTCC 19
DB 23 AGCGGACGCCCTCTAC 6

RESULT 6
AX523638/c
LOCUS AX523638 81 bp DNA linear PAT 24-OCT-2002
DEFINITION Sequence 18 from Patent WO02064760.
ACCESSION AX523638
VERSION AX523638.1 GI:24412440
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Mueller,R., Thalhofer,J.P., Geipel,F., Glaser,S., Hoelke,W.,
Schoen,H. and Kirschbaum,T.
TITLE Expression of recombinant proteinase k from tritirachium album in
yeast
JOURNAL Patent: WO 02064760-A 18 22-AUG-2002;
Roche Diagnostics GmbH (DE) ; F.HOFFMANN-LA ROCHE AG (CH)
FEATURES
source 1..81
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

ORIGIN
Query Match 74.0%; Score 14.8; DB 6; Length 81;
Best Local Similarity 88.9%; Pred. No. 7.5e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GCGGACGCCCTCTCCA 20
DB 75 GCGGACGACCCGCTCCA 58

RESULT 7
AX538742/c
LOCUS AX538742 81 bp DNA linear PAT 23-NOV-2002
DEFINITION Sequence 18 from Patent WO02072634.
ACCESSION AX538742
VERSION AX538742.1 GI:25271389
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Mueller,R., Thalhofer,J.P., Rexer,B., Schmuck,R., Geipel,F.,
Glaser,S., Schoen,H., Meier,T., Rudolph,R., Lalle,H. and Schott,B.
TITLE Recombinant proteinase k
JOURNAL Patent: WO 02072634-A 18 19-SEP-2002;
Roche Diagnostics GmbH (DE) ; F. HOFFMANN-LA ROCHE AG (CH)
FEATURES
source 1..81
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

ORIGIN
Query Match 74.0%; Score 14.8; DB 6; Length 81;
Best Local Similarity 88.9%; Pred. No. 7.5e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GCGGACGCCCTCTCCA 20
DB 75 GCGGACGACCCGCTCCA 58

RESULT 8
CQ008211
LOCUS CQ008211 50 bp DNA linear PAT 16-JAN-2004
DEFINITION Sequence 6851 from Patent WO0147944.
ACCESSION CQ008211
VERSION CQ008211.1 GI:41014903
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shinkels,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0147944-A 6851 05-JUL-2001;
Curagen Corporation (US)
FEATURES
source 1..50
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Nucleotide deleted between bases 25 and 26
Accession number cg43950268"

misc_Feature
ORIGIN
Query Match 72.0%; Score 14.4; DB 6; Length 50;
Best Local Similarity 93.8%; Pred. No. 1.2e+05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCGAGCCCTCTCCA 20
DB 17 GCGAGCCCACTCCA 32

RESULT 9
AX073623
LOCUS AX073623 55 bp DNA linear PAT 06-FEB-2001
DEFINITION Sequence 14 from Patent WO0104335.
ACCESSION AX073623
VERSION AX073623.1 GI:12710046
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Buchholz,U., Collins,P.L., Murphy,B.R., Whitehead,S.S. and
Kremp,C.D.
TITLE Human-bovine chimeric respiratory syncytial virus vaccines
JOURNAL Patent: WO 0104335-A 14 18-JAN-2001;
THE GOVERNMENT OF THE UNITED STATES OF AMERICA (US)
FEATURES
source 1..55
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic respiratory syncytial virus"

ORIGIN
Query Match 72.0%; Score 14.4; DB 6; Length 55;
Best Local Similarity 93.8%; Pred. No. 1.2e+05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCGGACGCCCTCTC 18
DB 22 GCGGCGCCCTCTC 37

RESULT 10
AX359862
LOCUS AX359862 55 bp DNA linear PAT 13-FEB-2002

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DEFINITION Sequence 13 from Patent WO0200693.
ACCESSION AX359862
VERSION AX359862.1 GI:18675538
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Krempel,C.D., Collins,P.L., Murphy,B.R., Buchholz,U. and
TITLE Whitehead,S.S.
JOURNAL Respiratory syncytial virus vaccines expressing protective antigens
from promotor-proximal genes
Patent: WO 0200693-A 13 03-JAN-2002;
FEATURES
location/Qualifiers
source
1..55
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Artificial Respiratory Syncytial Virus"
ORIGIN
Query Match 72.0%; Score 14.4; DB 6; Length 55;
Best Local Similarity 93.8%; Pred. No. 1.2e+05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCGGCGAGCCCTCTC 18
Db 22 GCGGCGCCCTCTC 37

RESULT 11
LOCUS AX286671 60 bp DNA linear PAT 21-NOV-2001
DEFINITION Sequence 12 from Patent WO0181554.
ACCESSION AX286671
VERSION AX286671.1 GI:17048739
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Conzelmann,K.K.
TITLE Pneumovirus ns proteins antagonising the interferon (ifn) response
JOURNAL Patent: WO 0181554-A 12 01-NOV-2001;
FEATURES
location/Qualifiers
source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer mNS1-NC1BCORVS"
ORIGIN
Query Match 72.0%; Score 14.4; DB 6; Length 60;
Best Local Similarity 93.8%; Pred. No. 1.2e+05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCGGCGAGCCCTCTC 18
Db 10 GCGGCGCCCTCTC 25

RESULT 12
LOCUS CQ818711 71 bp DNA linear PAT 07-JUN-2004
DEFINITION Sequence 141 from Patent WO2004039825.
ACCESSION CQ818711
VERSION CQ818711.1 GI:48427317
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS
TITLE
JOURNAL
FEATURES
location/Qualifiers
source
1..71
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Artificially produced"
ORIGIN
Query Match 72.0%; Score 14.4; DB 6; Length 71;
Best Local Similarity 93.8%; Pred. No. 1.1e+05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAGCGGAGCCCTCTC 16
Db 17 GAGCGGAGCCCTCTC 32

RESULT 13
LOCUS CQ818717 71 bp DNA linear PAT 07-JUN-2004
DEFINITION Sequence 147 from Patent WO2004039825.
ACCESSION CQ818717
VERSION CQ818717.1 GI:48427323
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS
TITLE
JOURNAL
FEATURES
location/Qualifiers
source
1..71
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Artificially produced"
ORIGIN
Query Match 72.0%; Score 14.4; DB 6; Length 71;
Best Local Similarity 93.8%; Pred. No. 1.1e+05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAGCGGAGCCCTCTC 16
Db 17 GAGCGGAGCCCTCTC 32

RESULT 14
LOCUS CQ818720 71 bp DNA linear PAT 07-JUN-2004
DEFINITION Sequence 150 from Patent WO2004039825.
ACCESSION CQ818720
VERSION CQ818720.1 GI:48427326
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS
TITLE
JOURNAL
FEATURES
location/Qualifiers
source
1..71
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Artificially produced"
ORIGIN
Query Match 72.0%; Score 14.4; DB 6; Length 71;
Best Local Similarity 93.8%; Pred. No. 1.1e+05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAGCGGAGCCCTCTC 16
Db 17 GAGCGGAGCCCTCTC 32

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REFERENCE
1
AUTHORS freskg Rd,P.O., Franch,T., Gouliayev,A.H., Lundorf,M.D., Felding,J.,
Olsen,E.K., Holtmann,A., Jakobsen,S.R., Sams,C., Glad,S.S.,
Jensen,K.B. and Pedersen,H.
TITLE Enzymatic encoding
JOURNAL Patent: WO 2004039825-A 141 13-MAY-2004;
FEATURES
location/Qualifiers
source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Artificially produced"
misc_feature
47..51
/note="n represents inosine (I)"
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Query Match 72.0%; Score 14.4; DB 6; Length 71;
Best Local Similarity 93.8%; Pred. No. 1.1e+05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAGCGGAGCCCTCTC 16
Db 17 GAGCGGAGCCCTCTC 32

RESULT 13
LOCUS CQ818717 71 bp DNA linear PAT 07-JUN-2004
DEFINITION Sequence 147 from Patent WO2004039825.
ACCESSION CQ818717
VERSION CQ818717.1 GI:48427323
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS freskg Rd,P.O., Franch,T., Gouliayev,A.H., Lundorf,M.D., Felding,J.,
Olsen,E.K., Holtmann,A., Jakobsen,S.R., Sams,C., Glad,S.S.,
Jensen,K.B. and Pedersen,H.
TITLE Enzymatic encoding
JOURNAL Patent: WO 2004039825-A 147 13-MAY-2004;
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location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Artificially produced"
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Query Match 72.0%; Score 14.4; DB 6; Length 71;
Best Local Similarity 93.8%; Pred. No. 1.1e+05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAGCGGAGCCCTCTC 16
Db 17 GAGCGGAGCCCTCTC 32

RESULT 14
LOCUS CQ818720 71 bp DNA linear PAT 07-JUN-2004
DEFINITION Sequence 150 from Patent WO2004039825.
ACCESSION CQ818720
VERSION CQ818720.1 GI:48427326
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS freskg Rd,P.O., Franch,T., Gouliayev,A.H., Lundorf,M.D., Felding,J.,
Olsen,E.K., Holtmann,A., Jakobsen,S.R., Sams,C., Glad,S.S.,
Jensen,K.B. and Pedersen,H.
TITLE Enzymatic encoding
JOURNAL Patent: WO 2004039825-A 150 13-MAY-2004;
FEATURES
location/Qualifiers
source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Artificially produced"
ORIGIN
Query Match 72.0%; Score 14.4; DB 6; Length 71;
Best Local Similarity 93.8%; Pred. No. 1.1e+05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAGCGGAGCCCTCTC 16
Db 17 GAGCGGAGCCCTCTC 32

```


TITLE Jensen, K.B. and Pedersen, H.
Enzymatic encoding
JOURNAL Patent: WO 2004039825-A 150 13-MAY-2004;
Nuevolution A/S (DK)

FEATURES
source 1..71
Location/Qualifiers

/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Artificially produced"

ORIGIN

Query Match 72.0%; Score 14.4; DB 6; Length 71;
Best Local Similarity 93.8%; Pred. No. 1.1e+05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAGCGGAGCCCCCTC 16
Db 17 GAGCGGAGCCCCCCC 32

RESULT 15

AX204378 51 bp DNA linear PAT 30-AUG-2001
LOCUS AX204378/c
DEFINITION Sequence 484 from Patent WO0148245.
ACCESSION AX204378
VERSION AX204378.1 GI:15393911
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0148245-A 484 05-JUL-2001;
Curagen Corporation (US)

FEATURES
source 1..51
Location/Qualifiers

/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

variation

26
/note="single nucleotide polymorphism"
Accession number CG40310734"

ORIGIN

Query Match 71.0%; Score 14.2; DB 6; Length 51;
Best Local Similarity 84.2%; Pred. No. 1.5e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAGCGGAGCCCCCTCCTCC 19
Db 19 GAGCAGCAGCACCACTCC 1

Search completed: December 24, 2005, 14:06:00
Job time : 585 secs

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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 01:41:40 ; Search time 171.4 Seconds
(without alignments)
777.677 Million cell updates/sec

Title: US-09-296-264-1

Perfect score: 20
Sequence: 1 gagcgagcagccccctccca 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 3390896

Minimum DB seq length: 20

Maximum DB seq length: 100

Post-processing: Minimum Match 10%
Maximum Match 100%
Listing first 45 summaries

Database :

N_Geneseq_21:*
1: geneeqn1980s:*
2: geneeqn1990s:*
3: geneeqn2000s:*
4: geneeqn2001s:*
5: geneeqn2001bs:*
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7: geneeqn2002bs:*
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12: geneeqn2004s:*
13: geneeqn2004bs:*
14: geneeqn2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3 AA231431	Aa231431 Human neu
2	20	100.0	20	2 ADA74683	Ada74683 GTT3601 a
3	20	100.0	35	8 ACC80168	Acc80168 Human neu
4	15.2	76.0	28	10 ADK71246	Adk71246 Drug-tole
5	15.2	76.0	45	14 AEA31362	Aea31362 Human DNA
6	14.8	74.0	21	12 ADP75955	Adp75955 Human leu
7	14.8	74.0	81	6 ABO81759	Abg81759 Trilicrch
8	14.8	74.0	81	6 ABV73412	Abv73412 Trilicrch
9	14.4	72.0	50	4 AAL33643	Aal33643 Human SNP
10	14.4	72.0	55	5 AAF25148	Aaf25148 Nucleocid
11	14.4	72.0	55	6 AAK13065	Aak13065 Recombina
12	14.4	72.0	71	12 ADO04209	Ado04209 Identifie
13	14.4	72.0	71	12 ADO04205	Ado04205 Identifie
14	14.2	71.0	30	2 AAO97261	Aao97261 Nor-dc ol
15	14.2	71.0	51	4 AAH79869	Aah79869 Human DNA
16	14.2	71.0	71	10 ADE93755	Ade93755 Human tra
17	13.8	69.0	65	6 AAN52872	Aan52872 Mouse spl
18	13.8	69.0	90	2 AAO49420	Aao49420 Cytochrom
19	13.6	68.0	30	13 ADU86387	Adu86387 U6 promot

20	13.6	68.0	50	6 AB200178	Abz00178 Human leu
21	13.6	68.0	55	6 ABA91984	Abz91984 Single nu
22	13.6	68.0	57	2 ABA96211	Abz96211 Extracell
23	13.6	68.0	65	6 ABN57612	Abn57612 Mouse spl
24	13.6	68.0	70	14 ADZ27568	Adz27568 Chemosen
25	13.6	68.0	84	2 AAX87463	Aax87463 Plaemid p
26	13.6	68.0	92	3 AAC07582	Aac07582 Human sec
27	13.4	67.0	31	11 ADI35330	Adi35330 Ant-i-PCga
28	13.4	67.0	37	5 AAH43131	Aah43131 Primer: F
29	13.4	67.0	42	5 AAH43133	Aah43133 Primer: F
30	13.4	67.0	50	4 AAH78099	Aah78099 Human gll
31	13.4	67.0	51	4 AAH73503	Aah73503 Human gll
32	13.4	67.0	51	4 AAH78098	Aah78098 Human gll
33	13.4	67.0	51	4 AAH73502	Aah73502 Human gll
34	13.4	67.0	93	10 ADG38769	Adg38769 Frog fibr
35	13.4	67.0	100	10 ADE94000	Ade94000 Multiclon
36	13.4	67.0	100	10 ADE94001	Ade94001 Multiclon
37	13.2	66.0	20	4 AAH48586	Aah48586 Human Fas
38	13.2	66.0	20	8 ABZ75980	Abz75980 Human GAV
39	13.2	66.0	24	12 ADL67243	Adl67243 Human 4-1
40	13.2	66.0	24	14 AEB93504	Aeb93504 Human SIP
41	13.2	66.0	25	9 ACT12192	Act12192 Human mlg
42	13.2	66.0	27	2 AAV21278	Aav21278 Tissue pl
43	13.2	66.0	29	12 ADO22496	Ado22496 Human EDG
44	13.2	66.0	29	12 ADO22495	Ado22495 Human EDG
45	13.2	66.0	30	2 AAT09304	Aat09304 Murine an

ALIGNMENTS

RESULT 1	AA231431	AA231431 standard; DNA; 20 BP.
ID	AA231431	
XX	AA231431;	
AC		
XX		
DT	07-FEB-2000	(first entry)
XX		
DE	Human neuropilin mRNA specific antisense oligo GTT3601.	
XX		
KW	Neuropilin; human; growth; metastasis; tumor; neovascularisation; cancer;	
XX	papilloma; diabetic retinopathy; antisense; ss.	
OS	Synthetic.	
XX	Homo sapiens.	
XX	WO955855-A2.	
XX		
PD	04-NOV-1999.	
XX		
PF	23-APR-1999;	99WO-CA000324.
XX		
FR	23-APR-1998;	98US-0082791P.
XX		
PA	(GENE-) GENESENSE TECHNOLOGIES INC.	
XX		
PI	Wright JA, Young AH, Lee YS;	
XX		
DR	WPI; 2000-023357/02.	
XX		
PT	Antisense oligonucleotides that inhibit neuropilin expression, useful for	
XX	treating cancer.	
XX		
PS	Claim 4; Page 16; 57pp; English.	
XX		
CC	Sequences AA231431-460 represent antisense oligonucleotides which inhibit	
CC	human neuropilin expression. The antisense oligonucleotides can be used	
CC	to inhibit the growth or metastasis of a mammalian tumor and inhibit	
CC	neovascularisation. The oligonucleotides may be used to treat various	
CC	forms of cancers or tumors, such as sarcomas, melanomas, adenomas,	
CC	carcinomas of solid tissue, hypoxic tumors, squamous cell carcinomas of	
CC	the mouth, throat, larynx and lung, genitourinary cancers such as	

CC cervical and bladder cancer, hematopoietic cancers, colon cancer, breast
CC cancer, pancreatic cancer, renal cancer, brain cancer, skin cancer, liver
CC cancer, head and neck cancers, and nervous system cancers, as well as
CC benign lesions such as papillomas. The methods may be used to treat
CC neovascularisation disorders such as diabetic retinopathy, and
CC retinopathy of prematurity and age related macular degeneration
CC
SQ Sequence 20 BP; 3 A; 10 C; 5 G; 2 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAGCGGACAGCCCCCTCTCCA 20
Db 1 GAGCGGACAGCCCCCTCTCCA 20
RESULT 2
ADA74683
ID ADA74683 standard; DNA; 20 BP.
XX
AC ADA74683;
XX
DT 20-NOV-2003 (first entry)
XX
DE GT13601 antisense oligonucleotide targeted to human neuropilin mRNA.
XX
KW neuropilin; VEGF165R; vascular endothelial growth factor receptor;
KM cytosolic; growth; tumour metastasis; angiogenesis; gene therapy;
KW GT13601; antisense; human; ss.
XX
OS Homo sapiens.
XX
PN US2003083274-A1.
XX
PD 01-MAY-2003.
XX
PF 22-APR-1999; 99US-00296264.
XX
PR 23-APR-1998; 98US-0082791P.
XX
PA (WRIGHT) WRIGHT J A.
PA (YOUNG) YOUNG A H.
PA (LEEVY) LEEVY S.
XX
PI Wright JA, Young AH, Lee YS;
XX
DR WPI; 2003-576622/54.
XX
PT New antisense oligonucleotide that inhibits neuropilin expression, useful
PT for inhibiting growth of mammalian tumor or inhibiting metastasis of a
PT mammalian tumor.
XX
PS Claim 1; Page 5; 27pp; English.
XX
CC The invention relates to a novel antisense oligonucleotide that inhibits
CC the expression of neuropilin, also known as VEGF165R (vascular
CC endothelial growth factor receptor). The oligonucleotide of the invention
CC demonstrates cytostatic activity and may be useful for inhibiting the
CC growth or metastasis of a mammalian tumour and to inhibit angiogenesis in
CC mammals. Furthermore, the oligonucleotide may be utilised during gene
CC therapy. The current sequence is that of the GT13601 antisense
CC oligonucleotide of the invention which is targeted to human neuropilin
CC mRNA.
XX
SQ Sequence 20 BP; 3 A; 10 C; 5 G; 2 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAGCGGACAGCCCCCTCTCCA 20

Db 1 GAGCGGACAGCCCCCTCTCCA 20
RESULT 3
ACC80168/c
ID ACC80168 standard; DNA; 35 BP.
XX
AC ACC80168;
XX
DT 04-AUG-2003 (first entry)
XX
DE Human neuropilin-1 gene PCR primer #1.
XX
KW Cytostatic; Neuropilin-1 receptor; NP-1 receptor; angiogenesis; cancer;
KW Vascular Endothelial Growth Factor Receptor-2; VEGFR-2; PlGF; VEGF;
KW Placental Growth Factor; Vascular Endothelial Growth Factor;
KW anti-angiogenic; human; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO2003029275-A2.
XX
PD 10-APR-2003.
XX
PF 02-OCT-2002; 2002WO-US031386.
XX
PR 03-OCT-2001; 2001US-0326712P.
XX
PA (REGG-) REGENERON PHARM INC.
PA (PROC) PROCTER & GAMBLE CO.
XX
PI Rosenbaum JS, Jones DR, Whitaker GB;
XX
DR WPI; 2003-371982/35.
XX
PT New anti-angiogenic peptides that are capable of binding to NP-1 or
PT vascular endothelial growth factor receptor (VEGFR)-2/NP-1 complex,
PT useful for treating diseases characterized by abnormal angiogenesis, such
PT as cancer.
XX
PS Disclosure; Page 21; 115pp; English.
XX
CC The present invention relates to peptides that are capable of binding to
CC Neuropilin-1 (NP-1) receptor or the Vascular Endothelial Growth Factor
CC Receptor (VEGFR)-2/NP-1 complex. The peptides are derived from a
CC combination of peptides from Exon 6 of Placental Growth Factor (PlGF),
CC coupled at the carboxyl terminus to either Exon 8 of Vascular Endothelial
CC Growth Factor (VEGF) isoform 165 (VEGF165, also referred to as P6V8) or
CC Exon 7 of PlGF (referred to as P6P7). The peptides and compositions are
CC useful for treating diseases characterised by abnormal angiogenesis, such
CC as cancer. The present peptide is a PCR primer, which was used to
CC illustrate the invention
XX
SQ Sequence 35 BP; 7 A; 8 C; 11 G; 9 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 8; Length 35;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAGCGGACAGCCCCCTCTCCA 20
Db 31 GAGCGGACAGCCCCCTCTCCA 12
RESULT 4
ADK71246
ID ADK71246 standard; DNA; 28 BP.
XX
AC ADK71246;
XX
DT 06-MAY-2004 (first entry)
XX

DE Drug-tolerant gene related PCR primer.
XX
XX detection; drug-tolerant gene; gene chip; probe; PCR; amplification;
KM hybridisation; primer; ss.
XX
OS Synthetic.
XX
XX CN1396271-A.
XX
PD 12-FEB-2003.
XX
XX
PF 13-JUL-2001; 2001CN-00120441.
XX
PR 13-JUL-2001; 2001CN-00120441.
XX
PA (SANX-) SANXIONG HI TECH DEV CO LTD BEIJING.
XX
PI Liu Y, Wang H, Li L;
XX
XX WPI; 2003-442250/42.
DR
XX
XX
PT Detection to drug tolerant gene by gene chip technique.
XX
PS Claim 4; Page 15; 32pp; Chinese.
XX
CC The present invention describes a process for detecting a drug-tolerant
CC gene with a gene chip technique. The method comprises fixing the DNA
CC sequence of an oligonucleotide probe to a carrier of a gene chip, the DNA
CC sequence of an elongation primer for the PCR linear amplification of a
CC target drug-tolerant gene, PCR amplification, and hybridisation of the
CC PCR resultant with a probe on the chip. The present sequence represents a
CC PCR primer which is used in the exemplification of the present invention.
XX
SQ Sequence 28 BP; 6 A; 10 C; 6 G; 6 T; 0 U; 0 Other;
Query Match 76.0%; Score 15.2; DB 10; Length 28;
Best Local Similarity 85.0%; Pred. No. 7.3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GAGCGGAGCCCCCTCTCCA 20
DB 6 GAGCGGAGCACTATCTCCA 25
RESULT 5
ID AEA31362 standard; DNA; 45 BP.
XX
XX AEA31362;
AC
XX
DT 11-AUG-2005 (first entry)
XX
XX
DE Human DNA oligonucleotide #4.
XX
XX Transposon; retrotransposon; genetic disorder; hemophilia;
KM Parkinsons disease; Fabry disease; hypercholesterolemia;
KM Gauchers disease; cystic fibrosis; adrenoleukodystrophy;
KM adenosine deaminase deficiency; alpha-1 antitrypsin deficiency;
KM Duchenne dystrophy; phenylketonuria; sickle cell anemia;
KM Tay Sachs disease; thalassemia; lysosomal storage disease;
KM metabolic disorder; antiparkinsonian; hemostatic; metabolic; antileptic;
KM CNS-gen.; respiratory-gen.; antianemic; cerebroprotective; muscular-gen.;
KM dermatological; nootropic; antisticking; ss.
XX
XX Homo sapiens.
OS
XX
XX WO2005049789-A2.
PN
XX
XX 02-JUN-2005.
PD
XX
XX 18-MAY-2004; 2004WO-US015810.
PF
XX
XX 28-MAY-2003; 2003US-0473658P.
PR

XX
XX (UYXO) UNIV JOHNS HOPKINS.
PA
XX
XX Boeke JD, Han US;
PI
XX
XX WPI; 2005-396089/40.
DR
XX
XX
XX
PT New synthetic mammalian (retro)transposon open reading frame 2 (ORF2) or
PT ORF1 gene exhibiting a higher level of expression relative to a natural
PT L1 (retro)transposon ORF2 or ORF1 gene, useful for treating e.g.,
PT metabolic diseases.
XX
XX
PS Disclosure; SEQ ID NO 213; 66pp; English.
XX
XX
XX The invention relates to a synthetic mammalian (retro)transposon ORF2 or
CC ORF1 gene exhibiting a higher level of expression relative to a natural
CC L1 (retro)transposon ORF2 or ORF1 gene. The invention also relates to a
CC (retro)transposon comprising the synthetic gene, a mammalian L1
CC retrotransposon comprising the synthetic gene, a recombinant vector
CC construct comprising the synthetic gene, a eukaryotic cell transfected,
CC transformed or infected with the recombinant vector construct, a method
CC of delivering a desired gene, or its biologically active fragment, to the
CC cells of a mammal, a composition comprising a cassette comprising the
CC gene, a desired gene and a pharmaceutical carrier, and a method of
CC identifying an uncharacterized gene, or its biologically active fragment,
CC in cells. The composition is useful for treating a genetic disorder in a
CC mammal such as hemophilia, Parkinsons disease, Fabry disease,
CC hypercholesterolemia, Gauchers disease, cystic fibrosis,
CC adrenoleukodystrophy, disorders associated with mutations in the
CC dystrophin gene, adenosine deaminase deficiency, alpha-antitrypsin
CC deficiency, Duchenne muscular dystrophy, phenylketonuria, sickle cell
CC anemia, Tay Sachs disease, thalassemia, lysosomal storage diseases and
CC metabolic disorders. The synthetic gene is useful for treating the
CC diseases. This sequence represents a human DNA oligonucleotide used in
CC the scope of the invention.
XX
SQ Sequence 45 BP; 0 A; 12 C; 23 G; 10 T; 0 U; 0 Other;
Query Match 76.0%; Score 15.2; DB 14; Length 45;
Best Local Similarity 85.0%; Pred. No. 7.2e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GAGCGGAGCCCCCTCTCCA 20
DB 44 GAGCGGAGCCCCCCCCCA 25
RESULT 6
ID ADP75955 standard; DNA; 21 BP.
XX
XX ADP75955;
AC
XX
XX
DT 09-SEP-2004 (first entry)
XX
XX Human leukaemia inhibiting factor PCR primer SeqIDS.
DE
XX
XX matrix binding region; cell surface; extracellular matrix;
KM leukaemia inhibitory factor region; cell differentiation;
KM embryonic stem cell; PCR; primer; ss; human.
XX
XX Homo sapiens.
OS
XX
XX JP2004166641-A.
PN
XX
XX 17-JUN-2004.
PD
XX
XX 21-NOV-2002; 2002JP-00338373.
PF
XX
XX 21-NOV-2002; 2002JP-00338373.
PR
XX
XX (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
PA (AIZU/) AIZU Y.

XX WP1; 2004-445579/42.
 DR
 XX
 PT Novel protein which has matrix binding region which assembles to cell
 PT surface, or to extracellular matrix surrounding cell and leukemia
 PT inhibitory factor region that suppresses cell differentiation of
 PT embryonic stem cell.
 XX
 PS Example 1; SEQ ID NO 5; 49bp; Japanese.
 CC This invention relates to a novel protein (and the gene which encodes it)
 CC which has a matrix binding region which assembles to a cell surface, or
 CC extracellular matrix surrounding the cell, and a leukemia inhibitory
 CC factor region which suppresses cell differentiation of embryonic stem
 CC cells. The invention is useful for suppressing cell differentiation. The
 CC invention can be used for the efficient inhibition of embryonic stem cell
 CC differentiation. The invention thus enables efficient and continuous
 CC proliferation of embryonic stem cells. Therefore, embryonic stem cells
 CC can be prepared in large quantities and utilised for fundamental research
 CC and applications. The present sequence is that of a PCR primer which was
 CC used for amplification of a region of the human leukaemia inhibitory
 CC factor CDNA in the exemplification of the invention.
 CC
 SQ Sequence 21 BP; 2 A; 13 C; 4 G; 2 T; 0 U; 0 Other;
 Query Match 74.0%; Score 14.8; DB 12; Length 21;
 Best Local Similarity 88.9%; Pred. No. 1.1e+04;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 GCGGCGAGCCCTCTCCCA 20
 DB 2 GCGGCGAGCCCTCTCCCA 19
 RESULT 7
 AB081759/c
 ID AB081759 standard; DNA; 81 BP.
 XX
 AC AB081759;
 XX
 DT 29-AUG-2003 (revised)
 DT 29-NOV-2002 (first entry)
 XX
 DE Trifirachium album limber proteinase K PCR primer SEQ ID NO 18.
 XX
 DE Trifirachium album limber; proteinase K; enzyme; PCR; primer; ss.
 XX
 KW Trifirachium album; limber.
 OS
 XX Trifirachium album; limber.
 XX
 PN DE10105912-A1.
 XX
 PD 14-AUG-2002.
 XX
 PF 09-FEB-2001; 2001DE-01005912.
 XX
 PR 09-FEB-2001; 2001DE-01005912.
 XX
 PA (HOF) ROCHE DIAGNOSTICS GMBH.
 XX
 PI Mueller R, Schoen H, Schmuck R, Geipel F, Meier T, Glaser S;
 PI Rexer B, Thalhofer J, Scholt B, Rudolph R, Lill H;
 XX
 DR WP1; 2002-667991/72.
 XX
 PT Renaturing denatured zymogenic proteinase K, useful e.g. for analysis, by
 PT incubation in folding buffer, especially applied to material solubilized
 PT from inclusion bodies.
 XX
 PS Example 1; Page 18; 36pp; German.
 CC The invention relates to renaturing (M1) denatured, zymogenic proteinase
 CC K (I), at 0-3pMnOC, by transfer to a folding buffer (A) that has pH 7.5
 CC -10.5 and includes: (1) low molecular weight folding auxiliaries; (11) a

CC redox shuffling system; and (11) a complexing agent at less than the
 CC stoichiometric amount relative to calcium ions present. (I) is useful in
 CC analysis and diagnosis (no details given). M1 allows the high expression
 CC potential and quick, simple growth of Escherichia coli to be exploited;
 CC permits genetic modification of the recombinant DNA used; reduces the
 CC extent of purification required after renaturation, and avoids
 CC contamination with eukaryotic materials. (I) is produced in homogeneous
 CC form. The present sequence is that of a PCR primer used to generated
 CC vectors expressing the Trifirachium album limber proteinase K protein
 CC gene sequence, used in examples of the invention. However, the disclosed
 CC gene sequence (AB081743) does not encode the disclosed proteinase K
 CC sequence (AB083956) of the invention. (Updated on 29-AUG-2003 to
 CC standardise OS field)
 CC
 SQ Sequence 81 BP; 18 A; 19 C; 33 G; 11 T; 0 U; 0 Other;
 Query Match 74.0%; Score 14.8; DB 6; Length 81;
 Best Local Similarity 88.9%; Pred. No. 1e+04;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 GCGGCGAGCCCTCTCCCA 20
 DB 75 GCGGCGAGCACTCCCTCCA 58
 RESULT 8
 ABV73412/c
 ID ABV73412 standard; DNA; 81 BP.
 XX
 AC ABV73412;
 XX
 DT 29-AUG-2003 (revised)
 DT 05-DEC-2002 (first entry)
 XX
 DE Trifirachium album limber proteinase K PCR primer SEQ ID NO 18.
 XX
 DE Trifirachium album limber; proteinase K; enzyme; PCR; primer; ss.
 XX
 OS Trifirachium album; limber.
 XX
 PN DE10105911-A1.
 XX
 PD 14-AUG-2002.
 XX
 PF 09-FEB-2001; 2001DE-01005911.
 XX
 PR 09-FEB-2001; 2001DE-01005911.
 XX
 PA (HOF) ROCHE DIAGNOSTICS GMBH.
 XX
 PI Mueller R, Thalhofer J, Geipel F, Glaser S, Hoelke W, Schoen H;
 PI Kirchbaum T;
 XX
 DR WP1; 2002-667990/72.
 XX
 PT Preparing recombinant proteinase K in yeast, useful for analysis and
 PT diagnosis, using a signal peptide for secretion of a precursor which is
 PT activated autocatalytically.
 XX
 PS Example 1; Page 13; 18pp; German.
 CC The invention relates to preparing recombinant proteinase K (I) by: (a)
 CC transforming a yeast cell with a vector containing DNA (II) that encodes
 CC a zymogenic precursor of (I), fused, upstream and in frame, with a
 CC sequence encoding a signal peptide (SP); (b) expressing the precursor;
 CC and (c) secretion of (I) in soluble form, followed by autocatalytic
 CC activation. (I) is useful in analysis and diagnosis (no details given).
 CC The method provides economical amounts of (I) in soluble, homogeneous and
 CC active form. Secretion avoids the toxic effects of cytosolic (I); ensures
 CC correct formation of disulfide bonds and unexpectedly, (I) has no effect
 CC on the surface proteins of the host cell. Yeast have a higher growth rate
 CC and are easier to handle than Trifirachium album, the native source of
 CC (I). The present sequence is that of a PCR primer for amplification of

CC the Trifirachium album limber proteinase K encoding DNA sequence of the
CC invention. (Updated on 29-AUG-2003 to standardise OS field)
XX
SQ Sequence 81 BP; 18 A; 19 C; 33 G; 11 T; 0 U; 0 Other;
Query Match 74.0%; Score 14.8; DB 6; Length 81;
Best Local Similarity 88.9%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 GCGGACGCCCTCTCCA 20
DB 75 GCGGACGACCCGCTCCA 58
GGGACGACCCCTCTCCA 58
RESULT 9
AAL33643
ID AAL33643 standard; DNA; 50 BP.
XX
AC AAL33643;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human SNP oligonucleotide #6851.
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
KW amyloid protein; angiopoietin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX
OS Homo sapiens.
XX
FN WO200147944-A2.
XX
PD 05-JUL-2001.
XX
PP 28-DEC-2000; 2000WO-US035498.
XX
PR 28-DEC-1999; 99US-0173419P.
PR 27-DEC-2000; 2000US-00173419.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkels RA, Leach M;
XX
DR WPI; 2001-465210/50.
XX
FT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
FT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
FT autoimmune diseases and infections.
XX
PS Claim 1; Page 3341; 4133pp; English.
XX
CC The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiopoietin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-
CC protein coupled receptors and thioesterases. The present sequence is one
CC such oligonucleotide. The oligonucleotides and the peptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of the proteins listed above.
CC Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukaemia), diseases of the nervous system and an infection of pathogenic
CC organisms

SQ Sequence 50 BP; 10 A; 16 C; 18 G; 6 T; 0 U; 0 Other;
Query Match 72.0%; Score 14.4; DB 4; Length 50;
Best Local Similarity 93.8%; Pred. No. 1.5e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 GCGAGCCCTCTCCA 20
DB 17 GCGAGCCCTCTCCA 32
GGGAGCCCTCTCCA 32
RESULT 10
AAF25148
ID AAF25148 standard; DNA; 55 BP.
XX
AC AAF25148;
XX
DT 30-APR-2001 (first entry)
XX
DE Nucleotide sequence of a recombinant Respiratory syncytial virus.
XX
KW Respiratory syncytial virus; RSV; attenuated vaccine; RSV A; RSV B; BRSV;
KW HSRV; ss.
XX
OS Respiratory syncytial virus.
XX
FN WO200104335-A2.
XX
PD 18-JAN-2001.
XX
PP 23-JUN-2000; 2000WO-US017755.
XX
PR 09-JUL-1999; 99US-0143132P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Buchholz U, Collins PL, Murphy BR, Whitehead SS, Krempf CD;
XX
DR WPI; 2001-103088/11.
XX
PP Isolated chimeric human-bovine respiratory syncytial virus (RSV), useful
PP in an attenuated vaccine to elicits an immune response against either or
PP both human RSV A or RSV B.
XX
PS Disclosure; Page 145; 148pp; English.
XX
CC The specification describes a chimeric human-bovine respiratory syncytial
CC virus (RSV) that is infectious and attenuated in humans. The virus
CC comprises a major nucleocapsid protein, a nucleocapsid phosphoprotein, a
CC large polymerase protein, a RNA polymerase elongation factor, and a
CC partial or complete RSV background genome, or antigenome of a human RSV
CC or bovine RSV, combined with one or more heterologous genes or genome
CC segment of a different RSV to form a human-bovine chimeric RSV genome or
CC antigenome. The chimeric RSV is useful in an attenuated vaccine to
CC elicits an immune response against either or both human RSV A or RSV B.
XX
PS The present sequence represents a fragment of a recombinant RSV
XX
SQ Sequence 55 BP; 14 A; 16 C; 11 G; 14 T; 0 U; 0 Other;
Query Match 72.0%; Score 14.4; DB 5; Length 55;
Best Local Similarity 93.8%; Pred. No. 1.5e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 GCGGACGCCCTCTC 18
DB 22 GCGGACGCCCTCTC 37
GGGACGCCCTCTC 37
RESULT 11
ABK13065
ID ABK13065 standard; DNA; 55 BP.
XX
AC ABK13065;

```

XX 23-APR-2002 (first entry)
DE Recombinant BRSV genome construct rBRSV/A2-G1F2 leader sequence.
XX
XX Respiratory syncytial virus; RSV; vaccine; immunostimulatory; antiviral;
KW gene therapy; rBRSV/A2-G1F2; ds.
XX
OS Bovine respiratory syncytial virus.
OS Synthetic.
XX
XX WO200200693-A2.
XX
XX 03-JAN-2002.
XX
XX 22-JUN-2001; 2001WO-US020107.
XX
XX 23-JUN-2000; 2000US-0213708P.
XX
XX (USGO ) US GOVERNMENT.
XX
XX Krempf CD, Collins PL, Murphy BR, Buchholz U, Whitehead SS;
XX WPI; 2002-090518/12.
XX
XX An isolated infectious recombinant respiratory syncytial virus (RSV)
PT having one or more shifted RSV gene(s) or genome segment(s) within the
PT recombinant genome or antigenome, useful as an attenuated vaccine against
PT RSV strains.
XX
XX Example 3; Fig 6; 168pp; English.
XX
XX The invention relates to an isolated infectious recombinant respiratory
CC syncytial virus (RSV) having one or more shifted RSV gene(s) or genome
CC segment(s) within the recombinant genome or antigenome that is/are
CC positionally shifted to a more promoter-proximal or promoter-distal
CC position relative to a position of the RSV gene(s) or genome segment(s)
CC within a wild type RSV genome or antigenome. Also described is (1) a
CC method for stimulating the immune system of an individual to induce
CC protection against RSV which comprises administering to the individual an
CC immunologically sufficient amount of the recombinant RSV combined with a
CC physiologically acceptable carrier; and (2) an isolated infectious
CC chimeric RSV comprising a major nucleocapsid protein, a RNA polymerase elongation
CC phosphoprotein, a large polymerase protein, a RNA polymerase elongation
CC factor, and a partial or complete bovine RSV background genome or
CC antigenome combined with heterologous gene(s) and/or genome segment(s) of
CC a human RSV selected from heterologous gene(s) and/or genome segment(s)
CC of RSV NS1, NS2, M, SH, G, and/or F, to form a human-bovine chimeric RSV
CC genome or antigenome. The recombinant RSV is useful in an attenuated
CC vaccine to elicit an immune response against either human RSV A or RSV B
CC or both human RSV A and RSV B. The present sequence represents
CC recombinant BRSV genome construct rBRSV/A2-G1F2 leader sequence as
CC described in the method of the invention
XX
XX Sequence 55 BP; 14 A; 16 C; 11 G; 14 T; 0 U; 0 Other;
SQ
XX
XX Query Match 72.0%; Score 14.4; DB 6; Length 55;
XX Best Local Similarity 93.8%; Pred. No. 1.5e+04;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 GCGGCGAGCCCTCTC 18
DB 22 GCGGCGAGCCCTCTC 37

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DE Identifier oligonucleotide E58.
XX
XX Bifunctional complex; ss.
XX
XX Synthetic.
XX
XX WO2004039825-A2.
XX
XX 13-MAY-2004.
XX
XX 30-OCT-2003; 2003WO-DK000739.
XX
XX 30-OCT-2002; 2002DK-00001652.
XX
XX 30-OCT-2002; 2002US-0422167P.
XX
XX 19-DEC-2002; 2002DK-00001955.
XX
XX 19-DEC-2002; 2002US-0434425P.
XX
XX 11-JUL-2003; 2003DK-00001064.
XX
XX 11-JUL-2003; 2003US-0486199P.
XX
XX (NUEV-) NUEVOLUTION AS.
XX
XX
XX Freshgard P, Franch T, Gouliayev AH, Lundorf MD, Felding J;
XX Olsen EK, Holtmann A, Jakobsen SN, Sams C, Glad SS, Jensen KB;
XX Pedersen H;
XX WPI; 2004-376154/35.
XX
XX Obtaining bifunctional complex with display molecule and coding part,
PT where bifunctional complex with priming site for adding tag is reacted at
PT reaction site with reactants and provided with tag identifying reactant
PT at priming site.
XX
XX Example 13; Page 175; 220pp; English.
XX
XX The present invention relates to a method (M1) for obtaining a
CC bifunctional complex. (M1) comprises a display molecule part and a coding
CC part, where a nascent bifunctional complex comprising a chemical reaction
CC site and a priming site for enzymatic addition of a tag is reacted at the
CC chemical reaction site with reactant(s), and provided with respective
CC tag(s) identifying the reactant(s) at the priming site using one or more
CC enzymes. The present sequence was used to illustrate the invention.
XX
XX Sequence 71 BP; 14 A; 32 C; 14 G; 11 T; 0 U; 0 Other;
SQ
XX
XX Query Match 72.0%; Score 14.4; DB 12; Length 71;
XX Best Local Similarity 93.8%; Pred. No. 1.5e+04;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GAGCGGAGCCCTCTC 16
DB 17 GAGCGGAGCCCTCTC 32

```

```

RESULT 12
AD004209
ID AD004209 standard; DNA; 71 BP.
XX
XX AD004209;
AC
XX
XX 29-JUL-2004 (first entry)
DT
XX

```

```

RESULT 13
AD004205
ID AD004205 standard; DNA; 71 BP.
XX
XX AD004205;
AC
XX
XX 29-JUL-2004 (first entry)
DT
XX
XX Identifier oligonucleotide E57.
DE
XX
XX Bifunctional complex; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 47..51
XX /*tag= a
XX /mod_base= i
XX
XX WO2004039825-A2.
PN

```



```
XX 13-MAY-2004.
PD
XX
XX 30-OCT-2003; 2003WO-DK000739.
PF
XX
XX 30-OCT-2002; 2002DK-00001652.
PR
XX 30-OCT-2002; 2002US-0422167P.
PR 19-DEC-2002; 2002DK-00001955.
PR 19-DEC-2002; 2002US-0434425P.
PR 11-JUL-2003; 2003DK-00001064.
PR 11-JUL-2003; 2003US-0486199P.
XX
XX (NUEV-) NREVOLUTION AS.
PA
XX
XX Freekard P, Franch T, Goulinev AH, Lundorf MD, Felding J;
PI Olsen EK, Holtmann A, Jakobsen SN, Sams C, Glad SS, Jensen KB;
PI Pedersen H;
XX
XX WPI; 2004-376154/35.
DR
XX
XX WPI; 2004-376154/35.
PT
XX
XX Obtaining bifunctional complex with display molecule and coding part,
PT where bifunctional complex with priming site for adding tag is reacted at
PT reaction site with reactants and provided with tag identifying reactant
PT at priming site.
XX
XX
XX Example 13; Page 174; 220pp; English.
PS
XX
XX The present invention relates to a method (M1) for obtaining a
CC bifunctional complex. (M1) comprises a display molecule part and a coding
CC part, where a nascent bifunctional complex comprising a chemical reaction
CC site and a priming site for enzymatic addition of a tag is reacted at the
CC chemical reaction site with reactant(s), and provided with respective
CC tag(s) identifying the reactant(s) at the priming site using one or more
CC enzymes. The present sequence was used to illustrate the invention.
XX
XX
XX Sequence 71 BP; 14 A; 27 C; 14 G; 11 T; 0 U; 5 Other;
SQ
XX
XX
XX Query Match 72.0%; Score 14.4; DB 12; Length 71;
XX Best Local Similarity 93.8%; Pred. No. 1.5e+04;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 GAGCGGAGCCCCCTTC 16
DB |||||
17 GAGCGGAGCCCCCCC 32
```

```
XX WPI; 1995-240472/31.
DR
XX
XX New astrocyte-derived neurotrophic factor proteins - related nucleic
PT acid, vectors and transformed cells, useful for stimulating neuronal cell
PT survival and growth.
XX
XX
XX Example 2; Page 43; 107pp; English.
PS
XX
XX cDNA was synthesized from astrocyte total RNA using reverse transcriptase
CC primed by a Not-dt oligo (given in AAQ97260). Products were used for non-
CC sequence specific cDNA amplification, using Not-dt (AAQ97260) and Not-dc,
CC asymmetric PCR and subtractive hybridization to isolate novel astrocyte
CC type 1 cDNA clones (AAQ97243-46)
XX
XX
XX Sequence 30 BP; 1 A; 21 C; 7 G; 1 T; 0 U; 0 Other;
SQ
XX
XX
XX Query Match 71.0%; Score 14.2; DB 2; Length 30;
XX Best Local Similarity 84.2%; Pred. No. 1.9e+04;
XX Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 GAGCGGAGCCCCCTTCC 19
DB |||||
8 GAGCGGAGCCCCCCCC 26
```

RESULT 15

```
AAH79869/c
ID AAH79869 standard; DNA; 51 BP.
XX
XX
XX AAH79869;
AC
XX
XX 19-SEP-2001 (first entry)
DT
XX
XX Human DNA containing single nucleotide polymorphism SEQ ID NO. 484.
DE
XX
XX Human; single nucleotide polymorphism; SNP; angiotensin;
KW 4-hydroxybutyrate; dehydrogenase; protein therapy;
KW adenosine triphosphate-dependent RNA helicase;
KW major histocompatibility complex Class I histocompatibility antigen; MHC;
KW phosphoglycerate kinase; immunosuppressive; immunostimulatory;
KW antineumatic; antisclerotic; antidiabetic; antiinflammatory; cytostatic;
KW antileukemic; neuroprotective; antimicrobial; gene therapy; vaccine; de.
XX
XX
XX Homo sapiens.
OS
XX
XX WO200148245-A2.
PN
XX
XX 05-JUL-2001.
PD
XX
XX 27-DEC-2000; 2000WO-US035346.
PF
XX
XX 27-DEC-1999; 99US-00472688.
PR
XX
XX (CURA-) CURAGEN CORP.
PA
XX
XX Shinkets RA, Leach M;
PI
XX
XX WPI; 2001-418297/44.
DR
XX
XX Polymorphic nucleic acids encoding e.g. angiotensin, dehydrogenase,
PT adenosine triphosphate-dependent RNA helicase and/or phosphoglycerate
PT kinase, useful for diagnosing and treating, e.g. cancer, autoimmune
PT diseases and infections.
XX
XX
XX Claim 1; Page 195; 484pp; English.
PS
XX
XX The invention relates to nucleic acids (AAH79386-AAH80036) encoding
CC polymorphic variants of proteins (AAH98010-AAH98238) related to
CC angiotensin, 4-hydroxybutyrate, dehydrogenase, adenosine triphosphate
CC (ATP)-dependent RNA helicase, major histocompatibility complex (MHC)
CC Class I histocompatibility antigen and/or phosphoglycerate kinase. These
CC nucleic acid single nucleotide polymorphisms (SNPs) and the encoded
```

CC proteins have potential immunosuppressive, immunostimulatory,
 CC antirheumatic, antisclerotic, antidiabetic, antiinflammatory, cytostatic,
 CC antileukemic, neuroprotective and antimicrobial activity and may be
 CC useful in gene/protein therapy, vaccines, modulation of the expression
 CC and activity of proteins related to angiotensin, 4-hydroxybutyrate,
 CC dehydrogenase, adenosine triphosphate (ATP)-dependent RNA helicase, major
 CC histocompatibility complex (MHC) Class I histocompatibility antigen
 CC and/or phosphoglycerate kinase. Disorders that may be prevented,
 CC diagnosed and/or treated by the above methods include multifactorial
 CC diseases with a genetic component, such as autoimmune diseases (e.g.
 CC rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus
 CC erythematosus and Grave's disease), inflammation, cancer (e.g. cancers
 CC of the bladder, brain, breast, colon and kidney, leukemia), diseases of
 CC the nervous system, an infection of pathogenic organisms. They may also
 CC be used to alter phenotypic traits such as longevity, appearance,
 CC strength, speed and endurance

XX Sequence 51 BP; 3 A; 15 C; 20 G; 13 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 4; Length 51;

Best Local Similarity 84.2%; Pred. No. 1.9e+04;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAGCGGAGAGCCCCCTCTCC 19

Db 19 GAGCAGCAGCACCCTCTCC 1

Search completed: December 24, 2005, 12:28:50
 Job time : 174.4 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 10:37:31 : Search time 1572 Seconds
(without alignments)
595.256 Million cell updates/sec

Title: US-09-296-264-1

Perfect score: 20
Sequence: 1 gagcgccagcccccctccca 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 2339354128 residues

Total number of hits satisfying chosen parameters: 768474

Minimum DB seq length: 20
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15.2	76.0	98	2	BE425297 WHE0311_D
2	14.8	74.0	65	1	AI270452 qu88C06.x
3	14.8	74.0	76	9	BZ286339 KG09603.D
4	14.8	74.0	91	5	BU861576 S003H06.P
5	14.4	72.0	82	6	CD672055 FG09F02.Y
6	14.2	71.0	50	1	AU107434 AU107434
7	14.2	71.0	58	1	AI123506 qa01909.x
8	14.2	71.0	59	9	BH855612 SALK_0848
9	14.2	71.0	62	8	CH001505 iv41d08.g
10	14.2	71.0	85	5	BO808288 1030003A0
11	14.2	71.0	87	11	TA2H03P
12	14.2	71.0	93	8	DR731394 MG6.4.1.
13	14.2	71.0	95	4	AK217328 Mus muscu
14	14.2	71.0	97	5	BU862683 S018G02.P
15	13.8	69.0	60	10	CG716533 1119045G0
16	13.8	69.0	60	10	CG716535 1119045G0
17	13.8	69.0	74	2	BG315169 POL.0.136
18	13.8	69.0	82	8	DN428053 L184216-1
19	13.8	69.0	84	3	BM090905 1g17d06.x
20	13.8	69.0	86	1	AW593901 hg28h03.x
21	13.8	69.0	95	1	AI051259 oy49f02.x
22	13.8	69.0	96	1	AA835222 ak65b02.s

C 23	13.8	69.0	97	9	AZ356019	AM0095M22
C 24	13.8	69.0	100	1	AM605663	QV2-DT007
C 25	13.6	68.0	57	9	AZ962155	2M0230024
C 26	13.6	68.0	61	6	CB213009	OML03289
C 27	13.6	68.0	66	11	TA391A11P	AL498916 T. brucei
C 28	13.6	68.0	67	3	B1908580	603069979
C 29	13.6	68.0	77	6	CD285974	10 A19..ab
C 30	13.6	68.0	81	7	CR446349	CR446349
C 31	13.6	68.0	82	1	AA870618	vg24a01.r
C 32	13.6	68.0	83	7	CR291222	CR291222
C 33	13.6	68.0	89	1	AA579142	AA579142
C 34	13.6	68.0	89	9	CC941103	nF35906.8
C 35	13.4	67.0	53	10	BX979943	0150649-0
C 36	13.4	67.0	75	9	AZ339132	BX979943 Forward s
C 37	13.4	67.0	93	11	TA358C80	AZ339132 IM0070B03
C 38	13.4	67.0	96	1	AU713458	AL495379 T. brucei
C 39	13.2	66.0	43	9	BH855596	AU713458 AU713458
C 40	13.2	66.0	50	1	AU103490	BH855596 SALK_0849
C 41	13.2	66.0	53	11	CR185627	AU103490 AU103490
C 42	13.2	66.0	58	10	CG712685	CR185627 Forward s
C 43	13.2	66.0	61	7	CN482613	CG712685 119028D1
C 44	13.2	66.0	61	9	AZ791343	CN482613 hw22e05.Y
C 45	13.2	66.0	76	8	DN444762	AZ791343 2M0041A16
						DN444762 LIBS338-0

ALIGNMENTS

RESULT 1
LOCUS BE425297/c 98 bp RNA linear EST 24-JUN-2000
DEFINITION WHE0311_D02_D0225 wheat unstressed seedling shoot cDNA library
Triticum aestivum cDNA clone WHE0311_D02_D02, mRNA sequence.

ACCESSION BE425297
VERSION BE425297.1 GI:9423056
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum

REFERENCE Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han, P.S., Hsia, C.C., Kang, Y., Izzo, G.R., Miller, R., Rausch, C.J., Seaton, C.L., and Tong, D.C.
1 (bases 1 to 98)
Poaideae; Triticeae; Triticum.

AUTHORS The structure and function of the expressed portion of the wheat genomes

JOURNAL Unpublished (2000)
COMMENT Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818

FEATURES
source Email: oanderson@w.usda.gov
Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20
Seq primer: Stratiagene SK primer.
Location/Qualifiers
1..98
/organism="Triticum aestivum"
/mol_type="RNA"
/db_xref="taxon:4565"
/db_xref="taxon:4565"
/clone="WHE0311_D02_D02"
/issue_type="Etiolated shoot"
/dev stage="Five day old seedling"
/lab_host="E. coli SOLR"
/clone_id="Wheat unstressed seedling shoot cDNA library"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site 1: EcoRI; Site 2: XhoI; Seeds were surface-sterilized, germinated and grown aseptically in the dark at room temperature on filter paper with water.

mystatin and cefotaxime in covered crystallization dishes. Shoots were harvested. The tissue, total RNA, and poly(A) RNA were prepared. A cDNA library was made, and the cDNA clones were in vivo excised to give phagescript phagemids in the IV Close Lab (Choi, Close, Fenton) at the University of California, Riverside, Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

ORIGIN

Query Match 76.0%; Score 15.2; DB 2; Length 98;
Best Local Similarity 85.0%; Pred. No. 5.4e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAGCGGAGCCCTCTCCA 20
DB 94 GAGCGGAGCCCTCTCCA 75

RESULT 2
LOCUS AI270452 65 bp mRNA linear EST 17-NOV-1998
DEFINITION qu88c06.x1 NCI_CGAP_Gas4 Homo sapiens cDNA IMAGE:1979146 3',
mRNA sequence.
ACCESSION AI270452
VERSION AI270452.1 GI:3889619
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 65)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncigap>
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/dbdp/image/image.html
Seq primer: -40UP from Gibco.
Location/Qualifiers

FEATURES

source

1. 65
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1979146"
/issue_type="poorly differentiated adenocarcinoma with
signed ring cell features"
/lab_host="DH10B"
/clone_1ib="NCI_CGAP Gas4"
/note="Organ: Stomach; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo #1.
Average insert size 1.69 kb. Life Technologies catalog #:
11549-011"

ORIGIN

Query Match 74.0%; Score 14.8; DB 1; Length 65;
Best Local Similarity 88.9%; Pred. No. 8.1e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AGCGGAGCCCTCTCC 19
DB 1 AGCGGAGCCCTCTCC 18

RESULT 3
LOCUS BZ286339/c 76 bp DNA linear GSS 15-OCT-2002
DEFINITION KG09603 Drosophila melanogaster P(SUPor-P) P element insertion
lines Drosophila melanogaster genomic Sequence recovered from Both
5' and 3' ends of P element, genomic survey sequence.
ACCESSION BZ286339
VERSION BZ286339.1 GI:24018111
KEYWORDS GSS.

SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 76)
Levits, R., Hoskins, R., Liao, G., Mozen, N., Tsang, G., He, Y.,
Karpén, G., Belien, H., Rubin, G., and Spreading, A.,
The Berkeley Drosophila Genome Project Gene Disruption Project
Unpublished (2001)
CONTACT: Gerald Rubin
Berkeley Drosophila Genome Project
University of California, Berkeley
LSA Building, Berkeley, CA 94720-3200, USA
Fax: 5106433947
Email: germy@fruitfly.berkeley.edu
Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5' end of P
element

The P element insertion position is base 52 in the 76 bases. This
insertion position refers to the first base of the 8 base target
recognition sequence.
Class: transposon-tagged.
Location/Qualifiers

FEATURES

source

1. 76
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone_1ib="Drosophila melanogaster P(SUPor-P) P element
insertion lines"
/note="Inverse PCR was performed on Drosophila
melanogaster strains each of which contains one or more
P(SUPor-P) P-element transposon insertion. The resultant
fragment for each strain was directly sequenced to
determine the genomic sequence at the site of insertion.
Details of the protocols used can be found at
<http://www.fruitfly.org/about/methods/inverse.pcr.html>."

ORIGIN

Query Match 74.0%; Score 14.8; DB 9; Length 76;
Best Local Similarity 88.9%; Pred. No. 8.1e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GCGGAGCCCTCTCCA 20
DB 54 GCGGAGCCCTCTCCA 37

RESULT 4
LOCUS BU861576 91 bp mRNA linear EST 16-OCT-2002
DEFINITION S003H06 Populus imbed seed cDNA library Populus tremula cDNA 5
prime, mRNA sequence.
ACCESSION BU861576
VERSION BU861576.1 GI:24047636
KEYWORDS EST.

SOURCE Populus tremula
ORGANISM Populus tremula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.

REFERENCE 1 (bases 1 to 91)
Umeberg, P., Bhalerao, R.R., Jansson, S., and Sterky, F.
The poplar tree transcriptome: Analysis of expressed sequence tags

JOURNAL
COMMENT

from multiple libraries
Unpublished (2002)
Contact: BHALERAO RUPALI R.
Umea Plant Science Center
Department of Plant Physiology
University of Umea, 901 87 Umea, Sweden
Tel: +46 90 786 5279
Fax: +46 90 786 6676
Email: rupali.bhalerao@plantphys.umu.se.

FEATURES

source

1. .91
/organism="Populus tremula"
/mol_type="mRNA"
/db_xref="taxon:113636"
/tissue_type="imbibed seed"
/clone_lib="Populus imbibed seed cDNA library"

ORIGIN

Query Match 74.0%; Score 14.8; DB 5; Length 91;
Best Local Similarity 88.9%; Pred. No. 8e+04; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2;

Qy 2 AGCGGACGCCCCCTCTCC 19
|||||
2 AGCGGACGCTCTCTCC 19

RESULT 5

CD672055/c 82 bp mRNA linear EST 24-JUN-2003
LOCUS f609f02.y1 Human Iris cDNA (Normalized): fg Homo sapiens cDNA clone
DEFINITION CD672055.1 GI:32173786
ACCESSION CD672055.1 GI:32173786
VERSION EST.
KEYWORDS

SOURCE
ORGANISM

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
AUTHORS
1 (bases 1 to 82)
Wistow, G., Bernstein, S.L., Ray, S., Wyatt, M.K., Behal, A.,
Touchman, J.W., Bouffard, G., Smith, D. and Peterson, K.
Expressed sequence tag analysis of adult human iris for the NEIBank
Project: steroid-response factors and similarities with retinal
pigment epithelium

JOURNAL
PUBMED
Mol. Vis. 8 (4), 185-195 (2002)
12107412

COMMENT

Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: gisraeme@helix.nih.gov
Plate: 09 row: f column: 02
Seq primer: M13RPI reverse primer (ABI).
Location/Qualifiers

FEATURES

source

1. .82
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="f609f02"
/tissue_type="Iris"
/dev_stage="Adult"
/lab_host="EMD110B"

/note="Organ: Eye; Vector: pCMTSPORT6; A human iris
library (bx) was normalized by self-subtraction. One
portion of double stranded plasmid DNA representing the
library was linearized by NotI. This NotI digested library
was used as a template for biotinylated RNA synthesis
using SP6 RNA polymerase. Another portion of the double

ORIGIN

Query Match 72.0%; Score 14.4; DB 6; Length 82;
Best Local Similarity 93.8%; Pred. No. 1.2e+05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CGCGAGCCCTCTCTCC 19
|||||
16 CGCGAGCCCTCTCTCC 1

RESULT 6

AU107434 50 bp mRNA linear EST 28-JAN-2004
LOCUS AU107434 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION LNC15774, mRNA sequence.
ACCESSION AU107434
VERSION AU107434.1 GI:13556955
KEYWORDS EST.

SOURCE
ORGANISM

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
AUTHORS
1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isegai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
11375929

COMMENT

Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1 Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
Location/Qualifiers

FEATURES

source

1. .50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="LNC15774"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 71.0%; Score 14.2; DB 1; Length 50;
Best Local Similarity 84.2%; Pred. No. 1.5e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAGGCGAGCCCTCTCTCC 19
|||||
13 GAGGCGAGGCGCTCTCTCC 31

RESULT 7

A1123506 58 bp mRNA linear EST 01-OCT-1998
LOCUS A1123506
DEFINITION g601009.x1 Soares parathyroid tumor N0HPA Homo sapiens cDNA clone
IMAGE:163616 3' similar to SW.DIA.DROME P48608 DIAPHANOUS PROTEIN.
; contains element MSRI repetitive element ;, mRNA sequence.

stranded plasmid library was converted to single-stranded
circles in vitro using Gene II and Exonuclease III (Life
Technologies). Single-stranded DNA (1 mg) was hybridized
(Cot 500) with 41 mg of Bio-RNA and vector blocking
oligonucleotides. The hybridized Bio-RNA/ss-circles were
removed by streptavidin:phenol extraction. EST analysis
was performed on the library at the NIH Intramural
Sequencing Center (NISC)."

ACCESSION A1123506
 VERSION A1123506.1 GI:3539272
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 58)
 REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 TITLE Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bcr-rt@mail.nih.gov
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
 FEATURES
 source
 Trace considered overall poor quality
 Insert Length: 953 Std Error: 0.00
 Seq primer: -40m13 fwd. ET from Amersham
 High quality sequence stop: 1.
 Location/Qualifiers
 1..58
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1683616"
 /tissue_type="parathyroid tumor"
 /dev_stage="adult"
 /lab_host="PH10B (ampicillin resistant)"
 /clone_lib="Soares parathyroid tumor NDHPA"
 /note="Organ: parathyroid gland; Vector: pT7T3D
 (Pharmacia) with a modified polylinker; Site 1: Not I;
 Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
 oligo(dT) primer
 5'-TGTTCACATCTGAAGTGGAGCGGCCGACCAATTTTTTTTTTTTTTTT
 TTTT-3'1, double-stranded cDNA was size selected, ligated
 to Eco RI adapters (Pharmacia), digested with Not I and
 cloned into the Not I and Eco RI sites of a modified pT7T3
 vector (Pharmacia). Library went through one round of
 normalization to a Cot = 5. Library constructed by Bento
 Soares and M. Fatima Bonaldo. RNA from sporadic parathyroid
 adenomas was kindly provided by Dr. Stephen Marx, National
 Institute of Diabetes and Digestive and Kidney Diseases,
 NIH."

ORIGIN
 Query Match 71.0%; Score 14.2; DB 1; Length 58;
 Best Local Similarity 84.2%; Pred. No. 1.5e+05;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 AGCGGAGCCCTCTCCA 20
 |||
 Db 10 AGCGGAGCCCTCTCCA 28

RESULT 8
 LOCUS BH855612/c 59 bp DNA linear GSS 08-JUL-2002
 DEFINITION SALK_084890.49.05.x Arabidopsis thaliana TDNA insertion lines
 Arabidopsis thaliana genomic clone SALK_084890.49.05.x, genomic
 survey sequence.
 ACCESSION BH855612
 VERSION BH855612
 KEYWORDS GSS.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 1 (bases 1 to 59)
 AUTHORS Alonso,J.M., Leisbe,T.J., Barajas,P., Chen,H., Cheuk,R.,
 Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
 Shinn,P., Zimmerman,J. and Ecker,J.R.
 TITLE A Sequence-Indexed Library of Insertion Mutations in the
 Arabidopsis Genome
 JOURNAL Unpublished (2001)
 COMMENT Contact: Joseph R. Ecker
 The Salk Institute Genomic Analysis Laboratory (SIGAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: eckere@salk.edu
 This is single pass sequence recovered from the left border of
 TDNA. This sequence lies within an annotated exon of At4g31410.
 Class: TDNA tagged.
 FEATURES
 source
 Location/Qualifiers
 1..59
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /ecotype="Col-0"
 /db_xref="taxon:3702"
 /clone="SALK_084890.49.05.x"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
 Query Match 71.0%; Score 14.2; DB 9; Length 59;
 Best Local Similarity 84.2%; Pred. No. 1.5e+05;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GAGCGGAGCCCTCTCTCC 19
 |||
 Db 45 GAGCGGAGCTCTCTCTCC 27

RESULT 9
 LOCUS CX001505 62 bp mRNA linear EST 03-DEC-2004
 DEFINITION iiv4id08.g1 Left Cardiac Ventricle (DOGEST7) Canis familiaris cDNA,
 mRNA sequence.
 ACCESSION CX001505
 VERSION CX001505.1 GI:56272921
 KEYWORDS EST.
 SOURCE Canis familiaris (dog)
 ORGANISM Canis familiaris
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
 Canis.
 1 (bases 1 to 62)
 REFERENCE Balija,V.S., Nascento,L.U. and McCombie,W.R.
 AUTHORS Balija,V.S., Nascento,L.U. and McCombie,W.R.
 TITLE ESTs from Canis familiaris left cardiac ventricle (dog)
 JOURNAL Unpublished (2004)
 COMMENT Contact: W. Richard McCombie
 Lita Annenberg Hazen Genome Sequencing Center
 Cold Spring Harbor Laboratory
 PO Box 100, Cold Spring Harbor, NY 11724, USA
 Tel: 516 367 8884
 Fax: 516 367 8874
 Email: mcombie@cshl.org.
 FEATURES
 source
 Location/Qualifiers
 1..62
 /organism="Canis familiaris"
 /mol_type="mRNA"

/db_xref="taxon:9615"
 /sex="Unknown"
 /tissue_type="Cardiac muscle"
 /dev_stage="3 month old normal canine"
 /lab_host="X110 Gold"
 /clone_lib="Left Cardiac Ventricle (DOGERT7)"
 /note="Organ: Heart; Vector: pBluescript II SK; Site 1: EcoRI; Site 2: XhoI; Library constructed using pBluescript XR kit from Stratagene. Cloned cDNA was size selected between 1-3 kb. Tissue supplied by Mark Haskins VMD, PhD, Pathology and Medical Genetics, School of Veterinary Medicine, University of Pennsylvania, 3800 Spruce Street, Philadelphia, PA 19104-6051"

ORIGIN

Query Match 71.0%; Score 14.2; DB 8; Length 62;
 Best Local Similarity 84.2%; Pred. No. 1.4e+05;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAGCGGAGCCCCCTCTCC 19
 Db 36 GGGCCGAGCCCCCTCTTC 54

RESULT 10

LOCUS BQ808288 85 bp mRNA linear EST 01-AUG-2002
 DEFINITION 1030003A09.x2 C. reinhardtii CC-1690, Deflagellation (normalized),
 Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.

ACCESSION BQ808288
 VERSION BQ808288.1 GI:22048620
 KEYWORDS EST.
 SOURCE Chlamydomonas reinhardtii
 ORGANISM Chlamydomonas reinhardtii
 Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae;
 Chlamydomonadales; Chlamydomonadales; Chlamydomonas.

REFERENCE 1 (bases 1 to 85)
 Grossman, A., Chang, C.-W., Davies, J., Harris, E., Hauser, C.,
 Lefebvre, J., McDermott, J.P., Shreger, J., Siflow, C., and Stern, D.
 Analyses of the Chlamydomonas reinhardtii Genome: A Model,
 Unicellular System for Analyzing Gene Function and Regulation in
 Vascular Plants. Project: 1030

JOURNAL

COMMENT unpublished (2002)
 Contact: Charles Hauser
 DCMB Box 91000
 Duke University
 Durham, NC 27708-1000
 Tel: 919 613 8159
 Fax: 919 613 8177
 Email: chausser@duke.edu

FEATURES

Source

1. 85
 /organism="Chlamydomonas reinhardtii"
 /mol_type="mRNA"
 /strain="CC-1690 wild type mt+ 21gr"
 /db_xref="taxon:3055"
 /clone_lib="C. reinhardtii CC-1690, Deflagellation
 (normalized), Lambda Zap II"
 /note="Vector: pBluescript II SK-; Site 1: EcoRI; Site 2:
 XhoI; Deflagellation library, constructed by John Davies
 and Jeffrey McDermott, combines cDNAs from CC-1690 cells
 which had been re-synthesizing flagella for 15, 30 and 60
 min after being deflagellated by pH shock. PolyA mRNA was
 purified from each sample, pooled and cDNA synthesized.
 The cDNA was directionally cloned into lambda Zap II
 (Stratagene) in the EcoRI (5') and XhoI (3') sites.
 pBluescript II SK- plasmids were excised from the lambda
 Zap clones by superinfection with Exsist (Stratagene)
 phage. The library was normalized using method 4 described
 in Bonaldo et al., (1996) Genome Research 6: 791-806."

ORIGIN

Query Match 71.0%; Score 14.2; DB 5; Length 85;

Best Local Similarity 84.2%; Pred. No. 1.4e+05;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAGCGGAGCCCCCTCTCC 19
 Db 35 GAGCGGAGAGCCCCCCCC 53

RESULT 11

LOCUS TA2H03P/C 87 bp DNA linear GSS 16-SEP-2000
 DEFINITION T. brucei sheared genomic DNA clone 2h03, forward sequence, genomic
 survey sequence.

ACCESSION AL441676.1 GI:10185383
 VERSION AL441676
 KEYWORDS GSS.
 SOURCE Trypanosoma brucei
 ORGANISM Trypanosoma brucei
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE

1 (bases 1 to 87)
 Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
 Melville, S.E., Rajandream, M.A. and Barrell, B.G.
 Direct Submission

JOURNAL

Submitted (15-SEP-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA. E-mail: barrell@sanger.ac.uk and
 nh@sanger.ac.uk

COMMENT

Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU97/4 GUTat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb). The v+1 method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 insert Sequencing: A Practical Approach, eds. M. Vaudin and B.
 Barrell, Oxford University Press, 1999).

Email: nh@sanger.ac.uk
 Details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source

1. 87
 /organism="Trypanosoma brucei"
 /mol_type="genomic DNA"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="2h03"

ORIGIN

Query Match 71.0%; Score 14.2; DB 11; Length 87;
 Best Local Similarity 84.2%; Pred. No. 1.4e+05;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AGCGGAGAGCCCCCTCTCCA 20
 Db 53 ATCGGCACTCTCTCTCCA 35

RESULT 12

LOCUS DR731394 93 bp mRNA linear EST 18-JUL-2005
 DEFINITION MGC8.4.1.1.1.E06.R.1 NIH_MGC_331 Homo sapiens cDNA clone

ACCESSION DR731394
 VERSION DR731394.1 GI:70957773
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.

REFERENCE 1 (bases 1 to 93)

AUTHORS	Stevens, M., Wei, C., Gross, S.S., McPherson, J. and Brent, M.R.
TITLE	Exhaustive RT-PCR and sequencing of all novel TWINSKAN predictions in human
JOURNAL	Unpublished (2005)
COMMENT	Contact: Brent, MR

OY 2 AGCGGAGCCCCCTCTCCA 20
 |||||
 Db 35 AGCGGAGCCTTCTCTTA 53

RESULT 15
 CG716533/c
 LOCUS 1119045G02.x1 1119 - RescuerMu Grid AA Zea mays genomic, genomic
 DEFINITION survey sequence.

ACCESSION CG716533
 VERSION CG716533.1 GI:37744943
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays

REFERENCE 60 bp DNA linear GSS 20-OCT-2003
 AUTHORS Walbot V.
 TITLE Maize genomic sequences found using engineered RescuerMu transposon
 JOURNAL Unpublished (2001)
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu

Possible ligation site so sequence was trimmed. Post-ligation
 sequence submitted separately.
 Plate: 1119045 row: G column: 02
 Class: transposon-tagged.

FEATURES
 source Location/Qualifiers

1..60
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /cultivar="mixed background W23/A188/B73/K55"
 /db_xref="taxon:4577"
 /issue_type="leaf"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="1119 - RescuerMu Grid AA"
 /note="Organ: leaf; Vector: RescuerMu (engineered from
 pBluescript backbone); Site_1: BamHI; Site_2: BglII;
 RescuerMu is a 4.9 kb, modified maize Mu transposon
 designed to allow plasmid rescue from total genomic DNA.
 Mu elements insert preferentially into transcription
 units. For more information on RescuerMu, go to the web
 site 'www.zmdb.iastate.edu' and follow the links for
 'RescuerMu.' Grid AA was grown at UC San Diego in 2002. DNA
 was extracted from leaf strips, double digested using
 BamHI and BglII, and ligated to form circular plasmids.
 DH10B cells were transformed and then screened on LB
 plates with ampicillin."

ORIGIN

Query Match 69.0%; Score 13.8; DB 10; Length 60;
 Best Local Similarity 88.2%; Pred. No. 2.1e+05;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 4 CGGCAAGCCCCCTCTCCA 20
 |||||
 Db 19 CGCGAGCCCCCTCTCCA 3

Search completed: December 24, 2005, 18:28:12
 Job time : 1577 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 11:34:25 ; Search time 48.1 Seconds

(without alignments)
739.111 Million cell updates/sec

Title: US-09-296-264-1

Perfect score: 20

Sequence: 1 gagcgagagcccccctccca 20

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1134872

Minimum DB seq length: 20

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/1.COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5.COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/H.COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/PCITUS.COMB.seq:*
- 7: /cgn2_6/ptodata/1/ina/PP.COMB.seq:*
- 8: /cgn2_6/ptodata/1/ina/RE.COMB.seq:*
- 9: /cgn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	14.8	74.0	60	9	5252465-13
2	14.4	72.0	55	3	US-09-887-469-13
3	13.6	68.0	50	3	US-10-131-827-169
4	13.6	68.0	55	3	US-09-357-740-16
5	13.6	68.0	92	3	US-09-513-999C-11657
6	13.2	65.0	30	6	PCT-US95-07372-3
7	13	65.0	93	3	US-09-513-999C-23015
8	12.8	64.0	20	3	US-09-120-853-19
9	12.8	64.0	42	3	US-09-120-853-3
10	12.8	64.0	47	3	US-09-422-978-3328
11	12.8	64.0	48	3	US-09-400-653A-49
12	12.8	64.0	54	2	US-08-311-486C-1107
13	12.8	64.0	55	3	US-09-357-740-18
14	12.8	64.0	79	3	US-09-407-605-56
15	12.8	64.0	83	3	US-09-621-976-17097
16	12.8	64.0	91	2	US-07-752-101A-53
17	12.8	64.0	91	2	US-09-513-999C-27692
18	12.8	64.0	93	3	US-08-976-413A-420
19	12.8	64.0	100	3	US-09-861-893-41
20	12.6	63.0	21	2	US-08-465-590-136
21	12.6	63.0	21	3	US-08-711-417C-136
22	12.6	63.0	21	3	US-09-177-650-42
23	12.6	63.0	21	3	US-09-723-909-136
24	12.6	63.0	21	6	PCT-US93-08743-136

25	12.6	63.0	25	3	US-08-772-512A-18	Sequence 18, Appl
26	12.6	63.0	25	3	US-09-396-196G-66325	Sequence 66325, A
27	12.6	63.0	25	3	US-09-396-196G-66326	Sequence 66326, A
28	12.6	63.0	25	3	US-09-396-196G-66337	Sequence 66337, A
29	12.6	63.0	25	3	US-09-396-196G-66337	Sequence 66337, A
30	12.6	63.0	25	9	5504194-3	Patent No. 5504194
31	12.6	63.0	26	3	US-09-271-013-1	Sequence 1, Appl
32	12.6	63.0	35	2	US-07-832-905B-48	Sequence 48, Appl
33	12.6	63.0	35	2	US-08-700-757-48	Sequence 48, Appl
34	12.6	63.0	36	3	US-10-012-070A-16	Sequence 16, Appl
35	12.6	63.0	39	3	US-09-046-158A-9	Sequence 9, Appl
36	12.6	63.0	41	3	US-09-214-151-5	Sequence 5, Appl
37	12.6	63.0	41	3	US-09-908-660-5	Sequence 4, Appl
38	12.6	63.0	42	2	US-07-982-712-4	Sequence 47, Appl
39	12.6	63.0	44	2	US-07-832-905B-47	Sequence 47, Appl
40	12.6	63.0	44	2	US-08-700-757-47	Sequence 47, Appl
41	12.6	63.0	69	2	US-07-609-716-29	Sequence 29, Appl
42	12.6	63.0	69	2	US-08-175-155-27	Sequence 27, Appl
43	12.6	63.0	69	2	US-08-477-509B-62	Sequence 62, Appl
44	12.6	63.0	69	3	US-08-482-085B-62	Sequence 62, Appl
45	12.6	63.0	69	3	US-08-475-411A-29	Sequence 29, Appl

ALIGNMENTS

```
RESULT 1
5252465-13/C
; Patent No. 5252465
; APPLICANT: NIGON, VICTOR-MARC;VERDIER, GERARD;CHEBLONNE,
; YAHIA;COSSET, FRANCOIS-LOIC;LEGRAS, CATHERINE;REYS-BRION,
; ASPIRID,BELAKBEI, MUSTAPHA;MALLET, FRANCOIS;SAVATIER, PIERRE;
; THORAVAU, PIERICK;SAMARUT, JACQUES;PONCET, DIDIER;BAGNAT,
; CLAUDE;BENCHAIBI, MILOUD
; TITLE OF INVENTION: AVIAN ERYTHROBLASTOSIS VIRUS VECTORS FOR
; INTEGRATION AND EXPRESSION OF HETEROLOGOUS GENES IN AVIAN CELLS
; NUMBER OF SEQUENCES: 14
; CURRENT APPLICATION NUMBER:
; APPLICATION NUMBER: US/07/477,833
; FILING DATE: 03-OCT-1988
; SEQ ID NO:13:
; LENGTH: 60
5252465-13

Query Match      74.0%; Score 14.8; DB 9; Length 60;
Best Local Similarity 88.9%; Pred. No. 2.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      2  AGCGGAGAGCCCTCTCC 19
Db      22 AGCGGAGAGCCCTCTAC 5

RESULT 2
US-09-887-469-13
; Sequence 13, Application US/09887469
; Patent No. 6923971
; GENERAL INFORMATION:
; APPLICANT: Krempf, Christine D.
; APPLICANT: Collins, Peter L.
; APPLICANT: Murphy, Brian R.
; APPLICANT: Buchholz, Ursula
; APPLICANT: Whitehead, Stephen S.
; TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS VACCINES EXPRESSING
; FILE REFERENCE: 15280-424-IUS
; CURRENT APPLICATION NUMBER: US/09/887,469
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/213,708
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
```

LENGTH: 55
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Artificial
OTHER INFORMATION: Respiratory Syncytial Virus
US-09-887-469-13

Query Match 72.0%; Score 14.4; DB 3; Length 55;
Best Local Similarity 93.8%; Pred. No. 3.7e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GCGGCGAGCCCCCTCTC 18
Db 22 GCGGCGAGCCCCCTCTC 37

RESULT 3
US-10-131-827-169
Sequence 169, Application US/10131827
Patent No. 6905827
GENERAL INFORMATION:
APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
FILE REFERENCE: 506612000120
CURRENT APPLICATION NUMBER: US/10/131,827
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 9090
SOFTWARE: PatentIn version 3.1
SEQ ID NO 169
LENGTH: 50
TYPE: DNA
ORGANISM: Homo sapiens
US-10-131-827-169

Query Match 68.0%; Score 13.6; DB 3; Length 50;
Best Local Similarity 80.0%; Pred. No. 8.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GAGCGGAGCCCCCTCTCCA 20
Db 6 GAGCGGAGCCCCCTCTCCA 25

RESULT 4
US-09-357-740-16/c
Sequence 16, Application US/09357740
Patent No. 6348596
GENERAL INFORMATION:
APPLICANT: Lee, Linda G.
APPLICANT: Graham, Ronald J.
APPLICANT: Mullah, Khairuzzaman B.
APPLICANT: Haxo, Francis T.
TITLE OF INVENTION: ASYMMETRIC CYANINE DYE QUENCHERS
FILE REFERENCE: 9584-007
CURRENT APPLICATION NUMBER: US/09/357,740
CURRENT FILING DATE: 1999-07-20
EARLIER APPLICATION NUMBER: 09/012,525
EARLIER FILING DATE: 1998-01-23
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 16
LENGTH: 55
TYPE: DNA
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Oligonucleotide
US-09-357-740-16

Query Match 68.0%; Score 13.6; DB 3; Length 55;
Best Local Similarity 80.0%; Pred. No. 8.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GAGCGGAGCCCCCTCTCCA 20
Db 52 GATGGGCGAGCCCCGAGTCCA 33

RESULT 5
US-09-513-999C-11657/c
Sequence 11657, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclerc, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59.US2.REG
Patent No. 6783961
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 11657
LENGTH: 92
TYPE: DNA
ORGANISM: Homo sapiens
US-09-513-999C-11657

Query Match 68.0%; Score 13.6; DB 3; Length 92;
Best Local Similarity 80.0%; Pred. No. 8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GAGCGGAGCCCCCTCTCCA 20
Db 34 GAGCGGAGCCCCGCGCTCGCCA 15

RESULT 6
PCT-US95-07372-3
Sequence 3, Application PC/TUS9507372
GENERAL INFORMATION:
APPLICANT: Oklahoma Medical Research Foundation
TITLE OF INVENTION: Calcium Binding Recombinant
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07372
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.

```

; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMRP106CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; PCT-US95-07372-3

Query Match      66.0%; Score 13.2; DB 6; Length 30;
Best Local Similarity 83.3%; Pred. No. 1.2e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 AGCGGAGCCCTCTCC 19
Db      2 AGCGGAGCCCTCTCC 19

RESULT 7
US-09-513-999C-23015
; Sequence 23015, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclet, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59. US2, REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 23015
; LENGTH: 93
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-23015

Query Match      65.0%; Score 13; DB 3; Length 93;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GCAGGCCCTCTC 18
Db      62 GCAGGCCCTCTC 74

RESULT 8
US-09-120-853-19/c
; Sequence 19, Application US/09120853
; Patent No. 6057437
; GENERAL INFORMATION:
; APPLICANT: Kamiya, Kinya
; APPLICANT: Matsuda, Yoko
; APPLICANT: Uchida, Kiyoshi
; TITLE OF INVENTION: AN ANTISENSE NUCLEIC ACID COMPOUND
; FILE REFERENCE: 07898/030001
; CURRENT APPLICATION NUMBER: US/09/120,853
; CURRENT FILING DATE: 1998-07-21
; EARLIER APPLICATION NUMBER: JP 213838/1997
; EARLIER FILING DATE: 1997-07-25
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent Ver. 2.0
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```

; SEQ ID NO 19
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Artificial
US-09-120-853-19

Query Match      64.0%; Score 12.8; DB 3; Length 20;
Best Local Similarity 87.5%; Pred. No. 1.7e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4 CGGAGCCCTCTCC 19
Db      20 CTGGGAGCCCTCTCC 5

RESULT 9
US-09-120-853-3/c
; Sequence 3, Application US/09120853
; Patent No. 6057437
; GENERAL INFORMATION:
; APPLICANT: Kamiya, Kinya
; APPLICANT: Matsuda, Yoko
; APPLICANT: Uchida, Kiyoshi
; TITLE OF INVENTION: AN ANTISENSE NUCLEIC ACID COMPOUND
; FILE REFERENCE: 07898/030001
; CURRENT APPLICATION NUMBER: US/09/120,853
; CURRENT FILING DATE: 1998-07-21
; EARLIER APPLICATION NUMBER: JP 213838/1997
; EARLIER FILING DATE: 1997-07-25
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 3
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Artificial
US-09-120-853-3

Query Match      64.0%; Score 12.8; DB 3; Length 42;
Best Local Similarity 87.5%; Pred. No. 1.7e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4 CGGAGCCCTCTCC 19
Db      42 CTGGGAGCCCTCTCC 27

RESULT 10
US-09-422-978-3328
; Sequence 3328, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marla
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSRT 020CD1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 3328
; LENGTH: 47
```

```

; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-3335-53 : polymorphic base C or T
US-09-422-978-3328
```

```

Query Match
Best Local Similarity 64.0%; Score 12.8; DB 3; Length 47;
Pred. No. 1.7e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```

QY 5 GGCAGCCCCCTCTCCA 20
    |||||
Db 30 GCCAGCCCCCTCTCCA 45
```

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RESULT 11
US-09-400-653A-49
; Sequence 49, Application US/09400653A
; Patent No. 6348311
; GENERAL INFORMATION:
; APPLICANT: Kaetan, Michael
; APPLICANT: Canman, Christine
; APPLICANT: Kim, Seong-Tae
; APPLICANT: Lim, Dae-Sik
; APPLICANT: St. Jude Children's Research Hospital
; TITLE OF INVENTION: ATM Kinase Modulation for Screening and Therapies
; FILE REFERENCE: 24271/F142
; CURRENT APPLICATION NUMBER: US/09/400,653A
; PRIOR FILING DATE: 1999-09-21
; PRIOR APPLICATION NUMBER: 09/248,061
; PRIOR FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 49
; LENGTH: 48
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
US-09-400-653A-49
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Query Match
Best Local Similarity 64.0%; Score 12.8; DB 3; Length 48;
Pred. No. 1.7e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 1 GAGCGGAGCCCCCTC 16
    |||||
Db 7 GAGCGGAGCCCCCTC 22
```

```

RESULT 12
US-08-311-486C-1107/c
; Sequence 1107, Application US/08311486C
; Patent No. 5811300
; GENERAL INFORMATION:
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth Draper
; APPLICANT: Kevin Kleich
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: TNF-
; NUMBER OF SEQUENCES: 1157
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
```

```

; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,486C
; FILING DATE: September 23, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1107:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 54 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-311-486C-1107
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```

Query Match
Best Local Similarity 64.0%; Score 12.8; DB 2; Length 54;
Pred. No. 1.7e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```

QY 5 GGCAGCCCCCTCTCCA 20
    |||||
Db 21 GGTAGCCCCCTCTCCA 6
```

```

RESULT 13
US-09-357-740-18/c
; Sequence 18, Application US/09357740
; Patent No. 6348596
; GENERAL INFORMATION:
; APPLICANT: Lee, Linda G.
; APPLICANT: Graham, Ronald J.
; APPLICANT: Mullah, Khairuzaman B.
; APPLICANT: Haxo, Francis T.
; TITLE OF INVENTION: ASYMMETRIC CYANINE DYE QUENCHERS
; FILE REFERENCE: 9584-007
; CURRENT APPLICATION NUMBER: US/09/357,740
; PRIOR FILING DATE: 1999-07-20
; EARLIER APPLICATION NUMBER: 09/012,525
; EARLIER FILING DATE: 1998-01-23
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 18
; LENGTH: 55
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide
US-09-357-740-18
```

```

Query Match
Best Local Similarity 64.0%; Score 12.8; DB 3; Length 55;
Pred. No. 1.7e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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OY 5 GGCAGCCCCCTCTCCA 20
|||||
Db 48 GGCAGCCCCCTCTCCA 33

RESULT 14

US-09-407-605-56
; Sequence 56, Application US/09407605
; Patent No. 6924365
; GENERAL INFORMATION:
; APPLICANT: Selden, Richard F.
; APPLICANT: Miller, Allan M.
; APPLICANT: Treco, Douglas A.
; TITLE OF INVENTION: OPTIMIZED MESSENGER RNA
; FILE REFERENCE: 10278-009001
; CURRENT APPLICATION NUMBER: US/09/407,605
; CURRENT FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/130,241
; PRIOR FILING DATE: 1999-04-20
; PRIOR APPLICATION NUMBER: 60/102,239
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 79
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-407-605-56

Query Match

64.0%: Score 12.8; DB 3; Length 79;

Best Local Similarity 87.5%; Pred. No. 1.7e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GAGCGGAGCCCCCTC 16
|||||
Db 48 GAGCGGAGCCCCCTC 63

RESULT 15

US-09-621-976-17097/C
; Sequence 17097, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 17097
; LENGTH: 83
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-17097

Query Match

64.0%: Score 12.8; DB 3; Length 83;

Best Local Similarity 77.8%; Pred. No. 1.7e+04;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 AGCGGAGCCCCCTCTCC 19
|||||
Db 58 AGCGGAGCCCCCTCTCC 41

Search completed: December 24, 2005, 18:36:18
Job time : 48.1 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 14:06:30 : Search time 337.6 Seconds
(without alignments)
489.892 Million cell updates/sec

Title: US-09-296-264-1

Perfect score: 20
Sequence: 1 gagcgagcagccctctcca 20

Scoring table: IDENTITY_NUC
Gapop 10.0', Gapext 1.0

Searched: 9793542 seqs, 413468905 residues

Total number of hits satisfying chosen parameters: 9887334

Minimum DB seq length: 20
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA Main:

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBSCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBSCOMB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US09_PUBSCOMB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US10_PUBSCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBSCOMB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBSCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBSCOMB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBSCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBSCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBSCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3	US-09-296-264-1
2	20	100.0	35	6	US-10-263-162-56
3	15.4	77.0	57	6	US-10-258-825-9
4	15.2	76.0	25	6	US-10-056-229-218
5	14.8	74.0	25	7	US-10-719-956-427632
6	14.8	74.0	25	8	US-10-719-900-598148
7	14.8	74.0	81	7	US-10-468-252-18
8	14.4	72.0	55	3	US-09-887-469-13
9	14.4	72.0	55	3	US-09-887-469-13
10	14.4	72.0	55	9	US-10-704-116-13
11	14.4	72.0	60	6	US-10-258-825-12
12	14.2	71.0	25	7	US-10-719-956-54800
13	14.2	71.0	25	8	US-10-719-900-467289
14	14.2	71.0	25	9	US-10-956-157-282024
15	14.2	71.0	51	8	US-10-865-478-484
16	14.2	71.0	70	3	US-09-994-228-64
17	14.2	71.0	71	3	US-09-994-228-63
18	13.8	69.0	25	7	US-10-719-956-630092
19	13.8	69.0	25	10	US-11-036-317-815857
20	13.8	69.0	65	3	US-09-908-975-25620
21	13.6	68.0	25	7	US-10-719-956-265585
22	13.6	68.0	25	7	US-10-719-956-603362
23	13.6	68.0	25	8	US-10-719-900-481600

24	13.6	68.0	25	8	US-10-719-900-481601	Sequence 481601,
25	13.6	68.0	25	8	US-10-719-900-708812	Sequence 708812,
26	13.6	68.0	25	8	US-10-719-900-863112	Sequence 863112,
27	13.6	68.0	25	8	US-10-719-900-880696	Sequence 880696,
28	13.6	68.0	25	9	US-10-956-157-210521	Sequence 210521,
29	13.6	68.0	25	9	US-10-956-157-226246	Sequence 226246,
30	13.6	68.0	25	9	US-10-956-157-244559	Sequence 244559,
31	13.6	68.0	25	9	US-10-956-157-267671	Sequence 267671,
32	13.6	68.0	25	10	US-11-036-317-75400	Sequence 75400, A
33	13.6	68.0	25	10	US-11-036-317-76950	Sequence 76950, A
34	13.6	68.0	25	10	US-11-036-317-170159	Sequence 170159,
35	13.6	68.0	25	10	US-11-036-317-205561	Sequence 205561,
36	13.6	68.0	25	10	US-11-036-317-232211	Sequence 232211,
37	13.6	68.0	25	10	US-11-036-317-348344	Sequence 348344,
38	13.6	68.0	25	10	US-11-036-317-410480	Sequence 410480,
39	13.6	68.0	25	10	US-11-036-317-421744	Sequence 421744,
40	13.6	68.0	25	10	US-11-036-317-449511	Sequence 449511,
41	13.6	68.0	25	10	US-11-036-317-815913	Sequence 815913,
42	13.6	68.0	34	6	US-10-203-821-30	Sequence 30, Appl
43	13.6	68.0	50	6	US-10-131-827-169	Sequence 169, Appl
44	13.6	68.0	65	3	US-09-908-975-30360	Sequence 30360, A
45	13.6	68.0	70	9	US-10-957-432-258	Sequence 258, App

ALIGNMENTS

```

RESULT 1
US-09-296-264-1
; Sequence 1, Application US/09296264
; Publication No. US20030083274A1
; GENERAL INFORMATION:
; APPLICANT: WRIGHT, Jim A.
; APPLICANT: YOUNG, Aiping H.
; TITLE OF INVENTION: NEUROPEPTIDE ANTISENSE OLIGONUCLEOTIDE SEQUENCES AND
; TITLE OF INVENTION: METHODS OF USING SAME TO MODULATE CELL GROWTH
; FILE REFERENCE: 032396-043
; CURRENT APPLICATION NUMBER: US/09/296,264
; EARLIER FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 60/082,791
; EARLIER FILING DATE: 1998-04-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-09-296-264-1

Query Match      100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 GAGCGGAGCCCTCTCCA 20
Db      1 GAGCGGAGCCCTCTCCA 20

RESULT 2
US-10-263-162-56/C
; Sequence 56, Application US/10263162
; Publication No. US20030186868A1
; GENERAL INFORMATION:
; APPLICANT: Rosenbaum, et al.
; TITLE OF INVENTION: Anti-Angiogenic Peptides
; FILE REFERENCE: REG 810
; CURRENT APPLICATION NUMBER: US/10/263,162
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/326,712
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.0

```

SEQ ID NO 56
LENGTH: 35
TYPE: DNA
ORGANISM: homo sapiens
US-10-263-162-56

Query Match 100.0%; Score 20; DB 6; Length 35;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCGGAGCCCCCTCTCCA 20
DB 31 GAGCGGAGCCCCCTCTCCA 12

RESULT 3
US-10-258-825-9
Sequence 9, Application US/10258825
Publication No. US20030133911A1
GENERAL INFORMATION:

APPLICANT: Conzelmann, Karl-Klaus
TITLE OF INVENTION: Pneumovirus NS Proteins Antagonising the Interferon (IFN) Response
FILE REFERENCE: AML00751
CURRENT APPLICATION NUMBER: US/10/258,825
CURRENT FILING DATE: 2002-10-25
PRIOR APPLICATION NUMBER: PCT/EP01/04740
PRIOR FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: DE 100 20 505.4
PRIOR FILING DATE: 2000-04-26
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
LENGTH: 57
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Primer hns1-No. US20030133911A115
US-10-258-825-9

Query Match 77.0%; Score 15.4; DB 6; Length 57;
Best Local Similarity 94.1%; Pred. No. 2.4e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AGCGGAGCCCCCTCTC 18
DB 6 AGCGGAGCCCCCTCTC 22

RESULT 4
US-10-056-229-218/c
Sequence 218, Application US/10056229
Publication No. US20030198943A1
GENERAL INFORMATION:

APPLICANT: Remacle, Jose
APPLICANT: Hamels, Sandrine
APPLICANT: Zammateo, Nathalie
APPLICANT: Lockman, Laurence
APPLICANT: Dufour, Sophie
APPLICANT: Alexandre, Isabelle
APPLICANT: De Longueville, Françoise
TITLE OF INVENTION: IDENTIFICATION OF A LARGE NUMBER OF
TITLE OF INVENTION: BIOLOGICAL (MICRO)ORGANISMS GROUPS AT DIFFERENT
TITLE OF INVENTION: LEVELS BY THEIR DETECTION ON A SAME ARRAY
FILE REFERENCE: VAMW213-001CPI
CURRENT APPLICATION NUMBER: US/10/056,229
CURRENT FILING DATE: 2002-01-23
PRIOR APPLICATION NUMBER: EP 00870055.1
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: EP 00870204.5
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: US 09/817,014
PRIOR FILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 321

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 218
LENGTH: 25
TYPE: DNA
ORGANISM: Streptococcus pneumoniae
US-10-056-229-218

Query Match 76.0%; Score 15.2; DB 6; Length 25;
Best Local Similarity 85.0%; Pred. No. 3.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAGCGGAGCCCCCTCTCCA 20
DB 22 GAGCGGAGCACTACTCTCCA 3

RESULT 5
US-10-719-956-427632
Sequence 427632, Application US/10719956
Publication No. US20040146910A1
GENERAL INFORMATION:

APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527.1
CURRENT APPLICATION NUMBER: US/10/719,956
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,836
PRIOR FILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 427632
LENGTH: 25
TYPE: DNA
ORGANISM: Rattus norvegicus
US-10-719-956-427632

Query Match 74.0%; Score 14.8; DB 7; Length 25;
Best Local Similarity 88.9%; Pred. No. 5.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAGCGGAGCCCCCTCTC 18
DB 2 GAGCGGAGCTCTCTTTC 19

RESULT 6
US-10-719-900-598148
Sequence 598148, Application US/10719900
Publication No. US20050026164A1
GENERAL INFORMATION:

APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 598148
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-10-719-900-598148

Query Match 74.0%; Score 14.8; DB 8; Length 25;
Best Local Similarity 88.9%; Pred. No. 5.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAGCGGAGCCCCCTCTC 18
DB 2 GAGCGGAGCTCTCTTTC 19

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RESULT 7
US-10-468-252-18/C
; Sequence 18, Application US/10468252
; Publication No. US20040166560A1
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics Corporation
; TITLE OF INVENTION: Expression of recombinant proteinase K from
; TITLE OF INVENTION: Tetractin album in yeast
; FILE REFERENCE: RDID 01011
; CURRENT APPLICATION NUMBER: US/10/468,252
; CURRENT FILING DATE: 2003-08-07
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 81
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-468-252-18

Query Match          74.0%; Score 14.8; DB 7; Length 81;
Best Local Similarity 88.9%; Pred. No. 4.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GCGGACGCCCTCTCCA 20
    ||||| ||||| |||||
DB 75 GCGGACGACCGCTCCA 58

RESULT 8
US-09-887-469-13
; Sequence 13, Application US/09887469
; Patent No. US2002014643A1
; GENERAL INFORMATION:
; APPLICANT: Krempf, Christine D.
; APPLICANT: Collins, Peter L.
; APPLICANT: Murphy, Brian R.
; APPLICANT: Buchholz, Ursula
; APPLICANT: Whitehead, Stephen S.
; TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS VACCINES EXPRESSING
; TITLE OF INVENTION: PROTECTIVE ANTIGENS FROM PROMOTOR-PROXIMAL-GENES
; FILE REFERENCE: 15280-424-IUS
; CURRENT APPLICATION NUMBER: US/09/887,469
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/213,708
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 55
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Artificial
; OTHER INFORMATION: Respiratory Syncytial Virus
US-09-887-469-13

Query Match          72.0%; Score 14.4; DB 3; Length 55;
Best Local Similarity 93.8%; Pred. No. 6.7e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCGGACGCCCTCTC 18
    ||||| ||||| |||||
DB 22 GCGGCGCGCCCTCTC 37

RESULT 9
US-09-887-469-13
; Sequence 13, Application US/09887469
; Publication No. US20040258714A9
; GENERAL INFORMATION:
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; APPLICANT: Krempf, Christine D.
; APPLICANT: Collins, Peter L.
; APPLICANT: Murphy, Brian R.
; APPLICANT: Buchholz, Ursula
; APPLICANT: Whitehead, Stephen S.
; TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS VACCINES EXPRESSING
; TITLE OF INVENTION: PROTECTIVE ANTIGENS FROM PROMOTOR-PROXIMAL-GENES
; FILE REFERENCE: 15280-424-IUS
; CURRENT APPLICATION NUMBER: US/09/887,469
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/213,708
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 55
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Artificial
; OTHER INFORMATION: Respiratory Syncytial Virus
US-09-887-469-13

Query Match          72.0%; Score 14.4; DB 3; Length 55;
Best Local Similarity 93.8%; Pred. No. 6.7e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCGGACGCCCTCTC 18
    ||||| ||||| |||||
DB 22 GCGGCGCGCCCTCTC 37

RESULT 10
US-10-704-116-13
; Sequence 13, Application US/10704116
; Publication No. US2005015838A1
; GENERAL INFORMATION:
; APPLICANT: BUCHHOLZ, URSULA
; APPLICANT: COLLINS, PETER L.
; APPLICANT: MURPHY, BRIAN R.
; APPLICANT: WHITEHEAD, STEPHEN S.
; APPLICANT: KREMPF, CHRISTINE D.
; TITLE OF INVENTION: PRODUCTION OF ATTENUATED, HUMAN-BOVINE CHIMERIC
; TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUSES FOR USE IN IMMUNOGENIC
; FILE REFERENCE: 2303-022-05
; CURRENT APPLICATION NUMBER: US/10/704,116
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: 09/887,469
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 09/602,212
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/213,708
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/143,132
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 13
; LENGTH: 55
; TYPE: DNA
; ORGANISM: Bovine respiratory syncytial virus
US-10-704-116-13

Query Match          72.0%; Score 14.4; DB 9; Length 55;
Best Local Similarity 93.8%; Pred. No. 6.7e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCGGACGCCCTCTC 18
    ||||| ||||| |||||
DB 22 GCGGCGCGCCCTCTC 37
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RESULT 11
US-10-258-825-12
; Sequence 12, Application US/10258825
; Publication No. US20030133911A1
; GENERAL INFORMATION:
; APPLICANT: Conzelmann, Karl-Klaus
; TITLE OF INVENTION: Pneumovirus NS Proteins Antagonising the Interferon (IFN) Response
; FILE REFERENCE: AM100751
; CURRENT APPLICATION NUMBER: US/10/258,825
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/EP01/04740
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: DE 100 20 505.4
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Primer mns1-No. US20030133911A1ICORV5
US-10-258-825-12

Query Match
Best Local Similarity 72.0%; Score 14.4; DB 6; Length 60;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCGGACGCCCTCTC 18
Db 10 GCGGCCGCCCTCTC 25

RESULT 12
US-10-719-956-54800/c
; Sequence 54800, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 54800
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-54800

Query Match
Best Local Similarity 71.0%; Score 14.2; DB 7; Length 25;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AGCGGACGCCCTCTCCA 20
Db 23 AGCAGAGCTCCCTCTCCA 5

RESULT 13
US-10-719-900-467299/c
; Sequence 467299, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
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; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 467299
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-467299

Query Match
Best Local Similarity 71.0%; Score 14.2; DB 8; Length 25;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAGCGGACGCCCTCTCC 19
Db 25 GAGTGGACGCCCTCTCC 7

RESULT 14
US-10-956-157-282024/c
; Sequence 282024, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 282024
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-282024

Query Match
Best Local Similarity 71.0%; Score 14.2; DB 9; Length 25;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AGCGGACGCCCTCTCCA 20
Db 21 AGCGGACGCCCTCTCCA 3

RESULT 15
US-10-865-478-484/c
; Sequence 484, Application US/10865478
; Publication No. US20040235041A1
; GENERAL INFORMATION:
; APPLICANT: Shinketsu, Richard A.
; APPLICANT: Leach, Martin D.
; TITLE OF INVENTION: cSingle Nucleotide Polymorphisms for Known Genes
; FILE REFERENCE: 15966-534-CIP1
; CURRENT APPLICATION NUMBER: US/10/865,478
; PRIOR FILING DATE: 2004-06-10
; PRIOR APPLICATION NUMBER: 60/109,024
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 09/443,199
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 09/442,129
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 09/442,849
; PRIOR FILING DATE: 1999-11-17
; NUMBER OF SEQ ID NOS: 880
; SOFTWARE: Curagen Patent Formatter Version 0.9
; SEQ ID NO 484
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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; NAME/KEY: allele
; LOCATION: (26)...(0)
; OTHER INFORMATION: single nucleotide polymorphism
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Accession number cg40310734
US-10-865-478-484

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Query Match      71.0%; Score 14.2; DB 8; Length 51;
Best Local Similarity 84.2%; Pred. No. 8.4e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy      1 GAGCGGACAGCCCTCTCC 19
Db      19 GAGCGGACAGCCCTCTCC 1

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 Job time : 338.6 secs

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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 18:29:07 ; Search time 135.3 Seconds
(without alignments)
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Title: US-09-296-264-1

Perfect score: 20

Sequence: 1 gagcgagcagccctctcca 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4168288 seqs, 259477437 residues

Total number of hits satisfying chosen parameters: 1608458

Minimum DB seq length: 20

Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA_New:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Query Match	Length	ID	Description
1	14.2	71.0	25	US-11-121-849-233495	Sequence 233495,
2	14.2	71.0	25	US-11-121-849-278074	Sequence 278074,
3	13.8	69.0	25	US-11-121-849-151184	Sequence 151184,
4	13.8	69.0	25	US-11-121-849-464194	Sequence 464194,
5	13.6	68.0	25	US-11-121-849-151553	Sequence 151553,
6	13.6	68.0	25	US-11-121-849-315834	Sequence 315834,
7	13.6	68.0	25	US-11-121-849-315891	Sequence 315891,
8	13.6	68.0	25	US-11-121-849-409754	Sequence 409754,
9	13.6	68.0	25	US-11-121-849-409755	Sequence 409755,
10	13.6	68.0	25	US-11-121-849-409756	Sequence 409756,
11	13.6	68.0	25	US-11-121-849-409757	Sequence 409757,
12	13.6	68.0	25	US-11-121-849-411377	Sequence 411377,
13	13.6	68.0	25	US-11-121-849-411378	Sequence 411378,
14	13.6	68.0	25	US-11-121-849-411379	Sequence 411379,
15	13.6	68.0	25	US-11-121-849-411380	Sequence 411380,
16	13.2	66.0	25	US-11-121-849-124687	Sequence 124687,
17	13.2	66.0	25	US-11-121-849-124773	Sequence 124773,
18	13.2	66.0	25	US-11-121-849-124774	Sequence 124774,
19	13.2	66.0	25	US-11-121-849-233496	Sequence 233496,
20	12.8	64.0	25	US-11-121-849-13520	Sequence 13520, A
21	12.8	64.0	25	US-11-121-849-19002	Sequence 19002, A
22	12.8	64.0	25	US-11-121-849-264750	Sequence 264750,
23	12.8	64.0	25	US-11-121-849-264751	Sequence 264751,

24	12.8	64.0	25	US-11-121-849-265503	Sequence 265503,
25	12.8	64.0	25	US-11-121-849-307663	Sequence 307663,
26	12.8	64.0	25	US-11-121-849-307664	Sequence 307664,
27	12.8	64.0	25	US-11-121-849-426195	Sequence 426195,
28	12.8	64.0	34	US-10-525-710-60	Sequence 60, Appl
29	12.6	63.0	20	US-11-040-468-7	Sequence 7, Appl
30	12.6	63.0	25	US-11-121-849-18975	Sequence 28975, A
31	12.6	63.0	25	US-11-121-849-32420	Sequence 32420, A
32	12.6	63.0	25	US-11-121-849-38350	Sequence 38350, A
33	12.6	63.0	25	US-11-121-849-178326	Sequence 178326,
34	12.6	63.0	25	US-11-121-849-193304	Sequence 193304,
35	12.6	63.0	25	US-11-121-849-219241	Sequence 219241,
36	12.6	63.0	25	US-11-121-849-219492	Sequence 219492,
37	12.6	63.0	25	US-11-121-849-363351	Sequence 363351,
38	12.6	63.0	25	US-11-121-849-363352	Sequence 363352,
39	12.6	63.0	25	US-11-121-849-364925	Sequence 364925,
40	12.6	63.0	25	US-11-121-849-364926	Sequence 364926,
41	12.6	63.0	25	US-11-121-849-371701	Sequence 371701,
42	12.6	63.0	25	US-11-121-849-409753	Sequence 409753,
43	12.6	63.0	25	US-11-121-849-411376	Sequence 411376,
44	12.6	63.0	25	US-11-121-849-511145	Sequence 511145,
45	12.6	63.0	25	US-11-121-849-514701	Sequence 514701,

ALIGNMENTS

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RESULT 1
US-11-121-849-233495/c
; Sequence 233495, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3684.1
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 233495
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
; US-11-121-849-233495

Query Match      71.0%; Score 14.2; DB 7; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy      2 AGCGGAGCCCTCTCCA 20
Db      22 AGCGTAGCCTCTCTCCA 4

RESULT 2
US-11-121-849-278074/c
; Sequence 278074, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3684.1
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 278074
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LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-278074

Query Match 71.0%; Score 14.2; DB 7; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AGCGGAGCCCCCTCTCCA 20
DB 23 AGCGGAGCCACCTCTCCA 5

RESULT 3
US-11-121-849-151184/C
Sequence 151184, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
FILE REFERENCE: 3684.1
CURRENT FILING DATE: 2005-05-03
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 151184
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-151184

Query Match 69.0%; Score 13.8; DB 7; Length 25;
Best Local Similarity 88.2%; Pred. No. 2.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GCGGAGCCCCCTCTCC 19
DB 17 GCGGAGGTCCTCTCC 1

RESULT 4
US-11-121-849-464194
Sequence 464194, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
FILE REFERENCE: 3684.1
CURRENT FILING DATE: 2005-05-03
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 464194
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-464194

Query Match 69.0%; Score 13.8; DB 7; Length 25;
Best Local Similarity 88.2%; Pred. No. 2.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCGGAGCCCCCTCTCCA 20
DB 9 GAGGAGCTCTCTCTCCA 25

RESULT 5
US-11-121-849-151553
Sequence 151553, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
FILE REFERENCE: 3684.1
CURRENT FILING DATE: 2005-05-03
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 151553
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-151553

Query Match 68.0%; Score 13.6; DB 7; Length 25;
Best Local Similarity 80.0%; Pred. No. 3.2e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAGCGGAGCCCCCTCTCCA 20
DB 5 GAGCGAGAGCCCCCTCTCCA 24

RESULT 6
US-11-121-849-315834/C
Sequence 315834, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
FILE REFERENCE: 3684.1
CURRENT FILING DATE: 2005-05-03
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 315834
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-315834

Query Match 68.0%; Score 13.6; DB 7; Length 25;
Best Local Similarity 80.0%; Pred. No. 3.2e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAGCGGAGCCCCCTCTCCA 20
DB 20 GAGCTGAGTCCCCGCTCCA 1

RESULT 7
US-11-121-849-315891
Sequence 315891, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
FILE REFERENCE: 3684.1
CURRENT FILING DATE: 2005-05-03
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 315891
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-315891

PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 315891
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-315891

Query Match 68.0%; Score 13.6; DB 7; Length 25;
Best Local Similarity 80.0%; Pred. No. 3.2e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GAGCGGAGCCCCCTCTCCA 20
DB 3 GAGCTGAGTCCCGCTCCA 22

RESULT 8
US-11-121-849-409754/c
Sequence 409754, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S

TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 409754
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-409754

Query Match 68.0%; Score 13.6; DB 7; Length 25;
Best Local Similarity 80.0%; Pred. No. 3.2e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GAGCGGAGCCCCCTCTCCA 20
DB 24 GAGCGGCTGCTCCACTTCA 5

RESULT 9
US-11-121-849-409755/c
Sequence 409755, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 409755
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-409755

Query Match 68.0%; Score 13.6; DB 7; Length 25;
Best Local Similarity 80.0%; Pred. No. 3.2e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GAGCGGAGCCCCCTCTCCA 20
DB 23 GAGCGGCTGCTCCACTTCA 4

RESULT 10
US-11-121-849-409756/c
Sequence 409756, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 409756
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-409756

Query Match 68.0%; Score 13.6; DB 7; Length 25;
Best Local Similarity 80.0%; Pred. No. 3.2e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GAGCGGAGCCCCCTCTCCA 20
DB 22 GAGCGGCTGCTCCACTTCA 3

RESULT 11
US-11-121-849-409757/c
Sequence 409757, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 409757
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-409757

Query Match 68.0%; Score 13.6; DB 7; Length 25;
Best Local Similarity 80.0%; Pred. No. 3.2e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GAGCGGAGCCCCCTCTCCA 20
DB 21 GAGCGGCTGCTCCACTTCA 2

RESULT 12
US-11-121-849-411377/c
Sequence 411377, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
TITLE OF INVENTION: Microarrays

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; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 411377
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-411377

Query Match
Best Local Similarity 68.0%; Score 13.6; DB 7; Length 25;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAGCGGCGAGCCCCCTCTCCA 20
DB 24 GAGCGGCGTCTCCCACTTCA 5

RESULT 13
US-11-121-849-411378/c
; Sequence 411378, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 411378
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-411378

Query Match
Best Local Similarity 68.0%; Score 13.6; DB 7; Length 25;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAGCGGCGAGCCCCCTCTCCA 20
DB 23 GAGCGGCGTCTCCCACTTCA 4

RESULT 14
US-11-121-849-411379/c
; Sequence 411379, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 411379
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-411379
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Query Match
Best Local Similarity 68.0%; Score 13.6; DB 7; Length 25;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAGCGGCGAGCCCCCTCTCCA 20
DB 22 GAGCGGCGTCTCCCACTTCA 3

RESULT 15
US-11-121-849-411380/c
; Sequence 411380, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 411380
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-411380

Query Match
Best Local Similarity 68.0%; Score 13.6; DB 7; Length 25;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAGCGGCGAGCCCCCTCTCCA 20
DB 21 GAGCGGCGTCTCCCACTTCA 2

Search completed: December 25, 2005, 04:37:01
Job time : 135.3 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 10:28:41 ; Search time 582 Seconds
(without alignments)
1953.383 Million cell updates/sec

Title: US-09-296-264-2

Perfect score: 20

Sequence: 1 cgagcagcgccgagagagc 20

Scoring table: IDENTITY_NUC

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 1858228

Minimum DB seq length: 20

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ha: *
2: gb_in: *
3: gb_env: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pr: *
9: gb_ro: *
10: gb_scs: *
11: gb_sy: *
12: gb_un: *
13: gb_vl: *
14: gb_htg: *
15: gb_pl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6	BD211659
2	15.4	77.0	99	6	AX435605
3	15.2	76.0	27	6	AX356224
4	15.2	76.0	87	6	E27048
5	14.8	74.0	100	6	AX93844
6	14.4	72.0	21	6	A91560
7	14.4	72.0	21	6	AR441815
8	14.4	72.0	21	6	AR477004
9	14.4	72.0	21	6	AX454812
10	14.4	72.0	21	6	BD023342
11	14.2	71.0	50	6	AX156996
12	14.2	71.0	51	6	AR444342
13	14.2	71.0	51	6	AX156995
14	14.2	71.0	100	9	RATMAP
15	13.8	69.0	37	6	ARI70305
16	13.8	69.0	37	6	E51079
17	13.8	69.0	37	6	AX007133
18	13.8	69.0	65	6	COS60111

19	13.8	69.0	100	6	AX989123	AX989123 Sequence
20	13.8	69.0	100	6	AX989124	AX989124 Sequence
21	13.6	68.0	23	6	ARI12201	ARI12201 Sequence
22	13.6	68.0	23	6	ARI49243	ARI49243 Sequence
23	13.6	68.0	27	6	127230	127230 Sequence 36
24	13.6	68.0	27	6	AR364785	AR364785 Sequence
25	13.6	68.0	30	6	AX611269	AX611269 Sequence
26	13.6	68.0	35	6	A07810	A07810 Sequence
27	13.6	68.0	43	6	A07815	A07815 Sequence
28	13.6	68.0	45	6	AR012045	AR012045 Sequence
29	13.6	68.0	45	6	AR062287	AR062287 Sequence
30	13.6	68.0	50	6	BD205008	BD205008 Gene enco
31	13.6	68.0	50	6	AX014759	AX014759 Sequence
32	13.6	68.0	60	6	125129	125129 Sequence 17
33	13.6	68.0	60	6	AX613020	AX613020 Sequence
34	13.6	68.0	60	6	AX613021	AX613021 Sequence
35	13.6	68.0	60	6	AX613022	AX613022 Sequence
36	13.6	68.0	60	6	AX613023	AX613023 Sequence
37	13.6	68.0	65	6	C0556568	C0556568 Sequence
38	13.6	68.0	75	6	AR078717	AR078717 Sequence
39	13.6	68.0	75	6	125146	125146 Sequence 42
40	13.6	68.0	75	6	ARI98697	ARI98697 Sequence
41	13.6	68.0	75	15	MZEMTATP92	L38813 Maize mtloc
42	13.6	68.0	78	6	AR365016	AR365016 Sequence
43	13.6	68.0	81	6	A10907	A10907 DNA for sec
44	13.6	68.0	81	6	BD205009	BD205009 Gene enco
45	13.6	68.0	81	6	AX014760	AX014760 Sequence

ALIGNMENTS

RESULT 1
LOCUS BD211659 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Antisense oligonucleotide sequence of neuropilin and method of using the same for controlling cell proliferation.

ACCESSION BD211659.1 GI:33021429
VERSION JP 2002512793-A/2.

KEYWORDS Homo sapiens (human)

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BD211659
Antisense oligonucleotide sequence of neuropilin and method of using the same for controlling cell proliferation.
Patent: JP 2002512793-A 2 08-MAY-2002;
GENESENSE TECHNOLOGIES INC
OS Homo sapiens (human)
PN JP 2002512793-A/2
PD 08-MAY-2002
PF 23-APR-1998 JP 2000545999
PR 23-APR-1998 US 60/082791
PT JIM A WRIGHT, AIPING H YOUNG, YOON S LEE
PC C12N15/09, A61K31/711, A61K48/00, A61P35/00, C12N15/00 CC
Antisense oligonucleotide sequence of neuropilin and method of using the same for controlling cell proliferation
CC same for controlling cell proliferation
FH key Location/Qualifiers
FT source 1..20
Location/Qualifiers
1..20 /organism="Homo sapiens (human)"
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGAGCAGCGCGCAGAGAGC 20
1 CGAGCAGCGCGCAGAGAGC 20

Db 1 CGAGCAGCGCGCAGAGAGC 20

RESULT 2
AX35605
LOCUS Sequence 4020 from Patent WO0229113. 99 bp DNA 1linear PAT 28-JUN-2002
DEFINITION
ACCESSION AX435605
VERSION AX435605.1 GI:21660413
KEYWORDS
SOURCE Bacillus licheniformis
ORGANISM Bacillus licheniformis
REFERENCE 1 Berka, R. and Clausen, I. G.
AUTHORS Methods for monitoring multiple gene expression
TITLE Patent: WO 0229113-A 4020 11-APR-2002;
JOURNAL Novozymes Biotech, Inc. (US); Novozymes A/S (DK)
FEATURES
source 1. .99
/organism="Bacillus licheniformis"
/mol_type="unassigned DNA"
/db_xref="taxon:1402"

ORIGIN

Query Match 77.0%; Score 15.4; DB 6; Length 99;
Best Local Similarity 94.1%; Pred. No. 7.2e+04;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GCACGCGCAGAGAGC 20
31 GCACGCGCAGAGAGC 47

Db 31 GCACGCGCAGAGAGC 47

RESULT 3
AX356224
LOCUS Sequence 18 from Patent WO0200905. 27 bp DNA 1linear PAT 06-FEB-2002
DEFINITION
ACCESSION AX356224
VERSION AX356224.1 GI:18620731
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 Conner, T. W., Dubois, P., Malven, M. and Maseucci, J. D.
AUTHORS Plant regulatory sequences for selective control of gene expression
TITLE Patent: WO 0200905-A 18 03-JAN-2002;
JOURNAL Monsanto Technology LLC (US)
FEATURES
source 1. .27
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic"

ORIGIN

Query Match 76.0%; Score 15.2; DB 6; Length 27;
Best Local Similarity 85.0%; Pred. No. 1.1e+05;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CGAGCAGCGCGCAGAGAGC 20
7 CGAGCAGCGCGCAGAGAGC 26

Db 7 CGAGCAGCGCGCAGAGAGC 26

RESULT 4
E27048/c
LOCUS E27048 87 bp DNA 1linear PAT 18-JUN-2001

DEFINITION Novel receptor protein and utilization of the same.
ACCESSION E27048
VERSION E27048.1 GI:13026378
KEYWORDS JP 1999152300-A/3.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 87)
AUTHORS Kazunori, N., Yasushi, A. and Takashi, H.
TITLE Novel receptor protein and utilization of the same
JOURNAL Patent: JP 1999152300-A 3 08-JUN-1999;
COMMENT
OS Unidentified
PN JP 1999152300-A/3
PD 08-JUN-1999
PF 24-APR-1998 JP 1998114450
PR
PI KAZUNORI NISHI, YASUSHI ARAI, TAKASHI HORIGUCHI
PC C07K14/715, A61K45/00, C07K16/28, C12N15/09, C12P21/02, PC
C1201/02//A61K48/00,
PC C12N5/10, (C12N15/09, C12R1:91), (C12P21/02, C12R1:91), C12N15/00,
PC C12N5/00, C12R1:91)
CC Strandedness: Double;
CC Topology: linear;
FH Key
FT source 1. .87
/organism="Unidentified".
FEATURES
source 1. .87
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN

Query Match 76.0%; Score 15.2; DB 6; Length 87;
Best Local Similarity 85.0%; Pred. No. 8.8e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CGAGCAGCGCGCAGAGAGC 20
64 CGAGCAGCGCGCAGAGAGC 45

Db 64 CGAGCAGCGCGCAGAGAGC 45

RESULT 5
AX93844
LOCUS Sequence 5307 from Patent EP1260592. 100 bp DNA 1linear PAT 16-JAN-2004
DEFINITION
ACCESSION AX93844
VERSION AX93844.1 GI:41000190
KEYWORDS
SOURCE Escherichia coli
ORGANISM Escherichia coli
REFERENCE 1 Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
AUTHORS Donner, H., Drescher, B., Huber, A. and Weber, J.
TITLE Biochip
JOURNAL Patent: EP 1260592-A 5307 27-NOV-2002;
MWG -Biotech AG (DE)
FEATURES
source 1. .100
/organism="Escherichia coli"
/mol_type="unassigned DNA"
/db_xref="taxon:562"
/note="mode mode U00096 complement (793079_793867)"

ORIGIN

Query Match 74.0%; Score 14.8; DB 6; Length 100;
Best Local Similarity 88.9%; Pred. No. 1.2e+05;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GAGCAGCGCGCAGAGAG 19

Db 50 GAGCGCGCGCAGAGCAG 67
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RESULT 6
A91560
LOCUS A91560 21 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 87 from Patent WO9824928.
ACCESSION A91560
VERSION A91560.1 GI:6740515
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 21)
AUTHORS Pallsgaard,N. and Hokland,P.
TITLE DETECTION OF CHROMOSOMAL ABNORMALITIES
JOURNAL Patent: WO 9824928-A 87 11-JUN-1998;
PALLSGAARD NIELS (DK); HOKLAND PETER (DK)
FEATURES
Location/Qualifiers
1..21
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
ORIGIN
Query Match 72.0%; Score 14.4; DB 6; Length 21;
Best Local Similarity 93.8%; Pred. No. 2.4e+05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 3 AGCAGCGCGCAGAGGA 18
|||||
Db 1 AGCAGCGCGCAGAGGA 16
RESULT 7
AR441815/c
LOCUS AR441815 21 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 14 from patent US 6667164.
ACCESSION AR441815
VERSION AR441815.1 GI:42668042
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 21)
AUTHORS Miller,M.M., Afanassieff,M. and Briles,W.E.
TITLE Method for determining the MHC genotype of chickens
JOURNAL Patent: US 6667164-A 14 23-DEC-2003;
The Board of Trustees for Northern Illinois University and City of
Hope; DeKalb, IL
FEATURES
Location/Qualifiers
1..21
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 72.0%; Score 14.4; DB 6; Length 21;
Best Local Similarity 93.8%; Pred. No. 2.4e+05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 5 CACGCGCGCAGAGGAGC 20
|||||
Db 16 CACGCGCGCAGAGGAGC 1
RESULT 8
AR477004/c
LOCUS AR477004 21 bp DNA linear PAT 14-MAY-2004
DEFINITION Sequence 14 from patent US 6696253.
ACCESSION AR477004
VERSION AR477004.1 GI:47234260
KEYWORDS

SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 21)
AUTHORS Miller,M.M., Briles,W.E. and Afanassieff,M.
TITLE Method for determining the MHC genotype of chickens
JOURNAL Patent: US 6696253-A 14 24-FEB-2004;
City of Hope; Duarte, CA
FEATURES
Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 72.0%; Score 14.4; DB 6; Length 21;
Best Local Similarity 93.8%; Pred. No. 2.4e+05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 5 CACGCGCGCAGAGGAGC 20
|||||
Db 16 CACGCGCGCAGAGGAGC 1
RESULT 9
AX454812/c
LOCUS AX454812 21 bp DNA linear PAT 06-JUL-2002
DEFINITION Sequence 14 from Patent WO0206535.
ACCESSION AX454812
VERSION AX454812.1 GI:21714041
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Miller,M.M., Afanassieff,M. and Briles,W.E.
TITLE Method for breeding disease resistant domesticated fowl
JOURNAL Patent: WO 0206535-A 14 24-JAN-2002;
City of Hope (US)
FEATURES
Location/Qualifiers
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer for SSCP analysis of MHC B class II-beta
genotype of fowl"
ORIGIN
Query Match 72.0%; Score 14.4; DB 6; Length 21;
Best Local Similarity 93.8%; Pred. No. 2.4e+05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 5 CACGCGCGCAGAGGAGC 20
|||||
Db 16 CACGCGCGCAGAGGAGC 1
RESULT 10
BD023342
LOCUS BD023342 21 bp DNA linear PAT 27-AUG-2002
DEFINITION Method for detecting abnormality in chromosome.
ACCESSION BD023342
VERSION BD023342.1 GI:22564565
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 21)
AUTHORS Pallsgaard,N. and Hokurando,P.
TITLE Method for detecting abnormality in chromosome
JOURNAL Patent: JP 2001505428-A 87 24-APR-2001;
NIELLS PALLSGAARD

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COMMENT      PN      JP 2001505428-A/87
              PD      24-APR-2001
              PF      08-DEC-1997 JP 1998525090
              PI      NEILIS PARISGARD,PATER HOKURANDO
              PC      C12N15/09,C12Q1/68,G01N33/50,C12N15/00
              CC      Strandedness: Single;
              CC      Topology: Linear;
              CC      /desc = 'DNA (synthetic)'
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ORIGIN
Query Match      72.0%; Score 14.4; DB 6; Length 21;
Best Local Similarity 93.8%; Pred. No. 2.4e+05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3 AGCAGCGCGCAGAGGA 18
        |||||
Db      1 AGCAGCGAGCAGAGGA 16

RESULT 11
AX156996      50 bp      DNA      linear      PAT 22-JUN-2001
LOCUS
DEFINITION      Sequence 324 from Patent WO0140521.
ACCESSION      AX156996
VERSION      AX156996.1 GI:14538327
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Homiinae; Homo.
REFERENCE
  AUTHORS      1 Shinkets,R.A. and Leach,M.
  TITLE      Nucleic acids containing single nucleotide polymorphisms and
              methods of use thereof
  JOURNAL      Patent: WO 0140521-A 324 07-JUN-2001;
              Curagen Corporation (US)
FEATURES
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              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
              /note="Nucleotide deleted between bases 25 and 26
              Accession number cg20436198"
              /note="2 of 2 allelic variants (323 is other entry)"

ORIGIN
Query Match      71.0%; Score 14.2; DB 6; Length 50;
Best Local Similarity 84.2%; Pred. No. 2.4e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 CGAGCAGCGCGCAGAGGAG 19
        |||||
Db      30 CGAGCAGCGCGCGCAGAG 48

RESULT 12
AR444342      51 bp      DNA      linear      PAT 20-FEB-2004
LOCUS
DEFINITION      Sequence 753 from patent US 6670464.
ACCESSION      AR444342
VERSION      AR444342.1 GI:42672121
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.

```

```

Unclassified.
REFERENCE
  AUTHORS      1 (bases 1 to 51)
              Shinkets,R.A. and Leach,M.
  TITLE      Nucleic acids containing single nucleotide polymorphisms and
              methods of use thereof
  JOURNAL      Patent: US 6670464-A 753 30-DEC-2003;
              Curagen Corporation; New Haven, CT
FEATURES
  source      1..51
              /organism="unknown"
              /mol_type="genomic DNA"

ORIGIN
Query Match      71.0%; Score 14.2; DB 6; Length 51;
Best Local Similarity 84.2%; Pred. No. 2.4e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 GAGCAGCGCGCAGAGGAGC 20
        |||||
Db      26 GAGCAGCGGAGAGAGGAGC 44

RESULT 13
AX156995      51 bp      DNA      linear      PAT 22-JUN-2001
LOCUS
DEFINITION      Sequence 323 from Patent WO0140521.
ACCESSION      AX156995
VERSION      AX156995.1 GI:14538326
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Homiinae; Homo.
REFERENCE
  AUTHORS      1 Shinkets,R.A. and Leach,M.
  TITLE      Nucleic acids containing single nucleotide polymorphisms and
              methods of use thereof
  JOURNAL      Patent: WO 0140521-A 323 07-JUN-2001;
              Curagen Corporation (US)
FEATURES
  source      1..51
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
              /note="1 of 2 allelic variants (324 is other entry)
              Accession number cg20436198"

ORIGIN
Query Match      71.0%; Score 14.2; DB 6; Length 51;
Best Local Similarity 84.2%; Pred. No. 2.4e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 CGAGCAGCGCGCAGAGGAG 19
        |||||
Db      31 CGAGCAGCGCGCGCAGAG 49

RESULT 14
RATMAP/c      100 bp      mRNA      linear      ROD 27-APR-1993
LOCUS
DEFINITION      Rat major acute phase protein mRNA (alpha1-MAP gene), partial cds.
ACCESSION      M26758
VERSION      M26758.1 GI:205301
KEYWORDS      major acute phase protein.
SOURCE      Rattus norvegicus (Norway rat)
ORGANISM      Rattus norvegicus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
              Sciurognathi; Muridae; Muridae; Murinae; Rattus.
REFERENCE
  AUTHORS      1 (bases 1 to 100)
              Anderson,K.P., Martin,A.D. and Heath,E.C.

```


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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 01:41:40 ; Search time 171.4 Seconds
(without alignments)
777.677 Million cell updates/sec

Title: US-09-296-264-2

Perfect score: 20

Sequence: 1 cgagcacgscgcagagagagc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 3390896

Minimum DB seq length: 20

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq_21.*
1: geneseqn1980s.*
2: geneseqn1990s.*
3: geneseqn2000s.*
4: geneseqn2001s.*
5: geneseqn2001bs.*
6: geneseqn2002as.*
7: geneseqn2002bs.*
8: geneseqn2003as.*
9: geneseqn2003bs.*
10: geneseqn2003cs.*
11: geneseqn2003ds.*
12: geneseqn2004as.*
13: geneseqn2004bs.*
14: geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3	AAZ31432
2	20	100.0	20	3	ADA74684
3	19	95.0	29	12	ADO48591
4	15.8	79.0	50	13	ADU24833
5	15.8	79.0	50	13	ADU22300
6	15.4	77.0	99	6	ABK76729
7	15.2	76.0	27	6	ABK27825
8	14.8	74.0	48	1	AAH80520
9	14.8	74.0	52	6	ADG69851
10	14.8	74.0	54	11	ADN88873
11	14.8	74.0	100	8	ACD74037
12	14.4	72.0	20	10	ADC38589
13	14.4	72.0	21	6	AAV40985
14	14.4	72.0	21	6	ABK8264
15	14.4	72.0	21	6	ABD29196
16	14.4	72.0	42	10	ADC38571
17	14.2	71.0	27	12	ADN06162
18	14.2	71.0	42	9	ADB39065
19	14.2	71.0	48	9	ADB39064

20	14.2	71.0	50	4	AAI73383
21	14.2	71.0	51	3	AAI77070
22	14.2	71.0	51	4	AAI77382
23	14.2	71.0	63	8	ACF57081
24	14.2	71.0	63	12	ADG39198
25	14.2	71.0	63	13	ADU81373
26	14.2	71.0	63	14	ABE84262
27	14.2	71.0	75	9	ADB39116
28	14.2	71.0	96	9	ADB39117
29	13.8	69.0	20	13	ADR86867
30	13.8	69.0	20	13	ADR82422
31	13.8	69.0	23	14	ADZ84685
32	13.8	69.0	37	3	AAZ57918
33	13.8	69.0	65	6	ABN56988
34	13.8	69.0	80	13	ADY5949
35	13.8	69.0	100	8	ACD69317
36	13.8	69.0	100	8	ACD69316
37	13.6	68.0	23	2	AAZ24557
38	13.6	68.0	23	2	AAZ24649
39	13.6	68.0	23	9	ACD45012
40	13.6	68.0	23	12	ADU6207
41	13.6	68.0	27	2	AAQ34929
42	13.6	68.0	28	3	AAZ49806
43	13.6	68.0	28	3	AAZ63976
44	13.6	68.0	45	2	AAI38929
45	13.6	68.0	45	2	AAI39278

ALIGNMENTS

RESULT 1
AAZ31432
ID AAZ31432 standard; DNA; 20 BP.
AC AAZ31432;
XX
DT 07-FEB-2000 (first entry)
XX
DE Human neuropilin mRNA specific antisense oligo GTI3602.
XX
KW Neuropilin; human; growth; metastasis; tumor; neovascularisation; cancer;
XX papilloma; diabetic retinopathy; antisense; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN W0955855-A2.
XX
PD 04-NOV-1999.
XX
PF 23-APR-1999; 99WO-CA000324.
XX
PR 23-APR-1998; 98US-0082791P.
XX
PA (GENE-) GENESENSE TECHNOLOGIES INC.
XX
PI Wright JA, Young AH, Lee YS;
XX WPI; 2000-023357/02.
XX
PT Antisense oligonucleotides that inhibit neuropilin expression, useful for
PT treating cancer.
XX
PS Claim 4; Page 16; 57pp; English.
XX
CC Sequences AAZ31431-460 represent antisense oligonucleotides which inhibit
CC human neuropilin expression. The antisense oligonucleotides can be used
CC to inhibit the growth or metastasis of a mammalian tumor and inhibit
CC neovascularisation. The oligonucleotides may be used to treat various
CC forms of cancers or tumors, such as sarcomas, melanomas, adenomas,
CC carcinomas of solid tissue, hypoxic tumors, squamous cell carcinomas of
CC the mouth, throat, larynx and lung, genitourinary cancers such as

```
CC cervical and bladder cancer, hematopoietic cancers, colon cancer, breast
CC cancer, pancreatic cancer, renal cancer, brain cancer, skin cancer, liver
CC cancer, head and neck cancers, and nervous system cancers, as well as
CC benign lesions such as papillomas. The methods may be used to treat
CC neovascularisation disorders such as diabetic retinopathy, and
CC retinopathy of prematurity and age related macular degeneration
XX
SQ Sequence 20 BP; 5 A; 6 C; 9 G; 0 T; 0 U; 0 Other;

Query Match          100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 CGAGCAGCGCGCAGAGAGC 20
        |||
Db      1 CGAGCAGCGCGCAGAGAGC 20

RESULT 2
ADA74684
ID ADA74684 strand; DNA; 20 BP.
AC ADA74684;
XX
XX
XX 20-NOV-2003 (first entry)
XX
DE GT13602 antisense oligonucleotide targeted to human neuropilin mRNA.
XX
XX neuropilin; VEGF165R; vascular endothelial growth factor receptor;
XX cytosolic; growth; tumour metastasis; angiogenesis; gene therapy;
XX GT13602; antisense; human; ss.
XX
XX Homo sapiens.
XX
XX US2003083274-A1.
XX
XX 01-MAY-2003.
XX
XX 22-APR-1999; 99US-00296264.
XX
XX 23-APR-1998; 98US-0082791P.
XX
XX (WRIG/) WRIGHT J A.
XX PA (YOUNG/) YOUNG A H.
XX PA (LEERY/) LEE Y S.
XX
XX Wright JA, Young AH, Lee YS;
XX
XX WPI; 2003-576622/54.
XX
XX New antisense oligonucleotide that inhibits neuropilin expression, useful
XX for inhibiting growth of mammalian tumor or inhibiting metastasis of a
XX mammalian tumor.
XX
XX Claim 1; Page 5; 27pp; English.
XX
XX The invention relates to a novel antisense oligonucleotide that inhibits
XX the expression of neuropilin, also known as VEGF165R (vascular
XX endothelial growth factor receptor). The oligonucleotide of the invention
XX demonstrates cytostatic activity and may be useful for inhibiting the
XX growth or metastasis of a mammalian tumour and to inhibit angiogenesis in
XX mammals. Furthermore, the oligonucleotide may be utilised during gene
XX therapy. The current sequence is that of the GT13602 antisense
XX oligonucleotide of the invention which is targeted to human neuropilin
XX mRNA.
XX
SQ Sequence 20 BP; 5 A; 6 C; 9 G; 0 T; 0 U; 0 Other;

Query Match          100.0%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 CGAGCAGCGCGCAGAGAGC 20
```

```
Db      1 CGAGCAGCGCGCAGAGAGC 20
        |||
RESULT 3
ADO48591/c
ID ADO48591 strand; DNA; 29 BP.
XX
XX ADO48591;
XX
XX 12-AUG-2004 (first entry)
XX
DE Human neuropilin 1 (NRP1) PCR primer #48.
XX
XX human; melanoma; single nucleotide polymorphism; SNP; neuropilin 1; NRP1;
XX mannose receptor C type 2; MRC2; PCR; primer; ss; genotyping.
XX
XX Homo sapiens.
XX
XX WO2004044163-A2.
XX
XX 27-MAY-2004.
XX
XX 06-NOV-2003; 2003WO-US035876.
XX
XX 06-NOV-2002; 2002US-0424475P.
XX
XX 23-JUL-2003; 2003US-0489703P.
XX
XX (SEQU-) SEQUENOM INC.
XX
XX Roth RB, Nelson MR, Braun A, Kammerer SM;
XX
XX WPI; 2004-411720/38.
XX
XX Identifying a subject at risk of melanoma, useful for treating melanoma,
XX comprises detecting the presence or absence of one or more polymorphic
XX variations associated with melanoma in a nucleic acid sample from a
XX subject.
XX
XX Example 3; Page 76; 176pp; English.
XX
XX The invention comprises a method for identifying a subject at risk of
XX melanoma. The invention involves detecting the presence or absence of one
XX or more polymorphic variations associated with melanoma in the neuropilin
XX 1 (NRP1) or mannose receptor C type 2 (MRC2) genes. The method of the
XX invention is useful for identifying subjects at risk and treating
XX melanoma. The present DNA sequence represents a PCR primer that was used
XX to detect single nucleotide polymorphisms within human NRP1.
XX
SQ Sequence 29 BP; 2 A; 10 C; 9 G; 8 T; 0 U; 0 Other;

Query Match          95.0%; Score 19; DB 12; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      2 GAGCAGCGCGCAGAGAGC 20
        |||
Db      29 GAGCAGCGCGCAGAGAGC 11

RESULT 4
ADU24833/c
ID ADU24833 strand; DNA; 50 BP.
XX
XX ADU24833;
XX
XX 27-JAN-2005 (first entry)
XX
XX Retroelement consensus sequence identifier oligonucleotide #203.
XX
XX Expression pattern; transposable element; developmental potential;
XX stem cell; cellular differentiation induction factor;
XX methylation pattern; chromatin status pattern; endogenous retrovirus;
```

KM ERV; short interspersed nuclear element; SINE;
 XX long interspersed nuclear element; LINE; retroelement; ss.
 OS Synthetic.
 XX WO2004097005-A2.
 XX 11-NOV-2004.
 PD 29-APR-2004; 2004WO-US013667.
 XX 29-APR-2004; 2004WO-US013667.
 PR 29-APR-2003; 2003US-0466801P.
 XX (UYGE-) UNIV GEORGIA RES FOUND INC.
 PA Mcdonald JF;
 XX Mcdonald JF;
 PI WPI; 2004-804756/79.
 DR WPI; 2004-804756/79.
 XX
 PT Assigning an expression pattern of transposable elements to the level of
 PT developmental potential of a cell comprises determining expression of one
 PT or more families of transposable elements, and assigning the expression
 PT pattern.
 PS Disclosure; SEQ ID NO 303; 50pp; English.
 XX
 CC The invention relates to a method of assigning an expression pattern of
 CC transposable elements to the level of developmental potential of a cell.
 CC The method comprises determining the expression of one or more families
 CC of transposable elements, and assigning the expression pattern obtained
 CC to the level of developmental potential of a cell. Also disclosed are a
 CC method of determining the developmental potential of a stem cell, a
 CC method of identifying a cellular differentiation induction factor, a
 CC method of identifying a factor that increases the developmental potential
 CC of a cell, a method of assigning a methylation pattern of transposable
 CC elements to the level of developmental potential of a cell, and a method
 CC of assigning a chromatin status pattern of transposable elements to the
 CC level of developmental potential of a cell. In assigning an expression
 CC pattern of transposable elements to the level of developmental potential
 CC of a cell, the cell is a fully pluripotent stem cell, a pluripotent stem
 CC cell, or a differentiated cell. The expression pattern is determined by
 CC microarray analysis. One or more of the families of transposable elements
 CC are retroelement families, or DNA element families. One or more of the
 CC families of retroelements is selected from the group consisting of
 CC endogenous retroviruses (ERVs), a family of short interspersed nuclear
 CC elements (SINEs) and a family of long interspersed nuclear elements
 CC (LINEs). The expression of the transposable elements is measured by
 CC assaying for the mRNA transcribed from the genes or proteins translated
 CC from an mRNA transcribed from the genes. The expression of two or more
 CC families of transposable elements is determined and used to form the
 CC pattern of expression. The methylation of the transposable element genes
 CC is monitored by enzymatic means, microarray analysis, or methylation-
 CC specific PCR. The methylation pattern is determined by microarray
 CC analysis. The methods of the invention are useful for assigning an
 CC expression pattern of transposable elements to the level of developmental
 CC potential of a cell. This sequence represents an oligonucleotide
 CC identifier of a retroelement consensus sequence.
 XX
 SQ Sequence 50 BP; 8 A; 22 C; 6 G; 14 T; 0 U; 0 Other;
 QY Query Match 79.0%; Score 15.8; DB 13; Length 50;
 DB Best Local Similarity 89.5%; Pred. No. 3.1e+03;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGCAGCGCGCAGAGAGC 20
 |||||
 DB 26 GAGCAGCGCGAGAGAGC 8

RESULT 5
 ADU22300/c
 ID ADU22300 standard; DNA; 50 BP.
 XX

AC ADU22300;
 XX 27-JAN-2005 (first entry)
 DT
 XX Human transposable element representative sequence, SEQ ID 303.
 DE
 XX Human transposable element; DNA methylation; chromatin; cancer;
 KM LINE; long interspersed nuclear element; SINE;
 KM short interspersed nuclear element; HERV; human endogenous retrovirus;
 XX microarray.
 OS Homo sapiens.
 XX
 OS WO2004096021-A2.
 XX 11-NOV-2004.
 PD 29-APR-2004; 2004WO-US013522.
 XX 29-APR-2004; 2004WO-US013522.
 PR 29-APR-2003; 2003US-0466798P.
 XX (UYGE-) UNIV GEORGIA RES FOUND INC.
 PA Mcdonald JF;
 XX Mcdonald JF;
 PI WPI; 2004-804580/79.
 DR WPI; 2004-804580/79.
 XX
 PT Determining expression, methylation or chromatin status pattern of
 PT families of transposable elements in a sample e.g. for diagnosing cancer,
 PT comprises determining the expression, methylation or chromatin status of
 PT the elements.
 XX
 PS Disclosure; SEQ ID NO 303; 68pp; English.
 XX
 CC The invention relates to determining expression, methylation or chromatin
 CC status pattern of one or more families of transposable elements in a
 CC sample comprises determining expression, methylation or chromatin status
 CC of one or more families of transposable elements. Also included are a
 CC method of assigning an expression pattern of transposable elements to a
 CC type of cancerous cell in a sample, a method of diagnosing cancer, a
 CC method of determining the effectiveness of an anti-cancer therapeutic in
 CC a subject, a method of assigning a methylation pattern of one or more
 CC families of transposable elements to a type of cancerous cell in a sample
 CC and a method of assigning a chromatin status pattern of transposable
 CC elements to a type of cancerous cell in a sample. The method is useful in
 CC determining an expression, methylation or chromatin status pattern of one
 CC or more families of transposable elements (e.g. LINE, long interspersed
 CC nuclear element, SINE, short interspersed nuclear element, or HERV, human
 CC endogenous retrovirus) in a sample for diagnosing cancer or determining
 CC the effectiveness of an anti-cancer therapeutic. The present sequence is
 CC a representative sequence for a human transposable element, used in a
 CC microarray to study the expression, methylation or chromatin status
 CC pattern of the transposable elements.
 XX
 SQ Sequence 50 BP; 8 A; 22 C; 6 G; 14 T; 0 U; 0 Other;
 QY Query Match 79.0%; Score 15.8; DB 13; Length 50;
 DB Best Local Similarity 89.5%; Pred. No. 3.1e+03;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGCAGCGCGCAGAGAGC 20
 |||||
 DB 26 GAGCAGCGCGAGAGAGC 8

RESULT 6
 ABK76729
 ID ABK76729 standard; DNA; 99 BP.
 XX
 AC ABK76729;
 XX 13-AUG-2002 (first entry)
 DT
 XX

DE	Bacillus licheniformis genomic sequence tag (GST) #4020.
XX	
KM	Differential gene expression; genomic sequenced tag; GST;
KW	altered culture condition; environmental stress;
KW	physiological provocation; ds.
XX	
OS	Bacillus licheniformis.
XX	
FN	WO200229113-A2.
XX	
PD	11-APR-2002.
XX	
PF	05-OCT-2001; 2001WO-US031437.
XX	
PR	06-OCT-2000; 2000US-00680598.
PR	27-MAR-2001; 2001US-02795269.
XX	
PA	(NOVO) NOVOZYMES BIOTECH INC.
XX	(NOVO) NOVOZYMES AS.
XX	
PI	Berka R, Clausen IG;
XX	
DR	WPI, 2002-416684/44.
XX	
PT	Monitoring differential expression of several genes in first Bacillus
PT	cell relative to expression of same genes in one or more second Bacillus
PT	cells, by using substrate containing Bacillus genomic sequenced tag
PT	array.
XX	
PS	Claim 4; SEQ ID NO 4020; 200pp; English.
XX	
CC	The invention describes a method of monitoring differential expression of
CC	genes in a first Bacillus cell relative to expression of the genes in
CC	other Bacillus cells, comprising hybridising labelled nucleic acid probes
CC	isolated from Bacillus cells to a substrate containing array of Bacillus
CC	genomic sequenced tags (GST), examining the array, and determining
CC	relative gene expression by an observed hybridisation reporter signal of
CC	a spot in the array. The method is useful for measuring the expression of
CC	genes in a first Bacillus cell relative to expression of the same genes
CC	in one or more second Bacillus cells. The method is useful for monitoring
CC	global expression of several genes from a Bacillus cell, discovering new
CC	genes, identifying possible functions of unknown open reading frames and
CC	monitoring gene copy number variation and stability. Monitoring changes
CC	in expression of genes may be used to provide a representation of the way
CC	in which Bacillus cells adapt to changes in culture conditions,
CC	environmental stress or other physiological provocation. Extensive follow
CC	up characterisation is unnecessary, when one spot on an array equals one
CC	gene or one open reading frame, since sequence information is available.
CC	This sequence represents a genomic sequence tag (GST) used in the method
CC	of the invention. Note: The sequence data for this patent did not form
CC	part of the printed specification, but was obtained in electronic format
CC	directly from WIPD at fcp.wipo.int/pub/published_pct_sequences
XX	
XX	
SO	Sequence 99 BP; 32 A; 26 C; 20 G; 20 T; 0 U; 1 Other;
Query Match	77.0%; Score 15.4; DB 6; Length 99;
Best Local Similarity	94.1%; Pred. No. 4.5e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0	
QY	4 GCACGCCGACGAGAGC 20
Db	31 GCACGCCGACGAGAGC 47
RESULT 7	
ABK27825	ABK27825 standard; DNA; 27 BP.
XX	
AC	ABK27825;
XX	
DT	09-APR-2002 (first entry)
XX	
DE	Corn male reproductive tissue promoter, PCR primer #15.

XX	Corn; male reproductive tissue; promoter; plant; gene stacking;
KM	fertility; insect; pathogen; herbicide tolerance; primer; ss.
XX	
OS	Zea mays.
PN	MO200200905-A2.
XX	
PD	03-JAN-2002.
XX	
PF	26-JUN-2001; 2001WO-US020658.
XX	
PR	28-JUN-2000; 2000US-0214357P.
XX	
PA	(MONS) MONSANTO TECHNOLOGY LLC.
XX	
PI	Conner TW, Dubois P, Malven M, Masucci JD;
XX	
DR	WPI; 2002-147890/19.
XX	
PT	New plant regulatory sequences or promoters and nucleic acids encoding
PT	them, useful for regulating gene expression, especially in male
PT	reproductive tissues.
XX	
PS	Example 3; Page 96; 131pp; English.
XX	
CC	The invention relates to an isolated nucleic acid (I) promoter capable of
CC	regulating transcription of an operably linked DNA sequence. The promoter
CC	sequences may be used for selectively modulating expression of any
CC	operatively linked gene and provide additional regulatory element
CC	diversity in a plant expression vector in gene stacking approaches, and
CC	for regulating gene expression in male reproductive tissues or gene
CC	transcription of any target gene (e.g. for controlling fertility, insect,
CC	pathogen or herbicide tolerance). The nucleic acids are useful as
CC	hybridisation probes or primers in hybridisation assays of other plant
CC	tissues to identify closely related or homologous genes and associated
CC	regulatory sequences. ABK27808-ABK27918 represent corn male reproductive
CC	tissue promoter sequences and PCR primers of the invention
XX	
SO	Sequence 27 BP; 8 A; 6 C; 11 G; 2 T; 0 U; 0 Other;
	Query Match 76.0%; Score 15.2; DB 6; Length 27;
	Best Local Similarity 85.0%; Pred. No.5.6e+03;
	Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0
OY	1 CGAGCAGCGCGCAGAGGAGC 20
DB	7 CGAGGACGCGAGAGGATC 26
RESULT 8	
AA080520	
ID	AA080520 standard; DNA; 48 BP.
XX	
AC	AA080520;
XX	
DT	25-MAR-2003 (revised)
DT	03-OCT-2002 (revised)
DT	11-DEC-1990 (first entry)
XX	
DE	Synthetic oligonucleotide used in prodn. of hybrid gene.
XX	
XX	Synthetic oligonucleotide; hybrid gene; RESA 3'repeat;
KM	Plasmodium falciparum; malaria; vaccine.
XX	
OS	Synthetic.
XX	
FH	Key Location/Qualifiers
FT	1..24
FT	/*tag= a
FT	/note= "claimed peptide"
XX	
FN	WO8602757-A.

```

XX 21-APR-1988.
PD
XX
XX 16-OCT-1987; 87WO-AU000352.
PF
XX
XX 17-OCT-1986; 86AU-00008551.
PR
XX 17-OCT-1986; 87AU-00081506.
XX
PA (SARA-) SARAFANE PTY LTD.
PA (LANG/) LANGFORD C J.
XX
XX Langford CJ, Edwards SJ;
PI
XX WPI; 1988-119462/17.
DR
XX P-PSDB; AAP80519.
XX
PT New hybrid protein or polypeptide - contg. epitope(s) or mimotope(s) of
PT several antigens esp. useful as antimalarial vaccines.
XX
XX Disclosure; Page ?; 37pp; English.
PS
XX
XX Several antigens esp. useful as antimalarial antigens. The
CC oligonucleotide encodes an epitope of a P.falciparum antigen. The peptide
CC can be used in an antimalarial vaccine. (Updated on 03-OCT-2002 to add
CC missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 48 BP; 14 A; 12 C; 20 G; 2 T; 0 U; 0 Other;

Query Match 74.0%; Score 14.8; DB 1; Length 48;
Best Local Similarity 88.9%; Pred. No. 8.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGCACGGCGCAGAGAG 19
DB 13 GAGCACGACGCCGAGAG 30

RESULT 9
ADG69851
ID ADG69851 standard; DNA; 52 BP.
XX
XX ADG69851;
XX
XX 11-MAR-2004 (first entry)
DT
XX
XX Rat saliv transferase (RST) related PCR primer RST-FLB.
DE
XX
XX transgenic plant; ferulic acid esterase; FAE; enzyme; phenolic acid;
KW plant; cell wall; improved digestibility; biomass conversion;
KW highly fermentable carbohydrate; PCR primer; ss.
XX
XX Synthetic.
OS
XX Rattus sp.
XX
XX WO20026866-A1.
XX
XX 06-SEP-2002.
PD
XX
XX 16-NOV-2001; 2001WO-US043588.
PF
XX
XX 17-NOV-2000; 2000US-0249608P.
PR
XX
XX (GEMV ) GENENCOR INT INC.
PA
XX
XX Dunn-Coleman N, Langdon T, Morris P;
PI
XX WPI; 2002-698675/75.
DR
XX
XX New transgenic plant comprising an expression cassette with a promoter
PT operably linked to a ferulic acid esterase encoding polynucleotide,
PT useful in improving digestibility for livestock and enhancing biomass
PT conversion.
XX

```

```

PS Example 2; Page 34; 208pp; English.
XX
XX The present invention describes a transgenic plant (I) comprising an
CC expression cassette with a promoter operably linked to a ferulic acid
CC esterase encoding polynucleotide. Also described: (1) controlling (M1)
CC the level of phenolic acids in plant cell walls of a transgenic plant by
CC introducing into the plant an expression cassette comprising a promoter
CC operably linked to a ferulic acid esterase encoding polynucleotide; and
CC (2) a transgenic plant (II) produced by (M1). The transgenic plants are
CC useful in improving digestibility for livestock and enhancing biomass
CC conversion. The method is useful for enhancing the production of more
CC highly fermentable carbohydrates in plants, especially forage grasses.
CC The expression cassette is useful for controlling the level of phenolic
CC acids in plant cell walls of a transgenic plant. The present sequence is
CC used in the exemplification of the present invention.
XX
SQ Sequence 52 BP; 19 A; 6 C; 21 G; 6 T; 0 U; 0 Other;

Query Match 74.0%; Score 14.8; DB 6; Length 52;
Best Local Similarity 88.9%; Pred. No. 8.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGCACGGCGCAGAGAG 19
DB 6 GATCACGGCGAAGAGAG 23

RESULT 10
ADN88873
ID ADN88873 standard; DNA; 54 BP.
XX
XX ADN88873;
XX
XX 01-JUN-2004 (first entry)
DT
XX
XX RST-FLB PCR primer.
DE
XX
XX Transgenic plant; ferulic acid esterase; fermentable carbohydrate;
KW animal feed; phenolic acid; PCR; primer; ss.
XX
XX Synthetic.
OS
XX WO2003043411-A2.
XX
XX 30-MAY-2003.
PD
XX
XX 21-MAY-2002; 2002WO-US016239.
PF
XX
XX 16-NOV-2001; 2001US-00991209.
PR
XX 16-NOV-2001; 2001WO-US043588.
XX
XX (GEMV ) GENENCOR INT INC.
PA
XX
XX Dunn-Coleman N, Langdon T, Morris P;
PI
XX WPI; 2003-457563/43.
DR
XX
XX New transgenic plant comprising an expression cassette with a promoter
PT operably linked to ferulic acid esterase encoding polynucleotide, useful
PT for enhancing availability of fermentable carbohydrates as feed for grass
PT -fed animals.
XX
XX Example 2; Page 32; 190pp; English.
PS
XX
XX The present invention relates to transgenic plants comprising an
CC expression cassette having a promoter operably linked to a ferulic acid
CC esterase (FAE) encoding polynucleotide. The transgenic plants are useful
CC for enhancing the availability of fermentable carbohydrates as feed for
CC grass-fed animals. The methods are useful for reducing the levels of
CC phenolic acids in the cell walls available for cross-linking either by
CC directly disrupting ester bonds linking phenolics and lignins to cell
CC wall polysaccharides or by preventing excessive fermentation of cell wall
CC carbohydrates. The present sequence is a primer used to illustrate the

```

CC invention.
XX
SQ Sequence 54 BP; 19 A; 6 C; 21 G; 8 T; 0 U; 0 Other;
Query Match 74.0%; Score 14.8; DB 11; Length 54;
Best Local Similarity 88.9%; Pred. No. 8.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 GAGCAGCGCGCAGAGGAG 19
DB 6 GATCAGCGCGAAGAGGAG 23
RESULT 11
ACD74037
ID ACD74037 strand; DNA; 100 BP.
AC ACD74037;
XX
DT 18-SEP-2003 (first entry)
XX
DE E. coli K12 MG1655 biochip probe SEQ ID 5307.
XX
KW Biochip; gene expression; gut; diagnostic; detection; probe; ss.
XX
OS Escherichia coli.
XX
PN EP1260592-A1.
XX
PD 27-NOV-2002.
XX
PF 17-MAY-2001; 2001EP-00112179.
XX
PR 17-MAY-2001; 2001EP-00112179.
XX
PA (MMGB-) MMG-BIOTECH AG.
XX
PI Donner H, Drescher B, Huber A, Weber J;
XX
DR WPI; 2003-241155/24.
PT Biochip containing probes complementary with open reading frames in
PT Escherichia coli K12, useful for detecting gene expression and expression
PT patterns.
PS Claim 3; Page 833; 2004pp; German.
XX
CC This invention describes a novel biochip comprising probe spots, each
CC containing many identical probes. The probes are nucleotide sequences of
CC 30-80 bases, are prepared ex situ from synthetic oligonucleotides and at
CC least one includes a segment of at least 20 bases identical with, or
CC complementary to, a segment of an open reading frame (orf) of Escherichia
CC coli K12. The biochip is used for specific detection of gene expression
CC in K12 and for determining the gene expression pattern, e.g. for
CC diagnostic determination of which E. coli strains are present in the gut,
CC and to determine the effects of e.g. growth media on gene expression. The
CC biochip provides as comprehensive as possible detection of the K12
CC genome, with simultaneous analysis of many different genes with a single
CC device, and comparison of gene expression between K12 and its mutants or
CC other E. coli strains in a single experiment. Apart from qualitative and
CC quantitative information about gene expression, it also allows
CC measurements of population densities for the various strains. The use of
CC synthetic oligonucleotides for preparation of probes allows free
CC variation in probe length and ensures high purity (and thus selectivity,
CC reactivity and reproducibility); also synthetic probes are generally
CC shorter than probes prepared by polymerase chain reaction. ACD68731 to
CC ACD81540 represent oligonucleotide probes used with the biochip described
CC in the invention
XX
SQ Sequence 100 BP; 28 A; 24 C; 29 G; 19 T; 0 U; 0 Other;
Query Match 74.0%; Score 14.8; DB 8; Length 100;
Best Local Similarity 88.9%; Pred. No. 8e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 GAGCAGCGCGCAGAGGAG 19
DB 50 GAGCGCGCGCAGAGGAG 67
RESULT 12
ADC38589
ID ADC38589 strand; DNA; 20 BP.
AC ADC38589;
XX
DT 18-DEC-2003 (first entry)
XX
DE Translocation SBE primer SEQ ID 66.
XX
KW Chromosome translocation; cancer; leukaemia; lymphoma; SBE; primer; ss.
XX
OS Synthetic.
XX
PN WO2003044486-A2.
XX
PD 30-MAY-2003.
XX
PF 20-NOV-2002; 2002WO-US037507.
XX
PR 20-NOV-2001; 2001US-0335716P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Nolan JP, Zhou F;
XX
DR WPI; 2003-468806/44.
PT Detecting chromosome translocations in a target nucleic acid sequence for
PT diagnosing cancers associated with chromosome translocations, by using
PT microsphere arrays.
XX
PS Claim 52; Fig 10; 57pp; English.
XX
CC The present invention relates to a method (M) for detecting chromosome
CC translocation. The method comprises amplifying a target nucleic acid
CC sequence from a sample, hybridizing oligonucleotides (ONTs) specific for
CC regions of the translocation to the amplified target, where the ONTs
CC comprise capture tags, extending the ONTs to produce labelled extended
CC ONTs, hybridizing the ONTs to address tags on solid support and detecting
CC the presence of labelled extended ONTs on the solid support. (M) is
CC useful for detecting a chromosomal translocation in a target nucleic acid
CC sequence, preferably a cDNA from a biological sample from a human. The
CC chromosome translocation is associated with cancer (e.g. leukaemia) and
CC this method is especially useful for diagnosing cancer, especially
CC leukaemia, and also lymphoma. The present sequence is a primer for single
CC base extension (SBE) of the translocation oligonucleotides.
XX
SQ Sequence 20 BP; 7 A; 4 C; 8 G; 1 T; 0 U; 0 Other;
Query Match 72.0%; Score 14.4; DB 10; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.2e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 AGCAGCGCGCAGAGGA 18
DB 2 AGCAGCGAGCAGAGGA 17
RESULT 13
AAV40985
ID AAV40985 strand; DNA; 21 BP.
AC AAV40985;
XX
DT 25-SEP-1998 (first entry)

```

XX DE Primer TELML1:1216L21 for abnormality detection.
XX KM PCR primer: chromosomal abnormality; abnormality detection; leukaemia;
XX KM lymphoma; carcinoma; adenocarcinoma; sarcoma; glioma; neuroblastoma;
XX KM medullablastoma; malignant melanoma; malignant neoplastic condition; ss.
XX OS Synthetic.
XX OS Homo sapiens.
XX FN WO9824928-A2.
XX PD 11-JUN-1998.
XX PF 08-DEC-1997; 97WO-DK000556.
XX PR 06-DEC-1996; 96DK-00001401.
XX PA (PALL/) PALLISGAARD N.
XX PI Pallsgaard N, Hokland P;
XX DR WPI; 1998-333344/29.
XX PT Detection of chromosomal abnormalities - by subjecting patient sample
XX PT nucleic acids to a multiplex molecular amplification procedure using
XX PT primers specific for characteristic nucleic acid sequence.
XX PS Claim 73; Page 85; 126pp; English.
XX CC This sequence represents a primer used in the method of the invention for
XX CC the detection of the presence or absence of chromosomal abnormalities,
XX CC each abnormality being associated with a condition in a subject and each
XX CC method defined by at least one characteristic nucleic acid sequence. The
XX CC method comprises: (a) obtaining a sample of nucleic acids derived from a
XX CC subject which may harbour one of the chromosomal abnormalities; (b)
XX CC subjecting the sample to a multiplex molecular amplification (MMA)
XX CC procedure, where a number of the characteristic sequences, if present in
XX CC a sufficient amount, will be amplified; (c) retrieving the product(s)
XX CC from step (b), and detecting the presence and/or absence of an amplicon
XX CC characteristic of the abnormal sequences to detect the presence or
XX CC absence of corresponding chromosomal abnormalities; where the MMA
XX CC procedure comprises the use of at least 7 mutually distinct primers (MDP)
XX CC in one single reaction mixture, each of the primers defining an end of at
XX CC least one characteristic nucleic acid sequence, and where at least one of
XX CC the primers defines the first end of at least two characteristic nucleic
XX CC acid sequences, the characteristic nucleic acid sequences each being
XX CC determined in their opposite ends by MDP selected from the remainder of
XX CC the MDP. The method can be used for detecting chromosomal abnormalities
XX CC associated with diseases including numerous leukaemia's, lymphoma's,
XX CC carcinoma's, adenocarcinoma's, sarcoma's, glioma's, neuroblastoma's,
XX CC medullablastoma, malignant melanoma, and malignant neoplastic conditions
XX SQ Sequence 21 BP; 7 A; 3 C; 9 G; 2 T; 0 U; 0 Other;
XX
XX Query March 72.0%; Score 14.4; DB 2; Length 21;
XX Best Local Similarity 93.8%; Pred. No. 1.2e+04;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 3 AGCAGCGCGCAGAGGA 18
XX DB 1 AGCAGCGCGCAGAGGA 16
XX
XX RESULT 14
XX ABR8264/c
XX ID ABR8264 standard; DNA; 21 BP.
XX AC ABR8264;
XX XX 07-OCT-2002 (first entry)
XX DT
XX EX Exon 2 (alpha domain) of chicken class I gene PCR primer RV69BL.

```

```

XX KM Chicken: exon 2; alpha domain; class I gene; Rfp-Y; B-F; B-L; B-G;
XX KM major histocompatibility complex; MHC; domesticated fowl;
XX KM Marek's disease; genetic disease resistance; PCR; primer; ss.
XX OS Gallus sp.
XX PN US2002083482-A1.
XX PD 27-JUN-2002.
XX PF 22-JUN-2001; 2001US-00886607.
XX PR 19-JUL-2000; 2000US-00619758.
XX PA (MILL/) MILLER M M.
XX PA (BRIL/) BRILES W E.
XX PA (AFAN/) AFANASSIEFF M.
XX PI Miller MM, Briles WE, Afanasieff M;
XX DR WPI; 2002-557335/59.
XX PT Determining the major histocompatibility complex genotypes of a
XX PT domesticated fowl useful for selecting fowl, particularly chickens,
XX PT genetically resistant to a variety of diseases, particularly Marek's
XX PT disease.
XX PS Claim 14; Page 7; 22pp; English.
XX CC The present invention relates to a new method for determining the major
XX CC histocompatibility complex (MHC) genotypes of a domesticated fowl. The
XX CC method of the invention involves amplifying and denaturing nucleic acid
XX CC from the fowl which contains a region with a sequence corresponding to an
XX CC Rfp-Y, B-F, B-L or B-G region of the genome and separating the denatured
XX CC products electrophoretically to produce a pattern characteristic to the
XX CC genotype of the fowl. The method is useful for determining the MHC
XX CC genotypes of domestic fowl. The method may be used to select for domestic
XX CC fowl, particularly chickens, genetically resistant to a variety of
XX CC diseases, particularly Marek's disease. The methods of the invention are
XX CC useful for producing offspring that carry genetic resistance to disease.
XX CC The present nucleic acid sequence represents an exon 2 (alpha domain) of
XX CC chicken class I gene PCR primer that was used in the methods of the
XX CC invention for MHC genotyping.
XX SQ Sequence 21 BP; 4 A; 7 C; 6 G; 4 T; 0 U; 0 Other;
XX
XX Query March 72.0%; Score 14.4; DB 6; Length 21;
XX Best Local Similarity 93.8%; Pred. No. 1.2e+04;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 5 CACGCGCGCAGAGGAGC 20
XX DB 16 CACGCGCGCAGAGGAGC 1
XX
XX RESULT 15
XX AAD29196/c
XX ID AAD29196 standard; DNA; 21 BP.
XX AC AAD29196;
XX XX 07-MAY-2002 (first entry)
XX DT
XX DE Fowl MHC B class II-beta genotype analysing PCR primer, RV69BL.
XX KM Fowl; haplotyping; breeding; domesticated fowl; disease resistance;
XX KM major histocompatibility; MHC; Marek's disease; PCR primer; ss.
XX OS Gallus sp.
XX XX WO200206535-A2.
XX PN
XX EX

```

```

PD 24-JAN-2002.
XX
XX 19-JUL-2001; 2001WO-US022519.
XX
XX 19-JUL-2000; 2000US-00619758.
XX
XX (CITY ) CITY OF HOPE.
XX
XX Miller MM, Afanasieff M, Briles WE;
XX
XX WPI, 2002-171822/22.
XX
XX Determining major histocompatibility complex genotypes of domesticated
XX fowl for breeding disease resistant fowl by comparing B and Rfp-Y systems
XX of genome from the fowl to corresponding known genotypes.
XX
XX Claim 14; Page 16; 37pp; English.
XX
XX The invention relates to a method for haplotyping and breeding
XX domesticated fowl for increased disease resistance. Disease resistance in
XX domesticated fowl has been associated with the B and Rfp-Y systems of
XX major histocompatibility (MHC) genes. The method is useful for
XX determining the Mhc genotypes of a domesticated fowl. The method is
XX useful in selecting domesticated fowl which are resistant to a
XX preselected disease preferably Marek's disease by determining a genotype
XX of Rfp-Y, B-F, B-L or B-G genes of the domesticated fowl, correlating the
XX determined genotypes with resistance to the preselected disease and
XX selecting a domesticated fowl having a determined genotype which
XX correlates with resistance to the preselected disease. The method is also
XX useful for breeding domesticated fowl to produce an offspring resistant
XX to a preselected disease by selecting a first domesticated fowl of a
XX gender which is resistant to a preselected disease, and mating the first
XX domesticated fowl with a second domesticated fowl of the opposite gender
XX to produce offspring. The present sequence is a PCR primer used for
XX genotyping fowl Mhc region
XX
XX Sequence 21 BP; 4 A; 7 C; 6 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 72.0%; Score 14.4; DB 6; Length 21;
XX Best Local Similarity 93.8%; Pred. No. 1.2e+04;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 5 CACGGCGCAGAGAGC 20
XX ||||| |||||
XX 16 CACGGTGCAGAGAGC 1
XX

```

Search completed: December 24, 2005, 12:28:52
 Job time : 173.4 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 10:37:31 ; Search time 1572 Seconds
(without alignments)
595.256 Million cell updates/sec

Title: US-09-296-264-2

Perfect score: 20

Sequence: 1 cgagcagcgscgacagagagc 20

Scoring table: IDENTITY_NUC

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 768474

Minimum DB seq length: 20
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18.4	92.0	94	1	AA197619
2	15.8	79.0	52	1	AM693858
3	15.8	79.0	95	10	CM456343
4	15.2	76.0	55	2	BI250613
5	15.2	76.0	90	2	BI104703
6	15.2	76.0	100	7	CF954727
7	15.2	76.0	100	11	CL954628
8	14.8	74.0	96	11	GA270142
9	14.4	72.0	68	7	CV304081
10	14.4	72.0	87	4	AK185845
11	14.4	72.0	100	10	AG195654
12	14.2	71.0	55	9	BH643795
13	14.2	71.0	79	3	BQ167594
14	14.2	71.0	84	7	CO911144
15	14.2	71.0	95	10	CM118187
16	13.8	69.0	40	10	CG715520
17	13.8	69.0	62	10	CG650832
18	13.8	69.0	63	10	CG728306
19	13.8	69.0	92	9	AZ595307
20	13.8	69.0	93	11	CNS03900
21	13.8	69.0	95	9	BH173450
22	13.8	69.0	98	3	BI768381

23	13.6	68.0	46	1	AA008276
24	13.6	68.0	50	1	AU104090
25	13.6	68.0	67	10	BX987261
26	13.6	68.0	69	8	CK943799
27	13.6	68.0	71	10	CM115297
28	13.6	68.0	72	6	CD949020
29	13.6	68.0	74	7	CV589750
30	13.6	68.0	75	10	CL266096
31	13.6	68.0	81	3	BM490089
32	13.6	68.0	81	9	BH849516
33	13.6	68.0	86	9	BH796584
34	13.6	68.0	87	9	AZ918012
35	13.6	68.0	88	10	CZ233884
36	13.6	68.0	91	10	CG785229
37	13.6	68.0	93	5	B0564305
38	13.6	68.0	95	4	AK189242
39	13.6	68.0	100	6	CB212828
40	13.4	67.0	25	9	AZ374695
41	13.4	67.0	47	10	BX224384
42	13.4	67.0	74	1	AA492659
43	13.4	67.0	88	1	AA574321
44	13.2	66.0	23	6	CF277473
45	13.2	66.0	38	10	CZ551355

ALIGNMENTS

RESULT 1
LOCUS AA197619 94 bp mRNA linear EST 19-FEB-1997
DEFINITION mu19a03.r1 Soares_thymus_2NBWT Mus musculus cDNA clone IMAGE:639820
5', mRNA sequence.
ACCESSION AA197619 GI:1793270
VERSION AA197619.1 GI:1793270
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 94)
REFERENCE Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Stepcoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
AUTHORS The WashU-HMNI Mouse EST Project
TITLE Unpublished (1996)
JOURNAL Contact: Marra M/Mouse EST Project
COMMENT WashU-HMNI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LBNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:391812
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 81.
Location/Qualifiers
1..94
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:639820"
/sex="male"
/issue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
/clone_1lb="Soares_thymus_2NBWT"

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Sciurognathi; Muroidae; Muridae; Murinae; Mus.
1 (bases 1 to 55)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Source
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLM11369 row: g column: 20
High quality sequence start: 2
High quality sequence stop: 55.
Location/Qualifiers
1..55
/organism="Mus musculus"
/mol_type="mRNA"
/strain="mix FVB/N, C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:5149483"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Mam5"
/note="Organ: mammary; Vector: PCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"

ORIGIN

Query Match 76.0%; Score 15.2; DB 2; Length 55;
Best Local Similarity 85.0%; Pred. No. 3.4e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGAGCAGCGCCGACAGAGC 20
|||
DB 41 CGGCACGCGACGACGAC 22

RESULT 5
BI04703/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BI104703 90 bp mRNA linear EST 26-JUN-2001
602891614F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5036690 5',
mRNA sequence.
BI104703
BI104703.1 GI:14555596
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Mus.
1 (bases 1 to 90)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLM11101 row: 1 column: 03
High quality sequence stop: 90.
Location/Qualifiers

FEATURES

source

1..90
/organism="Mus musculus"
/mol_type="mRNA"
/strain="Czech II"
/db_xref="taxon:10090"
/clone="IMAGE:5036690"
/tissue_type="spontaneous tumor, metastatic to mammary.
stem cell origin"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Lu29"
/note="Organ: lung; Vector: PCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Gilbert Smith, NIH"

ORIGIN

Query Match 76.0%; Score 15.2; DB 2; Length 90;
Best Local Similarity 85.0%; Pred. No. 3.4e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGAGCAGCGCCGACAGAGC 20
|||
DB 75 CGGCACGCGACGACGAC 56

RESULT 6
CP954727 100 bp mRNA linear EST 15-JAN-2004
5246r1c1cb.10479.y1 Oryza sativa cv. PA64s leaf cDNA library Oryza
sativa (indica cultivar-group) cDNA 5', mRNA sequence.
CP954727
CP954727.1 GI:36470596
EST.
Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretoidae; Oryzaceae; Oryza.
1 (bases 1 to 100)
YU,J., Wang,J., Lin,W., Li,S., Li,H., Zhou,J., Ni,P., Dong,W.,
Hu,S., Zeng,C., Zhang,J., Zhang,Y., Li,R., Xu,Z., Li,S., Li,X.,
Zheng,H., Cong,L., Lin,L., Yin,D., Geng,J., Li,G., Shi,J., Liu,J.,
Lv,H., Li,J., Wang,J., Deng,Y., Ran,L., Shi,X., Wang,X., Wu,O.,
Li,C., Ren,X., Wang,J., Wang,X., Li,D., Liu,D., Zhang,X., Ji,Z.,
Zhao,W., Sun,Y., Zhang,Z., Bao,J., Han,Y., Dong,L., Ji,J., Chen,P.,
Wu,S. and Liu,J.
The Genomes of Oryza sativa: A History of Duplications
PLoS Biol. 3 (2), e38 (2005)
15685292
Contact: Yan Zhou
Bioinformatics Department
Hangzhou Genomics Institute
No.51 ZhiJiang Road, Hangzhou 310008, China
Tel: 86-571-56805886
Fax: 86-571-56805884
Email: zhouyan@genomics.org.cn
Seq primer: M13 Forward
High quality sequence stop: 100
POLYA=yes.
Location/Qualifiers
1..100
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="mRNA"
/cultivar="PA64s"
/db_xref="taxon:39946"
/tissue_type="leaf"
/dev_stage="trifoli"
/clone_lib="Oryza sativa cv. PA64s leaf cDNA library"

FEATURES
source

ORIGIN
Query Match 76.0%; Score 15.2; DB 7; Length 100;
Best Local Similarity 85.0%; Pred. No. 3.4e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CGAGCAGCGCGCAGAGAGC 20
|||||
48 CGAGCAGCGAGAGAGAGAGC 67

RESULT 7
LOCUS CL954628

DEFINITION OsrRUA002883 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.

ACCESSION CL954628

VERSION CL954628.1 GI:52366637

KEYWORDS GSS.

SOURCE Oryza sativa (indica cultivar-group)

ORGANISM Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 100)
Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M., Zhao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L., Wong, G., K. S., Deng, X. W., and Wang, J.
An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis
Unpublished (2004)
Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80486756
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.

FEATURES
source
1..100
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="genomic DNA"
/db_xref="taxon:39946"
/clone_lib="Oryza sativa Express Library"
/note="Oryza sativa exon trapped genomic sequences"

ORIGIN

Query Match 76.0%; Score 15.2; DB 10; Length 100;
Best Local Similarity 85.0%; Pred. No. 3.4e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CGAGCAGCGCGCAGAGAGC 20
|||||
48 CGAGCAGCGAGAGAGAGAGC 67

Db

RESULT 8
GGA270142/c 96 bp DNA linear GSS 08-JUL-2000

LOCUS

DEFINITION Gallus gallus anonymous sequence from Cosmid mapping to chromosome 5 (Cosmid 27 - Contig 43), genomic survey sequence.

ACCESSION AJ231913.1 GI:3451731

VERSION

KEYWORDS GSS; genome survey sequence.

SOURCE Gallus gallus (chicken)

ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 96)
Smith, J., Bruley, C. K., Paton, I. R., Dunn, I., Jones, C. T., Windsor, D., Morris, R., and Burt, D. W., Masabanda, J., Saranov, A., Waddington, D., Fries, R., and Burt, D. W.
Differences in gene density on chicken macrochromosomes and microchromosomes
Anim. Genet. 31 (2), 96-103 (2000)

JOURNAL

PUBMED 10782207

REFERENCE 2 (bases 1 to 96)
Smith, J., Bruley, C. K., Paton, I. R., Law, A. S., Masabanda, J., Waddington, D., Fries, R., and Burt, D. W.

TITLE Direct Submission (12-AUG-1998) Division of Molecular Biology, Roslin Institute, Roslin, Midlothian EH25 9PS, Scotland, UK

JOURNAL

FEATURES
source
1..96
/organism="Gallus gallus"
/mol_type="genomic DNA"
/db_xref="taxon:9031"
/chromosome="5"
/map="5q"

ORIGIN

Query Match 74.0%; Score 14.8; DB 11; Length 96;
Best Local Similarity 88.9%; Pred. No. 5e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AGCAGCGCGCAGAGAGC 20
|||||
36 AGCAGCGAGCAGAGAGC 19

Db

RESULT 9
CV304081 68 bp mRNA linear EST 23-SEP-2004

LOCUS t988d01.g7 Mouse 5' RACE clones Mus musculus cDNA 5', mRNA sequence.

ACCESSION CV304081

VERSION CV304081.1 GI:52621414

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 68)
Dike, S., Ballja, V. S., Nascimento, L. U., Xuan, Z., Ou, J., Zutavern, T., Palmer, L. B., Hannon, G., Zhang, M. O., and McCombie, W. R.
The mouse genome: Experimental examination of gene predictions and transcriptional start sites
Genome Res. 14 (12), 2424-2429 (2004)

JOURNAL

PUBMED 15574821

CONTACT: Ballja VS
McCombie Laboratory
Cold Spring Harbor Laboratory
500 Sunnyside Blvd, Woodbury, NY 11797, USA
Fax: 516 422 4109
Email: ballja@cshl.org.

FEATURES
source
1..68
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone_lib="Mouse 5' RACE clones"
/note="Vector: PCR-TOPO2.1; Cloned 5' RACE fragments amplified from 5' RACE cDNA generated from 15 pooled mouse tissues and stages: 7, 11, 15, & 17-day total embryo, whole brain, eye, kidney, liver, lung, prostate, submaxillary gland, smooth muscle, spleen, testes and uterus."

ORIGIN

Query Match 72.0%; Score 14.4; DB 7; Length 68;
Best Local Similarity 93.8%; Pred. No. 7.5e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 AGCAGCGCGCAGAGAGC 18
|||||
35 AGCAGCGCAGAGAGC 20

Db

RESULT 10
AK185845/c
LOCUS
DEFINITION
AK185845
Mus musculus cDNA, clone: Y060135G22, strand: minus,
reference: ENSEMBL: Mouse-Transcript-ENST: ENSMUST0000070400, based
on BLAT search.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
COMMENT

AK185845.1 GI:56010022
HTC; ASSETS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
Watabiki, A., Waki, K., Hayatsu, N., Shiraki, T., Kondo, S.,
Nakamura, M., Sasaki, D., Arakawa, T., Kawai, J., Harbers, M.,
Hayashizaki, Y., and Carninci, P.
Libraries enriched for alternatively spliced exons reveal splicing
patterns in melanocytes and melanomas
Nat. Methods 1, 233-239 (2004)
2 (bases 1 to 87)
Arakawa, T., Carninci, P., Fukuda, S., Harbers, M., Hayatsu, N.,
Hori, F., Imotani, K., Kawai, J., Kondo, S., Murata, M., Nakamura, M.,
Nomura, K., Ohno, M., Sasaki, D., Shiraki, T., Waki, K., Watabiki, A. and
Hayashizaki, Y.
Direct Submission
Submitted (15-SEP-2004) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsunumi-ku, Yokohama,
Kanagawa, 230-0045, Japan (E-mail: genome-res@gs.c.riken.jp,
URL: http://genome.gsc.riken.jp, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
Alternative Splicing Libraries (ASLs) are prepared by: Preparing
of single-stranded DNA using a RNA template from full length cDNA
libraries, hybridizing of
single-stranded DNAs, removing of remaining single-stranded DNA,
digesting of regions comprising double-stranded DNA by a set of 4
bp-cutters, capturing of DNA hybrids with loop structures
(alternative spliced exon), ligation of Y-shaped primers to
isolated DNA hybrids with loop structures, PCR amplification of
ligation products and their cloning into pUC1 vector. (Reference).
Location/Qualifiers
1..87
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="Y060135G22"
/cell_line="mixture of B16-F10Y and melan-c"
/cell_type="mixture of melanoma cell and melanocyte cell"
/clone_lib="Alternative Splicing Library L2"
/note="strand: minus, reference: ENSEMBL: Mouse-Transcript-
ENST: ENSMUST0000070400, based on BLAT search"

ORIGIN
Query Match 72.0%; Score 14.4; DB 4; Length 87;
Best Local Similarity 93.8%; Pred. No. 7.5e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 3 AGCAGCGCGCAGAGGA 18
|||||
65 AGCAGCGAGCAGAGGA 50
|||||

RESULT 11
LOCUS
DEFINITION
SEQUENCE
ACCESSION
VERSION
AG195654
AG195654
AG195654.1 GI:45227830

AG195654
Pan troglodytes DNA, clone: RP43-074N17.T7, genomic survey
sequence.

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

GSS.
Pan troglodytes (chimpanzee)
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Pan.
1
Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
BAC end sequences of library RP-43
Unpublished
2 (bases 1 to 100)
Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
Direct Submission
Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
Bioscience and Biotechnology (KRIIB), Genome Research Center (GRC);
52, Oun-dong, Yuseong-gu, Daejeon 305-333, Korea
(E-mail: redstone@mail.kribb.re.kr, URL: http://phs.grc.kribb.re.kr/
Tel: 82-42-866-7181, Fax: 82-42-866-4409)
Clones are derived from the chimpanzee BAC library RP-43 This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.
PRIMERS
Sequencing: T7
LIBRARY
Vector : pBAC3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
Location/Qualifiers
1..100
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-074N17.T7"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RP-43 Chimpanzee Male BAC Library"

ORIGIN
Query Match 72.0%; Score 14.4; DB 10; Length 100;
Best Local Similarity 93.8%; Pred. No. 7.5e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 2 GAGCAGCGCGCAGAGG 17
|||||
43 GAGCAGCGCGCAGTGG 58
|||||

RESULT 12
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BH643795/c
1008060C01.2EL.Y1 1008 - Rescuedu Grid I Zea mays genomic, genomic
survey sequence.
BH643795
BH643795.1 GI:18672592
GSS.
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 55)
Walbot, V.
Maize genomic sequences found using engineered Rescuedu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1008060 row: 21
Class: transposon-tagged.

FEATURES

source

```
1..55
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/Al88/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1008 - RescueMu Grid I"
/note="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site_1: BamHI; Site_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site www.zmhd.iastate.edu and follow the links for 'RescueMu.' Grid I was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
```

ORIGIN

Query Match 71.0%; Score 14.2; DB 9; Length 55;
Best Local Similarity 84.2%; Pred. No. 9.2e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGCAGCGCGCAGAGGAGC 20
|||||
35 GAGCAGCGCAGCAGCGAGC 17

RESULT 13
B0167594/c 79 bp mRNA linear EST 20-MAY-2003

LOCUS WHE0077_H03_P05ZK Cheyenne wheat endosperm cDNA library Triticum aestivum
B0167594
B0167594.1 GI:20312113

VERSION
B0167594.1 GI:20312113
EST

KEYWORDS
Triticum aestivum (bread wheat)

SOURCE

ORGANISM
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE
1 (bases 1 to 79)
Altenbach, S., Anderson, O.D., Chao, S., Crossman, C., Galili, G.,

AUTHORS
Laudencia-Chinguanco, D., Lazo, G.R., Rausch, C.U., Stamova, B. and Vela, S.

TITLE
The structure and function of the expressed portion of the wheat genomes - Cheyenne endosperm cDNA library

JOURNAL
Unpublished (2003)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818

COMMENT
Email: oanderson@w.usda.gov
This EST was generated by sequencing from the 3' end of the clone. Sequences have been trimmed to remove vector sequence and low quality sequence with phred score less than 20.

Seq primer: Stratagene's KS primer.

location/Qualifiers
1..79

FEATURES
source
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Cheyenne"

```
/db_xref="taxon:4565"
/clone="WHE0077_H03_P05"
/tissue_type="Cheyenne endosperm"
/dev_stage="5 -30 days post anthesis seed"
/lab_host="E. coli SOLR"
/clone_lib="Cheyenne wheat endosperm cDNA library"
/note="Vector: Lambda ZAP II, excised phagemid; Site_1: EcoRI; Seeds collected, Cheyenne endosperm isolated, and RNA prepared by Susan Altenbach. Library constructed by Stratagene, Inc. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab."
```

ORIGIN

Query Match 71.0%; Score 14.2; DB 3; Length 79;
Best Local Similarity 84.2%; Pred. No. 9.2e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGCAGCGCGCAGAGGAGC 20
|||||
58 GAGCGCGCGCAGAGGAGC 40

RESULT 14
C0911144

LOCUS C0911144 84 bp mRNA linear EST 16-AUG-2004
DEFINITION BJ03015E02 BJ03 Capsicum annuum cDNA 5', mRNA sequence.
C0911144
C0911144.1 GI:51301447

VERSION
C0911144.1 GI:51301447
EST

KEYWORDS
Capsicum annuum
Capsicum annuum

SOURCE

ORGANISM
Capsicum annuum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Solanales; Solanaceae; Capsicum.

REFERENCE
1 (bases 1 to 84)
Song, W.Y., Jeon, W.B., Kim, K.S., Lee, H.H., Ko, M.K., Kim, Y.S.,

AUTHORS
Hong, J.C. and Oh, B.J.

TITLE
Generation of Hot Pepper (Capsicum annuum) ESTs (Express Sequence Tags) from Red Ripe Fruit (Song, et al.)

JOURNAL
Unpublished (2004)

COMMENT
Contact: Boun-Jun Oh
Jeonnam Biotechnology Research Center
Namyang Bld. #603, 10-4 Gwangsan-dong, Dong-gu, Gwangju 501-180, Korea

Tel: 82 62 607 2422

Fax: 82 62 607 6205

Email: bj@biohub.re.kr

Plate: 015 row: B column: 02.

location/Qualifiers

FEATURES

source

```
1..84
/organism="Capsicum annuum"
/mol_type="mRNA"
/cultivar="Nokkwang"
/db_xref="taxon:4072"
/tissue_type="red pepper fruit pericarp"
/clone_lib="BJ03"
/note="Vector: pBluescript II SK(+), Site 1: EcoRI; Site 2: XhoI; cDNA library was generated from red ripe fruit pericarp using lambda ZAP II phage vector. In vivo excision was done with helper phage to generate subclone in pBluescript II SK(+), vector."
```

ORIGIN

Query Match 71.0%; Score 14.2; DB 7; Length 84;
Best Local Similarity 84.2%; Pred. No. 9.2e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGAGCAGCGCGCAGAGGAG 19
|||||
64 CGAGCAGCGCAGAGGAG 82

RESULT 15

CW118187/c 95 bp DNA linear GSS 29-OCT-2004
 LOCUS 104 494 11108068 148 34621 006 Sorghum methylation filtered library
 DEFINITION (LibID:104) Sorghum bicolor genomic clone 11108068, genomic survey
 sequence.
 ACCESSION CW118187
 VERSION CW118187.1 GI:54810734
 KEYWORDS GSS.
 SOURCE Sorghum bicolor (sorghum)
 ORGANISM Sorghum bicolor (sorghum)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Sorghum.
 1 (bases 1 to 95)
 Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
 Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
 McNameamy,J., Smith,M., Holman,H., Roe,B.A., Wiley,G., Korf,I.F.,
 Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
 Martienssen,R.A.
 Sorghum genome sequencing by methylation filtration
 PLOS Biol. 3 (1), e13 (2005)
 15660154
 TITLE Sorghum genome sequencing by methylation filtration
 JOURNAL
 PUBMED
 COMMENT
 Contact: Bedell JA
 Orion Genomics, LLC
 4041 Forest Park Ave, St. Louis, MO 63108, USA
 Tel: 314 615 6979
 Fax: 314 615 5975
 Email: jbedell@oriongenomics.com
 Plate: 494 row: k column: 04
 Seq primer: SWfor Forward
 Class: methylation filtered
 High quality sequence stop: 95.
 Location/Qualifiers
 1..95
 /organism="Sorghum bicolor"
 /mol_type="genomic DNA"
 /cultivar="Atk623"
 /db_xref="taxon:4558"
 /clone="11108068"
 /clone_lib="Sorghum methylation filtered library (LibID:
 104)"
 /note="Organ: leaf; Vector: pBCSK(-); Site 1: HincII; DNA
 prepared from purified nuclei was randomly sheared,
 end-repaired, size fractionated to enrich for the 0.5 to 5
 kb fraction, ligated into HincII-digested pBCSK(-) vector
 and electroporated into E. coli cells. This is a
 methylation filtered library."
 ORIGIN
 Query Match 71.0%; Score 14.2; DB 10; Length 95;
 Best Local Similarity 84.2%; Pred. No. 9.2e+04;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 GAGCAGCGCGCAGAGAGC 20
 |||||
 Db 59 GGGCAGCGCTCACAGAGC 41
 |||||

Search completed: December 24, 2005, 18:28:16
 Job time : 1576 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 11:34:25 : Search time 48.1 Seconds
(without alignments)
739.111 Million cell updates/sec

Title: US-09-296-264-2

Perfect score: 20
Sequence: 1 cgcagcagcgagcagagc 20

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1134872

Minimum DB seq length: 20
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/1 COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5 COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6 COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6 COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/6 COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/PCUS COMB.seq:*
- 7: /cgn2_6/ptodata/1/ina/PCUS COMB.seq:*
- 8: /cgn2_6/ptodata/1/ina/RE COMB.seq:*
- 9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
C 1	14.4	72.0	21 3 US-09-619-758-14	Sequence 14, Appl
C 2	14.4	72.0	21 3 US-09-886-607-14	Sequence 14, Appl
C 3	14.2	71.0	25 3 US-09-396-196G-65948	Sequence 65948, A
4	14.2	71.0	25 3 US-09-396-196G-65949	Sequence 65949, A
5	14.2	71.0	25 3 US-09-396-196G-65950	Sequence 65950, A
6	14.2	71.0	25 3 US-09-396-196G-65951	Sequence 65951, A
7	14.2	71.0	25 3 US-09-396-196G-71454	Sequence 71454, A
C 8	14.2	71.0	25 3 US-09-396-196G-71470	Sequence 71470, A
C 9	14.2	71.0	25 3 US-09-396-196G-71471	Sequence 71471, A
10	14.2	71.0	51 3 US-09-443-199C-753	Sequence 753, App
11	13.8	69.0	25 3 US-09-396-196G-46316	Sequence 46316, A
12	13.8	69.0	25 3 US-09-396-196G-46317	Sequence 46317, A
13	13.8	69.0	25 3 US-09-396-196G-46318	Sequence 46318, A
14	13.8	69.0	25 3 US-09-396-196G-46319	Sequence 46319, A
15	13.8	69.0	25 3 US-09-396-196G-46320	Sequence 46320, A
16	13.8	69.0	37 3 US-09-344-888A-19	Sequence 19, Appl
17	13.6	68.0	23 3 US-09-033-894-90	Sequence 90, Appl
18	13.6	68.0	23 3 US-09-031-626-90	Sequence 90, Appl
19	13.6	68.0	27 2 US-08-170-095B-36	Sequence 36, Appl
20	13.6	68.0	27 2 US-08-170-095B-36	Sequence 36, Appl
21	13.6	68.0	45 2 US-08-785-448-6	Sequence 6, Appl
22	13.6	68.0	45 2 US-08-925-927-6	Sequence 6, Appl
23	13.6	68.0	45 2 US-08-875-154-8	Sequence 8, Appl
24	13.6	68.0	45 3 US-09-120-576-6	Sequence 6, Appl

25	13.6	68.0	50 3 US-09-673-274C-14	Sequence 14, Appl
C 26	13.6	68.0	60 2 US-08-009-265-17	Sequence 17, Appl
C 27	13.6	68.0	75 2 US-08-009-265-42	Sequence 42, Appl
C 28	13.6	68.0	75 2 US-08-322-679-10	Sequence 10, Appl
C 29	13.6	68.0	75 3 US-08-686-993A-22	Sequence 22, Appl
C 30	13.6	68.0	78 9 5457037-7	Patent No. 5457037
C 31	13.6	68.0	81 3 US-09-673-274C-15	Sequence 15, Appl
C 32	13.2	66.0	25 3 US-09-396-196G-23837	Sequence 23837, A
C 33	13.2	66.0	25 3 US-09-396-196G-23838	Sequence 23838, A
C 34	13.2	66.0	25 3 US-09-396-196G-92823	Sequence 92823, A
C 35	13.2	66.0	25 3 US-09-396-196G-92824	Sequence 92824, A
C 36	13.2	66.0	25 3 US-09-396-196G-92825	Sequence 92825, A
C 37	13.2	66.0	25 3 US-09-396-196G-93601	Sequence 93601, A
C 38	13.2	66.0	25 3 US-09-396-196G-107012	Sequence 107012, A
C 39	13.2	66.0	25 3 US-09-396-196G-108063	Sequence 108063, A
C 40	13.2	66.0	40 3 US-09-548-797B-157	Sequence 157, App
C 41	13.2	66.0	43 3 US-09-380-190A-46	Sequence 46, Appl
C 42	13.2	66.0	44 3 US-09-380-420C-13	Sequence 13, Appl
C 43	13.2	66.0	44 3 US-09-899-642A-13	Sequence 13, Appl
C 44	13.2	66.0	51 3 US-09-443-199C-754	Sequence 754, App
45	13.2	66.0	92 2 US-08-487-141B-109	Sequence 109, App

ALIGNMENTS

RESULT 1
US-09-619-758-14/c
Sequence 14, Application US/09619758
Patent No. 6667164
GENERAL INFORMATION:
APPLICANT: Miller, Marcia M
APPLICANT: Afanasieff, Marielle
TITLE OF INVENTION: Methods for Breeding Disease-resistant Domestic Fowl
FILE REFERENCE: 1954-322
CURRENT APPLICATION NUMBER: US/09/619, 758
CURRENT FILING DATE: 2000-07-19
PRIORITY FILING DATE: 1999-02-04
PRIORITY FILING DATE: 1999-02-04
PRIORITY FILING DATE: 1996-12-27
PRIORITY FILING DATE: 1996-12-27
PRIORITY FILING DATE: 1995-01-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 21
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer for
OTHER INFORMATION: SSCP analysis of Mhc B class II-beta genotype of
OTHER INFORMATION: fowl
US-09-619-758-14
Query Match 72.0%; Score 14.4; DB 3; Length 21;
Best Local Similarity 93.8%; Pred. No. 3.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 5 CACGGCGCAGAGGAGC 20
16 CACGGTCAGAGGAGC 1
RESULT 2
US-09-886-607-14/c
Sequence 14, Application US/09886607
Patent No. 6696253
GENERAL INFORMATION:
APPLICANT: Miller, Marcia
APPLICANT: Afanasieff, Marielle
APPLICANT: Brites, W. Elwood

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; TITLE OF INVENTION: Method for Breeding Disease Resistant Domesticated Fowl
; FILE REFERENCE: 1954-376
; CURRENT APPLICATION NUMBER: US/09/886,607
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 09/244,093
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: US 09/619,757
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US 08/774,025
; PRIOR FILING DATE: 1996-12-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Gallus sp.
US-09-886-607-14
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Query Match          72.0%; Score 14.4; DB 3; Length 21;
Best Local Similarity 93.8%; Pred. No. 3.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      5 CACGGCGCAGAGGAGC 20
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Db      16 CACGGTGCAGAGGAGC 1
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RESULT 3
US-09-396-196G-65948
; Sequence 65948, Application US/09396196G
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; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65948
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-65948
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Query Match          71.0%; Score 14.2; DB 3; Length 25;
Best Local Similarity 84.2%; Pred. No. 4.4e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY      1 CGAGCAGCGCGCAGAGGAG 19
        |||||
Db      7 CCAGAGGCGCGCAGAGGAG 25
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RESULT 4
US-09-396-196G-65949
; Sequence 65949, Application US/09396196G
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; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
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; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65949
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-65949
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Query Match          71.0%; Score 14.2; DB 3; Length 25;
Best Local Similarity 84.2%; Pred. No. 4.4e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
QY      1 CGAGCAGCGCGCAGAGGAG 19
        |||||
Db      6 CCAGAGGCGCGCAGAGGAG 24
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RESULT 5
US-09-396-196G-65950
; Sequence 65950, Application US/09396196G
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; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65950
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-65950
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Query Match          71.0%; Score 14.2; DB 3; Length 25;
Best Local Similarity 84.2%; Pred. No. 4.4e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
QY      1 CGAGCAGCGCGCAGAGGAG 19
        |||||
Db      5 CCAGAGGCGCGCAGAGGAG 23
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RESULT 6
US-09-396-196G-65951
; Sequence 65951, Application US/09396196G
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; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65951
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-65951
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Query Match 71.0%; Score 14.2; DB 3; Length 25;
Best Local Similarity 84.2%; Pred. No. 4.4e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 CGAGCAGCGCGCAGAGAGC 19
Db 3 CCAGAAAGCGCGCAGAGAGC 21

RESULT 7
US-09-396-196G-71454/C

; Sequence 71454, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71454
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-71454

Query Match 71.0%; Score 14.2; DB 3; Length 25;
Best Local Similarity 84.2%; Pred. No. 4.4e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 GAGCAGCGCGCAGAGAGC 20
Db 19 GAGCAGCGTTGCAGAGAGC 1

RESULT 8
US-09-396-196G-71470/C

; Sequence 71470, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71470
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-71470

Query Match 71.0%; Score 14.2; DB 3; Length 25;
Best Local Similarity 84.2%; Pred. No. 4.4e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 GAGCAGCGCGCAGAGAGC 20
Db 23 GAGCAGCGTTGCAGAGAGC 5

RESULT 9
US-09-396-196G-71471/C

; Sequence 71471, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71471
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-71471

Query Match 71.0%; Score 14.2; DB 3; Length 25;
Best Local Similarity 84.2%; Pred. No. 4.4e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 GAGCAGCGCGCAGAGAGC 20
Db 21 GAGCAGCGTTGCAGAGAGC 3

RESULT 10
US-09-443-199C-753

; Sequence 753, Application US/09443199C
; Patent No. 6670464
; GENERAL INFORMATION:
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Leach, Martin
; TITLE OF INVENTION: Nucleic Acids Containing Single Nucleotide
; FILE REFERENCE: 15966-534A
; CURRENT APPLICATION NUMBER: US/09/443,199C
; CURRENT FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/109,024
; PRIOR FILING DATE: 1998-11-17
; NUMBER OF SEQ ID NOS: 1272
; SOFTWARE: Curagen Patent Formatter Version 0.9
; SEQ ID NO 753
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (26)...(0)
; OTHER INFORMATION: 1 of 2 allelic variants (754 is other entry)
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Accession number cg43921619
US-09-443-199C-753

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Best Local Similarity 84.2%; Pred. No. 4.3e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 GAGCAGCGCGCAGAGAGC 20
Db 26 GAGCAGGAGAGAGAGAGC 44

RESULT 11
US-09-396-196G-46316
; Sequence 46316, Application US/09396196G

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; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46316
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-46316
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Query Match          69.0%; Score 13.8; DB 3; Length 25;
Best Local Similarity 88.2%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 4 GCACGCGCGAGAGAGC 20
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DB 8 GCACGCGCGAGATGAGC 24
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RESULT 12
US-09-396-196G-46317
; Sequence 46317, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46317
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-46317
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Query Match          69.0%; Score 13.8; DB 3; Length 25;
Best Local Similarity 88.2%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

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QY 4 GCACGCGCGAGAGAGC 20
    |||||
DB 7 GCACGCGCGAGATGAGC 23
```

```
RESULT 13
US-09-396-196G-46318
; Sequence 46318, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
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; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46318
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-46318
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Query Match          69.0%; Score 13.8; DB 3; Length 25;
Best Local Similarity 88.2%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 4 GCACGCGCGAGAGAGC 20
    |||||
DB 5 GCACGCGCGAGATGAGC 21
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RESULT 14
US-09-396-196G-46319
; Sequence 46319, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46319
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-46319
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```
Query Match          69.0%; Score 13.8; DB 3; Length 25;
Best Local Similarity 88.2%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 4 GCACGCGCGAGAGAGC 20
    |||||
DB 4 GCACGCGCGAGATGAGC 20
```

```
RESULT 15
US-09-396-196G-46320
; Sequence 46320, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46320
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
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US-09-396-196G-46320

Query Match

Best Local Similarity 69.0%; Score 13.8; DB 3; Length 25;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 Db 2 GCACGCGCGCAGATGAGC 18

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Title: US-09-296-264-2
Perfect score: 20
Sequence: 1 cgagcagcgccgagagc 20

Scoring table: IDENTITY_NUC
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Searched: 9793542 seqs, 4134689005 residues

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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	15.4	77.0	99	3	US-09-974-300-4020
4	15.2	76.0	25	7	US-10-719-956-362544
5	15.2	76.0	27	3	US-09-894-633A-18
6	14.8	74.0	25	10	US-11-036-317-855094
7	14.8	74.0	55	3	US-09-991-209-72
8	14.4	72.0	21	3	US-09-886-607-14
9	14.2	71.0	25	7	US-10-719-956-601919
10	14.2	71.0	25	9	US-10-809-189-65948
11	14.2	71.0	25	9	US-10-809-189-65949
12	14.2	71.0	25	9	US-10-809-189-65950
13	14.2	71.0	25	9	US-10-809-189-65951
14	14.2	71.0	25	9	US-10-809-189-71454
15	14.2	71.0	25	9	US-10-809-189-71470
16	14.2	71.0	25	9	US-10-809-189-71471
17	14.2	71.0	27	6	US-10-186-157-6
18	14.2	71.0	42	6	US-10-353-678-35
19	14.2	71.0	48	6	US-10-353-678-35
20	14.2	71.0	63	6	US-10-174-394-41
21	14.2	71.0	63	8	US-10-435-087-27
22	14.2	71.0	63	9	US-10-980-764-13
23	14.2	71.0	63	9	US-10-980-659-13

24	14.2	71.0	63	9	US-10-980-695-13	Sequence 13, Appl
25	14.2	71.0	75	6	US-10-353-678-65	Sequence 65, Appl
26	14.2	71.0	96	6	US-10-353-678-66	Sequence 66, Appl
27	13.8	69.0	20	9	US-10-800-350-165	Sequence 165, App
28	13.8	69.0	20	9	US-10-800-077-165	Sequence 165, App
29	13.8	69.0	23	9	US-10-980-002-7	Sequence 7, Appl1
30	13.8	69.0	25	8	US-10-719-900-1092310	Sequence 3092310,
31	13.8	69.0	25	8	US-10-719-900-1092310	Sequence 3092310,
32	13.8	69.0	25	9	US-10-809-189-46316	Sequence 46316, A
33	13.8	69.0	25	9	US-10-809-189-46317	Sequence 46317, A
34	13.8	69.0	25	9	US-10-809-189-46318	Sequence 46318, A
35	13.8	69.0	25	9	US-10-809-189-46319	Sequence 46319, A
36	13.8	69.0	25	9	US-10-809-189-46320	Sequence 46320, A
37	13.8	69.0	65	3	US-09-908-975-29746	Sequence 29746, A
38	13.6	68.0	23	3	US-09-778-152-80	Sequence 90, Appl
39	13.6	68.0	23	3	US-10-023-610-50	Sequence 90, Appl
40	13.6	68.0	23	7	US-10-212-848-50	Sequence 90, Appl
41	13.6	68.0	25	7	US-10-719-956-194261	Sequence 194261,
42	13.6	68.0	25	7	US-10-719-956-194262	Sequence 194262,
43	13.6	68.0	25	7	US-10-719-956-362545	Sequence 362545,
44	13.6	68.0	25	8	US-10-719-900-949166	Sequence 949166,
45	13.6	68.0	25	10	US-11-036-317-95368	Sequence 95368, A

ALIGNMENTS

RESULT 1
US-09-296-264-2
Sequence 2, Application US/09296264
Publication No. US20030083274A1
GENERAL INFORMATION:
APPLICANT: WRIGHT, Jim A.
APPLICANT: YOUNG, Aiping H.
APPLICANT: LEE, Yoon S.
TITLE OF INVENTION: NEUROPELIN ANTISENSE OLIGONUCLEOTIDE SEQUENCES AND
TITLE OF INVENTION: METHODS OF USING SAME TO MODULATE CELL GROWTH
FILE REFERENCE: 032396-043
CURRENT APPLICATION NUMBER: US/09/296,264
CURRENT FILING DATE: 1999-04-22
EARLIER APPLICATION NUMBER: US 60/082,791
EARLIER FILING DATE: 1998-04-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 20
TYPE: DNA
ORGANISM: Human
US-09-296-264-2

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGAGCAGCGCGCAGAGGC 20
Db 1 CGAGCAGCGCGCAGAGGC 20

RESULT 2
US-10-703-817-104/C
Sequence 104, Application US/10703817
Publication No. US2005011817A1
GENERAL INFORMATION:
APPLICANT: ROTH, RICHARD B.
APPLICANT: NELSON, MATTHEW ROBERTS
APPLICANT: KAMMERER, STEFAN M.
APPLICANT: BRAUN, ANDREAS
TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF MELANOMA AND TREATMENTS
TITLE OF INVENTION: THEREOF
FILE REFERENCE: SEQ-4061-UT
CURRENT APPLICATION NUMBER: US/10/703,817
CURRENT FILING DATE: 2003-11-06

```
/ PRIOR APPLICATION NUMBER: 60/489,703
/ PRIOR FILING DATE: 2003-07-23
/ PRIOR APPLICATION NUMBER: 60/424,475
/ PRIOR FILING DATE: 2002-11-06
/ NUMBER OF SEQ ID NOS: 255
/ SOFTWARE: Patent version 3.3
/ SEQ ID NO 104
/ LENGTH: 29
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer
US-10-703-817-104

Query Match          95.0%; Score 19; DB 9; Length 29;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 GAGCAGCGCGCAGAGAGC 20
      |||||
Db      29 GAGCAGCGCGCAGAGAGC 11

RESULT 3
US-09-974-300-4020
/ Sequence 4020, Application US/09974300
/ Patent No. US20020146721A1
/ GENERAL INFORMATION:
/ APPLICANT: Berka, Randy M.
/ APPLICANT: Clausen, Ib Groth
/ TITLE OF INVENTION: Methode For Monitoring Multiple Gene
/ FILE REFERENCE: 10085,500-US
/ CURRENT APPLICATION NUMBER: US/09/974,300
/ CURRENT FILING DATE: 2001-10-05
/ PRIOR APPLICATION NUMBER: 09/680,598
/ PRIOR FILING DATE: 2000-10-06
/ PRIOR APPLICATION NUMBER: 60/279,526
/ PRIOR FILING DATE: 2001-03-27
/ NUMBER OF SEQ ID NOS: 8481
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 4020
/ LENGTH: 99
/ TYPE: DNA
/ ORGANISM: Bacillus licheniformis
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)...(99)
/ OTHER INFORMATION: n = A,T,C or G
US-09-974-300-4020

Query Match          77.0%; Score 15.4; DB 3; Length 99;
Best Local Similarity 94.1%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      4 GCAGCGCGCAGAGAGC 20
      |||||
Db      31 GCAGCGCGCAGAGAGC 47

RESULT 4
US-10-719-956-362544/c
/ Sequence 362544, Application US/10719956
/ Publication No. US20040146910A1
/ GENERAL INFORMATION:
/ APPLICANT: Xue Mei Zhou
/ TITLE OF INVENTION: Methode of Genetic Analysis of Rat
/ FILE REFERENCE: 3527.1
/ CURRENT APPLICATION NUMBER: US/10/719,956
/ CURRENT FILING DATE: 2003-11-20
/ PRIOR APPLICATION NUMBER: 60/427,836
/ PRIOR FILING DATE: 2002 11 20
/ NUMBER OF SEQ ID NOS: 699466
```

```
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 362544
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Rattus norvegicus
US-10-719-956-362544

Query Match          76.0%; Score 15.2; DB 7; Length 25;
Best Local Similarity 85.0%; Pred. No. 2.9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 CGAGCAGCGCGCAGAGAGC 20
      |||||
Db      20 CGAGCAGCGCGCGTAGAGATC 1

RESULT 5
US-09-894-633A-18
/ Sequence 18, Application US/09894633A
/ Patent No. US20020124285A1
/ GENERAL INFORMATION:
/ APPLICANT: Comer, Timothy
/ APPLICANT: Dubois, Patrice
/ APPLICANT: Maiven, Marianne
/ APPLICANT: Masucci, James
/ TITLE OF INVENTION: PLANT REGULATORY SEQUENCES FOR SELECTIVE CONTROL OF GENE EXPRESSION
/ FILE REFERENCE: 38-21(1585)B
/ CURRENT APPLICATION NUMBER: US/09/894,633A
/ CURRENT FILING DATE: 2001-06-28
/ PRIOR APPLICATION NUMBER: 60/214,357
/ PRIOR FILING DATE: 2000-06-28
/ PRIOR APPLICATION NUMBER: 09/894,633
/ PRIOR FILING DATE: 2000-06-28
/ NUMBER OF SEQ ID NOS: 111
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 18
/ LENGTH: 27
/ TYPE: DNA
/ ORGANISM: artificial sequence
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)..(27)
/ OTHER INFORMATION: synthetic primer sequence
US-09-894-633A-18

Query Match          76.0%; Score 15.2; DB 3; Length 27;
Best Local Similarity 85.0%; Pred. No. 2.9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 CGAGCAGCGCGCAGAGAGC 20
      |||||
Db      7 CGAGCAGCGCGAGAGAGATC 26

RESULT 6
US-11-036-317-855094
/ Sequence 855094, Application US/11036317
/ Publication No. US20050214823A1
/ GENERAL INFORMATION:
/ APPLICANT: Williams, Alan
/ APPLICANT: Blume, John
/ TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
/ FILE REFERENCE: 3654.1
/ CURRENT APPLICATION NUMBER: US/11/036,317
/ CURRENT FILING DATE: 2005-01-13
/ PRIOR APPLICATION NUMBER: 60/536,639
/ PRIOR FILING DATE: 2004-01-13
/ NUMBER OF SEQ ID NOS: 991174
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 855094
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Mus musculus
```


US-11-036-317-855094

Query Match 74.0%; Score 14.8; DB 10; Length 25;

Best Local Similarity 88.9%; Pred. No. 4.4e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GAGCAGCGCGCAGAGAG 19

Db 8 GAGCAGCTGCGCAGAGAG 25

RESULT 7

US-09-991-209-72

Sequence 72, Application US/09991209

Publication No. US20030024009A1

GENERAL INFORMATION:

APPLICANT: Dunn-Coleman, Nigel

APPLICANT: Langdon, Timothy

APPLICANT: Morse, Phillip

TITLE OF INVENTION: Manipulation of the Phenolic Acid

TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted

FILE REFERENCE: GC648-2

CURRENT APPLICATION NUMBER: US/09/991,209

CURRENT FILING DATE: 2002-07-02

PRIOR APPLICATION NUMBER: US 60/249,608

PRIOR FILING DATE: 2000-11-17

NUMBER OF SEQ ID NOS: 97

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 72

LENGTH: 55

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: primer

US-09-991-209-72

Query Match 74.0%; Score 14.8; DB 3; Length 55;

Best Local Similarity 88.9%; Pred. No. 3.8e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GAGCAGCGCGCAGAGAG 19

Db 6 GATCAGCGCGAAGAGAG 23

RESULT 8

US-09-886-607-14/C

Sequence 14, Application US/09886607

Patent No. US20020083482A1

GENERAL INFORMATION:

APPLICANT: Miller, Marcia

APPLICANT: Afanasieff, Marielle

APPLICANT: Biles, W. Elwood

TITLE OF INVENTION: Method for Breeding Disease Resistant Domesticated Fowl

FILE REFERENCE: 1954-376

CURRENT APPLICATION NUMBER: US/09/886,607

CURRENT FILING DATE: 2001-06-22

PRIOR APPLICATION NUMBER: US 09/244,093

PRIOR FILING DATE: 1999-02-04

PRIOR APPLICATION NUMBER: US 09/619,757

PRIOR FILING DATE: 2000-07-19

PRIOR APPLICATION NUMBER: US 08/774,025

PRIOR FILING DATE: 1996-12-27

NUMBER OF SEQ ID NOS: 20

SOFTWARE: PatentIn version 3.0

SEQ ID NO 14

LENGTH: 21

TYPE: DNA

ORGANISM: Gallus sp.

US-09-886-607-14

Query Match 72.0%; Score 14.4; DB 3; Length 21;

Best Local Similarity 93.8%; Pred. No. 6.9e+03;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CACGCGCGCAGAGAGC 20

Db 16 CACGCTGCAGAGAGAGC 1

RESULT 9

US-10-719-956-601919/C

Sequence 601919, Application US/10719956

Publication No. US20040146910A1

GENERAL INFORMATION:

APPLICANT: Xue Mei Zhou

TITLE OF INVENTION: Methods of Genetic Analysis of Rat

FILE REFERENCE: 3527.1

CURRENT APPLICATION NUMBER: US/10/719,956

CURRENT FILING DATE: 2003-11-20

PRIOR APPLICATION NUMBER: 60/427,836

PRIOR FILING DATE: 2002.11.20

NUMBER OF SEQ ID NOS: 699466

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 601919

LENGTH: 25

TYPE: DNA

ORGANISM: Rattus norvegicus

US-10-719-956-601919

Query Match 71.0%; Score 14.2; DB 7; Length 25;

Best Local Similarity 84.2%; Pred. No. 8.2e+03;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GAGCAGCGCGCAGAGAGC 20

Db 24 GAGCCCGCGCAGAGAGC 6

RESULT 10

US-10-809-189-65948

Sequence 65948, Application US/10809189

Publication No. US20050048531A1

GENERAL INFORMATION:

APPLICANT: Michael Miltmann

APPLICANT: David Lockhart

APPLICANT: Atymetrix, Inc.

TITLE OF INVENTION: Methods of Genetic Analysis

FILE REFERENCE: 3101.1

CURRENT APPLICATION NUMBER: US/10/809,189

CURRENT FILING DATE: 2004-03-25

PRIOR APPLICATION NUMBER: US/09/396,196

PRIOR FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: 60/100,678

PRIOR FILING DATE: 1998-09-17

NUMBER OF SEQ ID NOS: 127806

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 65948

LENGTH: 25

TYPE: DNA

ORGANISM: mus musculus

US-10-809-189-65948

Query Match 71.0%; Score 14.2; DB 9; Length 25;

Best Local Similarity 84.2%; Pred. No. 8.2e+03;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CGAGCAGCGCGCAGAGAG 19

Db 7 CGAGAGCGCGCAGAGAG 25

RESULT 11

US-10-809-189-65949

```
/ Sequence 65949, Application US/10809189
/ Publication No. US20050048531A1
/ GENERAL INFORMATION:
/ APPLICANT: Michael Miltmann
/ APPLICANT: David Mack
/ APPLICANT: David Lockhart
/ APPLICANT: Affymetrix, Inc.
/ TITLE OF INVENTION: Methods of Genetic Analysis
/ FILE REFERENCE: 3101.1
/ CURRENT APPLICATION NUMBER: US/10/809,189
/ CURRENT FILING DATE: 2004-03-25
/ PRIOR APPLICATION NUMBER: US/09/396,196
/ PRIOR FILING DATE: 1999-09-15
/ PRIOR APPLICATION NUMBER: 60/100,678
/ PRIOR FILING DATE: 1998-09-17
/ NUMBER OF SEQ ID NOS: 127806
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 65949
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: mus musculus
US-10-809-189-65949
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```
Query Match          71.0%; Score 14.2; DB 9; Length 25;
Best Local Similarity 84.2%; Pred. No. 8.2e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 CGAGCAGCGCGCAGAGGAG 19
Db      6 CCGAAGAGCGCGCAGAGGAG 24
```

```
RESULT 12
US-10-809-189-65950
/ Sequence 65950, Application US/10809189
/ Publication No. US20050048531A1
/ GENERAL INFORMATION:
/ APPLICANT: Michael Miltmann
/ APPLICANT: David Mack
/ APPLICANT: David Lockhart
/ APPLICANT: Affymetrix, Inc.
/ TITLE OF INVENTION: Methods of Genetic Analysis
/ FILE REFERENCE: 3101.1
/ CURRENT APPLICATION NUMBER: US/10/809,189
/ CURRENT FILING DATE: 2004-03-25
/ PRIOR APPLICATION NUMBER: US/09/396,196
/ PRIOR FILING DATE: 1999-09-15
/ PRIOR APPLICATION NUMBER: 60/100,678
/ PRIOR FILING DATE: 1998-09-17
/ NUMBER OF SEQ ID NOS: 127806
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 65950
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: mus musculus
US-10-809-189-65950
```

```
Query Match          71.0%; Score 14.2; DB 9; Length 25;
Best Local Similarity 84.2%; Pred. No. 8.2e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 CGAGCAGCGCGCAGAGGAG 19
Db      5 CCGAAGAGCGCGCAGAGGAG 23
```

```
RESULT 13
US-10-809-189-65951
/ Sequence 65951, Application US/10809189
/ Publication No. US20050048531A1
/ GENERAL INFORMATION:
/ APPLICANT: Michael Miltmann
/ APPLICANT: David Mack
```

```
/ APPLICANT: David Lockhart
/ APPLICANT: Affymetrix, Inc.
/ TITLE OF INVENTION: Methods of Genetic Analysis
/ FILE REFERENCE: 3101.1
/ CURRENT APPLICATION NUMBER: US/10/809,189
/ CURRENT FILING DATE: 2004-03-25
/ PRIOR APPLICATION NUMBER: US/09/396,196
/ PRIOR FILING DATE: 1999-09-15
/ PRIOR APPLICATION NUMBER: 60/100,678
/ PRIOR FILING DATE: 1998-09-17
/ NUMBER OF SEQ ID NOS: 127806
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 65951
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: mus musculus
US-10-809-189-65951
```

```
Query Match          71.0%; Score 14.2; DB 9; Length 25;
Best Local Similarity 84.2%; Pred. No. 8.2e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 CGAGCAGCGCGCAGAGGAG 19
Db      3 CCGAAGAGCGCGCAGAGGAG 21
```

```
RESULT 14
US-10-809-189-71454/C
/ Sequence 71454, Application US/10809189
/ Publication No. US20050048531A1
/ GENERAL INFORMATION:
/ APPLICANT: Michael Miltmann
/ APPLICANT: David Mack
/ APPLICANT: David Lockhart
/ APPLICANT: Affymetrix, Inc.
/ TITLE OF INVENTION: Methods of Genetic Analysis
/ FILE REFERENCE: 3101.1
/ CURRENT APPLICATION NUMBER: US/10/809,189
/ CURRENT FILING DATE: 2004-03-25
/ PRIOR APPLICATION NUMBER: US/09/396,196
/ PRIOR FILING DATE: 1999-09-15
/ PRIOR APPLICATION NUMBER: 60/100,678
/ PRIOR FILING DATE: 1998-09-17
/ NUMBER OF SEQ ID NOS: 127806
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 71454
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: mus musculus
US-10-809-189-71454
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```
Query Match          71.0%; Score 14.2; DB 9; Length 25;
Best Local Similarity 84.2%; Pred. No. 8.2e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
QY      2 GAGCAGCGCGCAGAGGAGC 20
Db      19 GAGCAGCGTTGCGAGAGAGC 1
```

```
RESULT 15
US-10-809-189-71470/C
/ Sequence 71470, Application US/10809189
/ Publication No. US20050048531A1
/ GENERAL INFORMATION:
/ APPLICANT: Michael Miltmann
/ APPLICANT: David Mack
/ APPLICANT: David Lockhart
/ APPLICANT: Affymetrix, Inc.
/ TITLE OF INVENTION: Methods of Genetic Analysis
/ FILE REFERENCE: 3101.1
/ CURRENT APPLICATION NUMBER: US/10/809,189
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 18:29:07 ; Search time 135.3 Seconds
(without alignments)
76.712 Million cell updates/sec

Title: US-09-296-264-2
Perfect score: 20
Sequence: 1 GAGCAGCGCCGAGAGGAGC 20

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 4168288 seqs, 259477437 residues

Total number of hits satisfying chosen parameters: 1608458

Minimum DB seq length: 20
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA New:

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2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/FCI_NEW_PUB.seq.*
5: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
6: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
7: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
8: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
10: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14.2	71.0	32	US-10-939-294A-18367	Sequence 18367, A
2	14.2	71.0	63	US-10-842-206-27	Sequence 27, Appl
3	14.2	71.0	63	US-10-980-459-13	Sequence 13, Appl
4	13.8	69.0	20	US-10-949-720-165	Sequence 165, App
5	13.8	69.0	25	US-11-121-849-36542	Sequence 36542, A
6	13.6	68.0	25	US-11-121-849-213458	Sequence 213458, A
7	13.6	68.0	25	US-11-121-849-213523	Sequence 213523, A
8	13.6	68.0	25	US-11-121-849-357209	Sequence 357209, A
9	13.6	68.0	32	US-10-939-294A-15531	Sequence 15531, A
10	13.6	68.0	32	US-10-939-294A-15856	Sequence 15856, A
11	13.2	66.0	25	US-11-121-849-20944	Sequence 20944, A
12	13.2	66.0	25	US-11-121-849-34121	Sequence 34121, A
13	13.2	66.0	25	US-11-121-849-258042	Sequence 258042, A
14	13.2	66.0	25	US-11-121-849-356175	Sequence 356175, A
15	13.2	66.0	25	US-11-121-849-360121	Sequence 360121, A
16	13.2	66.0	25	US-11-121-849-438054	Sequence 438054, A
17	13.2	66.0	32	US-10-939-294A-15741	Sequence 15741, A
18	12.8	64.0	25	US-11-121-849-497643	Sequence 497643, A
19	12.6	63.0	25	US-11-121-849-38244	Sequence 38244, A
20	12.6	63.0	25	US-11-121-849-228556	Sequence 228556, A
21	12.6	63.0	25	US-11-121-849-291020	Sequence 291020, A
22	12.6	63.0	25	US-11-121-849-351476	Sequence 351476, A
23	12.6	63.0	25	US-11-121-849-543546	Sequence 543546, A

24	12.6	63.0	32	US-10-939-294A-17627	Sequence 17627, A
25	12.4	62.0	25	US-11-121-849-53508	Sequence 53508, A
26	12.4	62.0	25	US-11-121-849-275556	Sequence 275556, A
27	12.4	62.0	25	US-11-121-849-402445	Sequence 402445, A
28	12.4	62.0	25	US-11-121-849-497644	Sequence 497644, A
29	12.2	61.0	23	US-11-069-908-1811	Sequence 1811, Ap
30	12.2	61.0	23	US-11-069-908-1177	Sequence 1177, Ap
31	12.2	61.0	25	US-11-121-849-6570	Sequence 6570, Ap
32	12.2	61.0	25	US-11-121-849-401201	Sequence 401201, Ap
33	12.2	61.0	25	US-11-121-849-37985	Sequence 37985, Ap
34	12.2	61.0	25	US-11-121-849-37985	Sequence 37985, A
35	12.2	61.0	25	US-11-121-849-44934	Sequence 44934, A
36	12.2	61.0	25	US-11-121-849-64787	Sequence 64787, A
37	12.2	61.0	25	US-11-121-849-99747	Sequence 99747, A
38	12.2	61.0	25	US-11-121-849-293861	Sequence 293861, A
39	12.2	61.0	25	US-11-121-849-293861	Sequence 293861, A
40	12.2	61.0	25	US-11-121-849-392046	Sequence 392046, A
41	12.2	61.0	25	US-11-121-849-392871	Sequence 392871, A
42	12.2	61.0	25	US-11-121-849-392893	Sequence 392893, A
43	12.2	61.0	25	US-11-121-849-401201	Sequence 401201, A
44	12.2	61.0	25	US-11-121-849-437433	Sequence 437433, A
45	12.2	61.0	25	US-11-121-849-457690	Sequence 457690, A
			7	US-11-121-849-457987	Sequence 457987, A

ALIGNMENTS

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RESULT 1
US-10-939-294A-18367
; Sequence 18367, Application US/10939294A
; Publication No. US20050266417A1
; GENERAL INFORMATION:
; APPLICANT: Barany, Francis
; APPLICANT: Turner, Daniel
; APPLICANT: Pincas, Hanna
; APPLICANT: Manes, Hanna
; TITLE OF INVENTION: Methods for identifying target nucleic acid molecules
; FILE REFERENCE: 19603/4121 (CRF D-2995-02)
; CURRENT APPLICATION NUMBER: US/10/939,294A
; PRIOR FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: US 60/502/731
; PRIOR FILING DATE: 2003-09-12
; NUMBER OF SEQ ID NOS: 38895
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18367
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: oligonucleotide probe
US-10-939-294A-18367
Query Match 71.0%; Score 14.2; DB 6; Length 32;
Best Local Similarity 84.2%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Cy 2 GAGCAGCGCCGAGAGGAGC 20
Db 5 GAGCAGCGCCGAGAGGAGC 23
RESULT 2
US-10-842-206-27
; Sequence 27, Application US/10842206
; Publication No. US20050256039A1
; GENERAL INFORMATION:
; APPLICANT: Peterson, Jeffrey D
; APPLICANT: Sciore, Paul J
; TITLE OF INVENTION: NOVEL FIBROBLAST GROWTH FACTORS AND METHODS OF USE THEREOF
; FILE REFERENCE: Cura 570A
; CURRENT APPLICATION NUMBER: US/10/842,206
; CURRENT FILING DATE: 2004-05-10
; NUMBER OF SEQ ID NOS: 40
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```

; SOFTWARE: Curseseqlist version 0.1
; SEQ ID NO 27
; LENGTH: 63
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(63)
US-10-842-206-27
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```

Query Match          71.0%; Score 14.2; DB 6; Length 63;
Best Local Similarity 84.2%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```

QY      2 GAGCAGCGCGCAGAGAGC 20
        ||| ||| ||| ||| |||
Db      30 GAGCGCGCGGAGCGAGC 48
```

RESULT 3

```

US-10-980-459-13
; Sequence 13, Application US/10980459
; Publication No. US20050256042A1
; GENERAL INFORMATION:
; APPLICANT: Alvarez, Enrique
; APPLICANT: Chilikuru, Rajeev A.
; APPLICANT: Jeffers, Michael B.
; APPLICANT: LaRochele, William J.
; APPLICANT: Lichenstein, Henri
; APPLICANT: Namdev, Pradyumna Kumar
; APPLICANT: Valax, Pascal
; APPLICANT: Yim, Zachary
; APPLICANT: Hahne, William
; TITLE OF INVENTION: Methods of Preventing and Treating Alimentary Mucositis
; FILE REFERENCE: Cura-57 AM
; CURRENT APPLICATION NUMBER: US/10/980,459
; PRIOR APPLICATION NUMBER: 2004-11-03
; PRIOR FILING DATE: 2003-5-9
; PRIOR APPLICATION NUMBER: 10/842,179
; PRIOR FILING DATE: 2004-5-10
; PRIOR APPLICATION NUMBER: 60/541,728
; PRIOR FILING DATE: 2004-2-4
; PRIOR APPLICATION NUMBER: 60/545,278
; PRIOR FILING DATE: 2004-2-18
; PRIOR APPLICATION NUMBER: 60/
; PRIOR FILING DATE: 2004-10-28
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Curseseqlist version 0.1
; SEQ ID NO 13
; LENGTH: 63
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(63)
US-10-980-459-13
```

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Query Match          71.0%; Score 14.2; DB 6; Length 63;
Best Local Similarity 84.2%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```

QY      2 GAGCAGCGCGCAGAGAGC 20
        ||| ||| ||| ||| |||
Db      30 GAGCGCGCGGAGCGAGC 48
```

RESULT 4

```

US-10-949-720-165
; Sequence 165, Application US/10949720
; Publication No. US20050249736A1
; GENERAL INFORMATION:
; APPLICANT: Krasnoperov, Valery
```

```

; APPLICANT: Zozulya, Sergey
; APPLICANT: Kertesz, Nathalie
; APPLICANT: Reddy, Ramachandra
; APPLICANT: Gill, Parkash
; TITLE OF INVENTION: POLYPEPTIDE COMPOUNDS FOR INHIBITING
; TITLE OF INVENTION: ANGIOGENESIS AND TUMOR GROWTH
; FILE REFERENCE: VASG-P02-002
; CURRENT APPLICATION NUMBER: US/10/949,720
; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: US 60/454,432
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/454,300
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/800,350
; PRIOR FILING DATE: 2004-03-12
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 165
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-949-720-165
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```

Query Match          69.0%; Score 13.8; DB 6; Length 20;
Best Local Similarity 88.2%; Pred. No. 2.8e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```

QY      4 GCACGCGCGCAGAGAGC 20
        ||| ||| ||| ||| |||
Db      4 GCAGGCGCGCACAGAGC 20
```

RESULT 5

```

US-11-121-849-366542
; Sequence 366542, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 366542
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-366542
```

```

Query Match          69.0%; Score 13.8; DB 7; Length 25;
Best Local Similarity 88.2%; Pred. No. 2.7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```

QY      4 GCACGCGCGCAGAGAGC 20
        ||| ||| ||| ||| |||
Db      4 GCTCGCGCGCAGAGAGC 20
```

RESULT 6

```

US-11-121-849-213468/c
; Sequence 213468, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
```

CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 213468
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-213468

Query Match
Best Local Similarity 80.0%; Score 13.6; DB 7; Length 25;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGAGCAGCGCGGAGAGAGC 20
Db 20 CGAACACGCGGAGAGAGCATC 1

RESULT 7
US-11-121-849-213523/c
Sequence 213523, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 213523
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-213523

Query Match
Best Local Similarity 80.0%; Score 13.6; DB 7; Length 25;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGAGCAGCGCGGAGAGAGC 20
Db 20 CGAACACGCGGAGAGAGCATC 1

RESULT 8
US-11-121-849-357209/c
Sequence 357209, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 357209
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-357209

Query Match
Best Local Similarity 80.0%; Score 13.6; DB 7; Length 25;

Best Local Similarity 80.0%; Pred. No. 3.3e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGAGCAGCGCGGAGAGAGC 20
Db 21 CGGCACACGCGCTGAGCATC 2

RESULT 9
US-10-939-294A-15531
Sequence 15531, Application US/10939294A
Publication No. US20050266417A1
GENERAL INFORMATION:
APPLICANT: Barany, Francis
APPLICANT: Turner, Daniel
APPLICANT: Pingle, Maneesh
TITLE OF INVENTION: Methods for identifying target nucleic acid molecules
FILE REFERENCE: 19603/4121 (CRF D-2995-02)
CURRENT APPLICATION NUMBER: US/10/939,294A
CURRENT FILING DATE: 2004-09-10
PRIOR APPLICATION NUMBER: US 60/502/731
PRIOR FILING DATE: 2003-09-12
NUMBER OF SEQ ID NOS: 38895
SOFTWARE: PatentIn version 3.3
SEQ ID NO 15531
LENGTH: 32
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: oligonucleotide probe
US-10-939-294A-15531

Query Match
Best Local Similarity 80.0%; Score 13.6; DB 6; Length 32;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGAGCAGCGCGGAGAGAGC 20
Db 7 CGGAATGCGCGGAGAGC 26

RESULT 10
US-10-939-294A-15856
Sequence 15856, Application US/10939294A
Publication No. US20050266417A1
GENERAL INFORMATION:
APPLICANT: Barany, Francis
APPLICANT: Turner, Daniel
APPLICANT: Pingle, Maneesh
TITLE OF INVENTION: Methods for identifying target nucleic acid molecules
FILE REFERENCE: 19603/4121 (CRF D-2995-02)
CURRENT APPLICATION NUMBER: US/10/939,294A
CURRENT FILING DATE: 2004-09-10
PRIOR APPLICATION NUMBER: US 60/502/731
PRIOR FILING DATE: 2003-09-12
NUMBER OF SEQ ID NOS: 38895
SOFTWARE: PatentIn version 3.3
SEQ ID NO 15856
LENGTH: 32
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: oligonucleotide probe
US-10-939-294A-15856

Query Match
Best Local Similarity 80.0%; Score 13.6; DB 6; Length 32;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGAGCAGCGCGGAGAGAGC 20

```
Db          7 CCAGCGTGGCGAGCGAGC 26

RESULT 11
US-11-121-849-20944
; Sequence 20944, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 20944
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-20944

Query Match          66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 4.7e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy          3 AGCAGCGGCGAGAGAGC 20
Db          2 AGCAGCGGCTGAAGAAGAGC 19

RESULT 12
US-11-121-849-34121
; Sequence 34121, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 34121
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-34121

Query Match          66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 4.7e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy          3 AGCAGCGGCGAGAGAGC 20
Db          5 AGCGCTGGCGAGAGAGAGC 22

RESULT 13
US-11-121-849-258042
; Sequence 258042, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 258042
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-258042

Query Match          66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 4.7e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy          3 AGCAGCGGCGAGAGAGC 20
Db          1 AGGACGACTCAGAGAGAGC 18

RESULT 14
US-11-121-849-356175
; Sequence 356175, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 356175
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-356175

Query Match          66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 4.7e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy          2 GAGCAGCGGCGAGAGAGC 15
Db          3 GAAACGCGGCGAGAGAGAGC 20

RESULT 15
US-11-121-849-360121/C
; Sequence 360121, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 360121
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-360121

Query Match          66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 4.7e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Matches	15;	Conservative	0;	Mismatches	3;	Indels	0;	Gaps	0;
Qy	1	CGAGCAGCGCGCAGAGA	18						
Db	19	CAAGCACGTTGCAGAGA	2						

Search completed: December 25, 2005, 04:37:02
 Job time : 136.3 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 10:28:41 ; Search time 582 Seconds
(without alignments)
1953.383 Million cell updates/sec

Title: US-09-296-264-3

Perfect score: 20
Sequence: 1 ggcagcagcgagcagcagcgcg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 1858228

Minimum DB seq length: 20

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

GenEmbl:.*
1: gb_ba:.*
2: gb_in:.*
3: gb_env:.*
4: gb_om:.*
5: gb_ov:.*
6: gb_pat:.*
7: gb_ph:.*
8: gb_pr:.*
9: gb_ro:.*
10: gb_secs:.*
11: gb_sy:.*
12: gb_un:.*
13: gb_vi:.*
14: gb_htg:.*
15: gb_pl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6	BD211660
2	16.8	84.0	51	6	AX156995
3	15.2	76.0	96	6	CQ745222
4	15.2	76.0	99	6	A23183
5	14.8	74.0	100	6	AX997929
6	14.8	74.0	100	6	AX997930
7	14.2	71.0	26	6	AR559751
8	14.2	71.0	26	6	AX146654
9	14.2	71.0	40	6	AX490799
10	14.2	71.0	45	6	AX128401
11	14.2	71.0	45	6	AX429834
12	14.2	71.0	65	6	AX429833
13	14.2	71.0	66	6	AR038665
14	14.2	71.0	78	13	AF362846
15	14.2	71.0	78	13	AF362847
16	14.2	71.0	78	13	AF362848
17	13.8	69.0	60	6	AR009383
18	13.8	69.0	78	6	A67678

19	13.6	68.0	30	6	AR063475	AR063475 Sequence
20	13.6	68.0	30	6	I28155	I28155 Sequence 12
21	13.6	68.0	37	6	AX356235	AX356235 Sequence
22	13.6	68.0	49	10	AL823803	AL823803 Arabidops
23	13.6	68.0	51	6	CQ005836	CQ005836 Sequence
24	13.6	68.0	51	6	CQ005837	CQ005837 Sequence
25	13.6	68.0	64	8	HUMMACU	L37707 Homo saplen
26	13.6	68.0	86	6	AX236733	AX236733 Sequence
27	13.6	68.0	90	6	AX236627	AX236627 Sequence
28	13.6	68.0	97	11	AF430188	AF430188 Synthetic
29	13.6	68.0	100	2	AB182402	AB182402 Ceratina
30	13.6	68.0	100	10	AF235063	AF235063 Mus muscu
31	13.4	67.0	50	6	AR410670	AR410670 Sequence
32	13.4	67.0	50	6	AR439034	AR439034 Sequence
33	13.4	67.0	50	6	AR473054	AR473054 Sequence
34	13.4	67.0	50	6	AR527040	AR527040 Sequence
35	13.4	67.0	50	6	AR566073	AR566073 Sequence
36	13.4	67.0	50	6	AR592091	AR592091 Sequence
37	13.4	67.0	50	6	AR604365	AR604365 Sequence
38	13.4	67.0	50	6	AR604951	AR604951 Sequence
39	13.4	67.0	50	6	AR613616	AR613616 Sequence
40	13.4	67.0	50	6	AR635787	AR635787 Sequence
41	13.4	67.0	50	6	AR650516	AR650516 Sequence
42	13.4	67.0	50	6	AR657457	AR657457 Sequence
43	13.4	67.0	50	6	AR697498	AR697498 Sequence
44	13.4	67.0	60	6	COS37981	COS37981 Sequence
45	13.2	66.0	21	6	A86893	A86893 Sequence 3

ALIGNMENTS

RESULT 1
BD211660
LOCUS
DEFINITION
Antisense oligonucleotide sequence of neuropilin and method of using the same for controlling cell proliferation.

ACCESSION
BD211660
VERSION
BD211660.1 GI:33021430

KEYWORDS
JP 2002512793-A/3.
SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
Wright,J.A., Young,A.H. and Lee,Y.S.
1 (bases 1 to 20)

AUTHORS
Wright,J.A., Young,A.H. and Lee,Y.S.
TITLE
Antisense oligonucleotide sequence of neuropilin and method of using the same for controlling cell proliferation

JOURNAL
Patent: JP 2002512793-A 3 08-MAY-2002;

GENESENSE TECHNOLOGIES INC

COMMENT
OS Homo sapiens (human)

PN JP 2002512793-A/3
PD 08-MAY-2002

PR 23-APR-1998 JP 2000545999
PI 23-APR-1998 US 60/082791

PC C12N15/09,A61K31/711,A61K48/00,A61P35/00,C12N15/00 CC
Antisense oligonucleotide sequence of neuropilin and method of using the

CC same for controlling cell proliferation

FT key Location/Qualifiers

FT source Location/Qualifiers

FEATURES
source Location/Qualifiers

ORIGIN
1..20 /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGACGAGGCGGACGACGCGC 20
1 GGACGAGGCGGACGACGCGC 20

Db 1 GGACGAGGCGGACGACGCGC 20

RESULT 2
AX156995
LOCUS A23183/c
DEFINITION Sequence 323 from Patent WO0140521.
ACCESSION AX156995
VERSION AX156995.1 GI:14538326
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1
AUTHORS Shimkova, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 323 07-JUN-2001;
Curegen Corporation (US)
FEATURES
source 1.51
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 26
/note="1 of 2 allelic variants (324 is other entry)
Accession number CG20436198"

ORIGIN

Query Match 84.0%; Score 16.8; DB 6; Length 51;
Best Local Similarity 90.0%; Pred. No. 7e+04;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGACGAGGCGGACGACGCGC 20
22 GGACGCGGCGGACGACGCGC 41

Db 22 GGACGCGGCGGACGACGCGC 41

RESULT 3
CQ745222/c
LOCUS CQ745222
DEFINITION Sequence 31156 from Patent WO02068579.
ACCESSION CQ745222
VERSION CQ745222.1 GI:42362958
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE Kite, such as nucleic acid arrays, comprising a majority of
humanecons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 31156 06-SEP-2002;
PE Corporation (NY) (US)
FEATURES
source 1..96
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 76.0%; Score 15.2; DB 6; Length 96;
Best Local Similarity 85.0%; Pred. No. 2.2e+05;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGACGAGGCGGACGACGCGC 20
31 GGCTGAGGCGGACGACGCGC 12

Db 31 GGCTGAGGCGGACGACGCGC 12

RESULT 4
A23183
LOCUS A23183/c
DEFINITION Artificial DNA for DNA adapter (d. 7).
ACCESSION A23183
VERSION A23183.1 GI:833251
KEYWORDS
SOURCE
ORGANISM synthetic construct
synthetic construct
other sequences: artificial sequences.
REFERENCE 1
AUTHORS Stern, A., Hagemann, I. and Ziegler-Landeburger, D.
TITLE Method of introduction of nucleic acids in cells
JOURNAL Patent: EP 0544292-A 7 02-JUN-1993;
BOEHRINGER MANNHEIM GMBH
FEATURES
source 1..99
Location/Qualifiers
/organism="synthetic construct"
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/db_xref="taxon:32630"

ORIGIN

Query Match 76.0%; Score 15.2; DB 6; Length 99;
Best Local Similarity 85.0%; Pred. No. 2.2e+05;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGACGAGGCGGACGACGCGC 20
88 GGACGACGCGGACGACGCGC 69

Db 88 GGACGACGCGGACGACGCGC 69

RESULT 5
AX997929
LOCUS AX997929
DEFINITION Sequence 9392 from Patent EP1260592.
ACCESSION AX997929
VERSION AX997929.1 GI:41004275
KEYWORDS
SOURCE
ORGANISM Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
REFERENCE 1
AUTHORS Donner, H., Drescher, B., Huber, A. and Weber, J.
TITLE Biochip
JOURNAL Patent: EP 1260592-A 9392 27-NOV-2002;
MWG - Biotech AG (DE)
FEATURES
source 1..100
Location/Qualifiers
/organism="Escherichia coli"
/mol_type="unassigned DNA"
/db_xref="taxon:562"
/note="D1832 D1832 U00096 complement(1913655__1914206)"

ORIGIN

Query Match 74.0%; Score 14.8; DB 6; Length 100;
Best Local Similarity 88.9%; Pred. No. 3.1e+05;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GACGAGGCGGACGACGCGC 19
15 GACGAGGACGACGACGCGC 32

Db 15 GACGAGGACGACGACGCGC 32

RESULT 6
AX997930
LOCUS AX997930
DEFINITION Sequence 100 bp DNA
ACCESSION AX997930
VERSION AX997930.1 GI:41004275
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE Kite, such as nucleic acid arrays, comprising a majority of
humanecons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 31156 06-SEP-2002;
PE Corporation (NY) (US)
FEATURES
source 1..96
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 76.0%; Score 15.2; DB 6; Length 96;
Best Local Similarity 85.0%; Pred. No. 2.2e+05;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

DEFINITION Sequence 9393 from Patent EP1260592.
ACCESSION AX997930
VERSION AX997930.1 GI:41004276
KEYWORDS
SOURCE Escherichia coli
ORGANISM Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.

REFERENCE 1
AUTHORS Donner, H., Dreischer, B., Huber, A. and Weber, J.
TITLE Biochip
JOURNAL Patent: EP 1260592-A 9393 27-NOV-2002;
MMG - Biotech AG (DE)
FEATURES
source 1.100
Location/Qualifiers
/organism="Escherichia coli"
/mol_type="unassigned DNA"
/db_xref="taxon:562"
/note="b1832 b1832 U00096 complement (1913655_1914206) "

ORIGIN

Query Match 74.0%; Score 14.8; DB 6; Length 100;
Best Local Similarity 88.9%; Pred. No. 3.1e+05;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GACGAGGCGGACGACGCGC 19
Db 79 GACGAGGCGGACGACGCGC 96

RESULT 7
AR559751/c
LOCUS AR559751 26 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 5 from patent US 6750380.
ACCESSION AR559751.
VERSION AR559751.1 GI:53969849
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Johal, G.S. and Mullan, D.S.
TITLE Isolated nucleic acid molecules encoding the Dw3 P-glycoprotein of sorghum and methods of modifying growth in transgenic plants therewith
JOURNAL Patent: US 6750380-A 5 15-JUN-2004;
Plioneer HI-Bred International, Inc. and The Curators of the University of Missouri; Des Moines, IA
FEATURES
source 1..26
Location/Qualifiers
/organism="Unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 71.0%; Score 14.2; DB 6; Length 26;
Best Local Similarity 84.2%; Pred. No. 6.6e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GACGAGGCGGACGACGCGC 20
Db 24 GACGAGGCGGACGACGCGC 6

RESULT 8
AX146654/c
LOCUS AX146654 26 bp DNA linear PAT 31-MAY-2001
DEFINITION Sequence 5 from Patent WO0134818.
ACCESSION AX146654
VERSION AX146654.1 GI:14285047
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Johal, G.S. and Mullan, D.S.
TITLE Sorghum dwarfing genes and methods of use
JOURNAL Patent: WO 0134818-A 5 17-MAY-2001;
Johal, Gurmukh S. (US) ; Mullan, Dilbag S. (US)
FEATURES
source 1..26
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide primer designed from sequence of Zea mays Br2 gene"

ORIGIN

Query Match 71.0%; Score 14.2; DB 6; Length 26;
Best Local Similarity 84.2%; Pred. No. 6.6e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GACGAGGCGGACGACGCGC 20
Db 24 GACGAGGCGGACGACGCGC 6

RESULT 9
AX490799/c
LOCUS AX490799 40 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 13 from Patent WO0246400.
ACCESSION AX490799
VERSION AX490799.1 GI:22323749
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Kranz, D.M., Starwalt, S. and Bluestone, J.A.
TITLE Mutated class II major histocompatibility proteins
JOURNAL Patent: WO 0246400-A 13 13-JUN-2002;
The Board of Trustees of the University of Illinois (US)
FEATURES
source 1..40
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic nucleotide primer"

ORIGIN

Query Match 71.0%; Score 14.2; DB 6; Length 40;
Best Local Similarity 84.2%; Pred. No. 6e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GACGAGGCGGACGACGCGC 20
Db 39 GACGTGGCGGACGACGCGC 21

RESULT 10
AX128401
LOCUS AX128401 45 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 62 from Patent WO0130843.
ACCESSION AX128401
VERSION AX128401.1 GI:14134909
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Barbas, C.F., Kadon, M. and Beerli, R.
TITLE Ligand activated transcriptional regulator proteins
JOURNAL Patent: WO 0130843-A 62 03-MAY-2001;
Novartis AG (CH) ; The Scripps Research Institute (US)
FEATURES
source 1..45
Location/Qualifiers
/organism="synthetic construct"

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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Recombinant molecule"
ORIGIN

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Matches	16	Conservative	0	Mismatches 3, Indels 0, Gaps 0
Qy	1	GCACGAGGGCGACGACGCG	19	
Db	3	GCAGGAGGCGCGCGCCGCGC	21	

RESULT 11					
AX429834					
LOCUS	AX429834	45 bp	DNA		
DEFINITION	Sequence 26 from Patent WO0206463.			linear	PAT 21-JUN-2002
ACCESSION	AX429834				
VERSION	AX429834.1	GI:21541010			
KEYWORDS					
SOURCE	unidentified				
ORGANISM	unidentified				
	unclassified sequences.				

AUTHORS	Beerli, R., Schnopfer, U., and Bardas, C. F.
TITLE	Regulation of gene expression using single-chain, monomeric, ligand dependent polypeptide switches
JOURNAL	Patent: WO 0206463-A 26 24-JAN-2002; The Scripps Research Institute (US)
FEATURES	Location/Qualifiers
source	1..45 /organism="unidentified" /mol_type="unassigned DNA" /db_xref="taxon:32644" /note="Synthesized"

Query Match	71.0%	Score 14.2	DB 6	Length 45
Best Local Similarity	84.2%	Pred. No. 5	9e+05	
Matches 16	Conservative 0	Mismatches 3	Indels 0	Gaps 0
QY	1	GGACGAGGGCCGACACGGC	19	
db	3	GGACGAGGGCCGCGCCGGC	21	

LOCUS	AR038667	65 bp	DNA	linear	PAT 29-SEP-1995
DEFINITION	Sequence	5 from patent US 5807675.			
ACCESSION	AR038667				
VERSION	AR038667.1	GI:5958030			
KEYWORDS					
SOURCE	unknown.				
ORGANISM	unknown.				
REFERENCE	1 (bases 1 to 65)				
AUTHORS	Davallian,D., Singh,R. and Ullman,E.F.				
TITLE	Fluorescent oxygen channeling immunoassays				
JOURNAL	Patent: US 5807675-A 5 15-SEP-1995;				
FEATURES	Location/Qualifiers				
source	1..65				

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ORIGIN      /mol_type="unassigned DNA"

Query Match: 71.0%; Score 14.2; DB 6; Length 65;
Best Local Similarity 84.2%; Pred No. 5.4e-05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0.

OY      2 GATGAGGGCGAGACGCGC 20
      ||| ||||| ||||| |||||

```

```

DB              3  GAAGCGGGCGGCGATGGCG  21

RESULT  13
LOCUS   AR038665/c
DEFINITION
Sequence 3 from patent US 5807675.
ACCESSION AR038665
VERSION   AR038665.1  GI:5958028
KEYWORDS
SOURCE   Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 66)
AUTHORS Davalian,D., Singh,R. and Ullman,E.F.
TITLE    Fluorescent oxygen channeling immunoassays
JOURNAL  Patent: US 5807675-A 3 15-SEP-1998;
FEATURES
Location/Qualifiers
source    1..66
           /organism="Unknown"
           /mol_type="unassigned DNA"
ORIGIN

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Query Match	71.0%	Score 14.2	DB 6	Length 66
Best Local Similarity	84.2%	Pred. No. 5.4e+05		
Matches	16	Conservative	0	Mismatches 3
				Indels 0
				Gaps 0
QY	2	GACGAGGGCGAGCAGCGCG	20	
Db	28	GAAAGGGGGCGAGCAGCGCG	10	

RESULT	14	
LOCUS	AF362846	78 bp RNA linear VRL 09-MAY-2001
DEFINITION	HIV-1 isolate 3040PI from USA envelope glycoprotein, V3 region (env) gene, partial cds.	
ACCESSION	AF362846	
VERSION	AF362846.1	GI:14010375
KEYWORDS		
SOURCE		
ORGANISM	Human immunodeficiency virus 1 (HIV-1)	
REFERENCE	Human immunodeficiency virus 1	
AUTHORS	Vituses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae; Lentivirus; Primate lentivirus group.	
TITLE	1 (bases 1 to 78)	
JOURNAL	Freel,S.A., Williams,J.M., Nelson,J.A., Patton,L.L., Fiscus,S.A., Swanstrom,R. and Shugars,D.C.	
PUBMED	Characterization of human immunodeficiency virus type 1 in saliva and blood plasma by V3-specific heteroduplex tracking assay and genotype analyses	
REFERENCE	J. Virol. 75 (10), 4935-4940 (2001)	
AUTHORS	2 (bases 1 to 78)	
TITLE	Freel,S.A., Williams,J.M., Nelson,J.A., Patton,L.L., Fiscus,S.A., Swanstrom,R. and Shugars,D.C.	
JOURNAL	Direct Submission	
FEATURES	Submitted (21-MAR-2001) Dentistry and Microbiology, University of North Carolina at Chapel Hill, Chapel Hill, NC 27599, USA	
source	Location/Qualifiers	
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	/vifion	
	/mol_type="genomic RNA"	
	/isolate="3040PI"	
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	/tissue_type="blood plasma"	
	/country="USA"	
gene	<1..>78	
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CDS	<1..>78	
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	/note="V3 region"	
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 01:41:40 ; Search time 171.4 Seconds
(without alignments)
777.677 Million cell updates/sec

Title: US-09-296-264-3

Perfect score: 20

Sequence: 1 gacgagggcgagcagcagcg 20

Scoring table: IDENTITY_NUC

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 3390996

Minimum DB seq length: 20

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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9: geneseqn2003bs:*
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11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3	AAZ31433 Human neu
2	20	100.0	20	9	ADA74685 GT13603 a
3	16.8	84.0	51	4	AA173382 Human sil
4	15.4	77.0	27	10	ADD95271 Acalligene
5	15.2	76.0	51	12	ADP85110 PCR prime
6	15.2	76.0	95	2	AAQ42957 Encodes X
7	14.8	74.0	100	8	ACD78116 E. coli K
8	14.8	74.0	100	8	ACD78117 E. coli K
9	14.2	71.0	26	4	AAAD06342 Sorghum d
10	14.2	71.0	30	3	AAZ98666 Escherich
11	14.2	71.0	30	3	AAZ98642 Probe for
12	14.2	71.0	40	6	ABN84043 Single ch
13	14.2	71.0	45	4	AAAD06100 Drosophi
14	14.2	71.0	45	6	AA172470 D. melano
15	14.2	71.0	45	8	ACA02214 D. melano
16	14.2	71.0	50	3	AAZ98665 Escherich
17	14.2	71.0	50	3	AAZ98641 E. coli K
18	14.2	71.0	60	4	AAZ48615 Pseudomon
19	14.2	71.0	60	4	AAZ48592 Pseudomon

C	20	14.2	71.0	60	8	ACA15641 Prokaryot
C	21	14.2	71.0	60	8	ACA15759 Prokaryot
C	22	14.2	71.0	66	2	AAQ85876 "CITRAC-3
C	23	13.8	69.0	21	13	ADU43614 Knock-dow
C	24	13.8	69.0	27	10	ADD95213 Acalligene
C	25	13.8	69.0	33	14	ADZ64744 Bmal1 pro
C	26	13.8	69.0	45	14	ADZ67731 IBD SNP d
C	27	13.8	69.0	50	6	ABZ03249 Human leu
C	28	13.8	69.0	50	6	ABZ04801 Human leu
C	29	13.8	69.0	50	10	ADG33513 Human DNA
C	30	13.8	69.0	60	2	AAV60517 Cloned Pa
C	31	13.8	69.0	78	2	AAV19397 Signal se
C	32	13.6	68.0	22	14	ABZ8666 RT-PCR pr
C	33	13.6	68.0	30	2	AA174994 Herpes si
C	34	13.6	68.0	30	2	AAV72560 Herpes si
C	35	13.6	68.0	31	12	ADU08593 Positiona
C	36	13.6	68.0	32	11	ADM33282 Monocag P
C	37	13.6	68.0	32	11	ADM33282 Monocag P
C	38	13.6	68.0	32	12	ADU08587 Positiona
C	39	13.6	68.0	32	12	ADU08592 Positiona
C	40	13.6	68.0	32	12	ADU08598 Positiona
C	41	13.6	68.0	32	12	ADU08583 Positiona
C	42	13.6	68.0	32	12	ADU08596 Positiona
C	43	13.6	68.0	32	12	ADU08611 Positiona
C	44	13.6	68.0	32	12	ADU08585 Positiona
C	45	13.6	68.0	32	14	ABZ8663 Oligonuci

ALIGNMENTS

RESULT 1
AAZ31433
ID AAZ31433 standard; DNA, 20 BP.
AC AAZ31433;
XX
DT 07-FEB-2000 (first entry)
XX
DE Human neuropilin mRNA specific antisense oligo GT13603.
XX
KW Neuropilin; human; growth; metastasis; tumor; neovascularization; cancer;
XX papilloma; diabetic retinopathy; antisense; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN W0955855-A2.
XX
PD 04-NOV-1999.
XX
PF 23-APR-1999; 99WO-CA000324.
XX
PR 23-APR-1998; 98US-0082791P.
XX
FA (GENE-) GENSENSE TECHNOLOGIES INC.
XX
PI Wright JA, Young AH, Lee YS;
XX
DR WPI; 2000-023357/02.
XX
PT Antisense oligonucleotides that inhibit neuropilin expression, useful for
FT treating cancer.
XX
PS Claim 4; Page 16; 57pp; English.
CC Sequences AAZ31431-460 represent antisense oligonucleotides which inhibit
CC human neuropilin expression. The antisense oligonucleotides can be used
CC to inhibit the growth of a mammalian tumor and inhibit
CC neovascularization. The oligonucleotides may be used to treat various
CC forms of cancers or tumors, such as sarcomas, melanomas, adenomas,
CC carcinomas of solid tissue, hypoxic tumors, squamous cell carcinomas of
CC the mouth, throat, larynx and lung, genitourinary cancers such as

CC cervical and bladder cancer, hematopoietic cancers, colon cancer, breast
CC cancer, pancreatic cancer, renal cancer, brain cancer, skin cancer, liver
CC cancer, head and neck cancers, and nervous system cancers, as well as
CC benign lesions such as papillomas. The methods may be used to treat
CC neovascularisation disorders such as diabetic retinopathy, and
CC retinopathy of prematurity and age related macular degeneration
XX
SQ Sequence 20 BP; 4 A; 5 C; 11 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGACGAGGCGGACGCGG 20
DB 1 GGACGAGGCGGACGCGG 20

RESULT 2

ADA74685
ID ADA74685 standard; DNA; 20 BP.

XX ADA74685;

DT 20-NOV-2003 (first entry)

XX GT13603 antisense oligonucleotide targeted to human neuropilin mRNA.

XX neuropilin; VEGF165R; vascular endothelial growth factor receptor;

XX cytosolic; growth; tumour metastasis; angiogenesis; gene therapy;

XX GT13603; antisense; human; ss.

XX Homo sapiens.

XX US2003083274-A1.

XX PD 01-MAY-2003.

XX PF 22-APR-1999; 99US-00296264.

XX PR 23-APR-1998; 98US-0082791P.

XX PA (WRIGHT) WRIGHT J A.

XX PA (YOUNG) YOUNG A H.

XX PA (LEEVY) LEEVY S.

XX PI Wright JA, Young AH, Lee YS;

XX DR WPI; 2003-576622/54.

XX PT New antisense oligonucleotide that inhibits neuropilin expression, useful
XX for inhibiting growth of mammalian tumor or inhibiting metastasis of a
XX mammalian tumor.

XX PS Claim 1; Page 5; 27pp; English.

CC The invention relates to a novel antisense oligonucleotide that inhibits
CC the expression of neuropilin, also known as VEGF165R (vascular
CC endothelial growth factor receptor). The oligonucleotide of the invention
CC demonstrates cytostatic activity and may be useful for inhibiting the
CC growth or metastasis of a mammalian tumor and to inhibit angiogenesis in
CC mammals. Furthermore, the oligonucleotide may be utilised during gene
CC therapy. The current sequence is that of the GT13603 antisense
CC oligonucleotide of the invention which is targeted to human neuropilin
CC mRNA.
XX
SQ Sequence 20 BP; 4 A; 5 C; 11 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGACGAGGCGGACGCGG 20

DB 1 GGACGAGGCGGACGCGG 20

RESULT 3
AA173382
ID AA173382 standard; DNA; 51 BP.

XX AA173382;

DT 09-NOV-2001 (first entry)

XX Human silent SNP containing nucleic acid SEQ.323.

XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;

XX protein therapy; vaccine; probe; diagnostic assay; detection;

XX quantitation; restorative therapy; polymorphic; db.

XX Homo sapiens.

XX WO200140521-A2.

XX PD 07-JUN-2001.

XX PF 30-NOV-2000; 2000WO-US032758.

XX PR 30-NOV-1999; 99US-0168138P.

XX PR 29-NOV-2000; 2000US-00726173.

XX PA (CURA-) CURAGEN CORP.

XX PI Shinkets RA, Leach M;

XX DR WPI; 2001-356160/37.

XX PT Polymorphic nucleic acid sequences, useful in genetic testing and
XX therapy.

XX PS Claim 1; Page 153; 2653pp; English.

CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AA173114 to AA175329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (I) may be used to treat disorders by rectifying mutations or
CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patient's own
CC production of polypeptide. Additionally, (I) and its complementary
CC sequences may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC polypeptides encoded by (I) may be used as antigens in the production of
CC antibodies specific for polymorphic polypeptides. The antibodies may also
CC be used to down regulate expression and activity. The antibodies may also
CC be used as diagnostic agents for detecting the presence of polymorphic
CC polypeptides in samples
XX
SQ Sequence 51 BP; 5 A; 14 C; 29 G; 3 T; 0 U; 0 Other;

Query Match 84.0%; Score 16.8; DB 4; Length 51;
Best Local Similarity 90.0%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGACGAGGCGGACGCGG 20
DB 22 GGACCGGCGGACGAGCGGCG 41

RESULT 4
ADD95271

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ID ADP95271 standard; DNA; 27 BP.
XX
XX ADB95271;
XX
XX 29-JAN-2004 (first entry)
XX
XX Acaligenes faecalis M3A 3-HP dehydrogenase PCR primer SEQ ID NO:19.
DE
XX alanine 2; 3-aminomutase; enzyme; beta-alanine; alpha-alanine; 1;
XX 3-propanediol; pantothenate; coenzyme A; CoA; cell; PCR primer; ss.
XX
XX Synthetic.
OS
XX Alcaligenes faecalis.
XX
XX WO2003062173-A2.
XX
XX 31-JUL-2003.
XX
XX 17-JAN-2003; 2003WO-US001635.
XX
XX 18-JAN-2002; 2002US-0350727P.
XX
XX 25-APR-2002; 2002US-0375785P.
XX
XX (CRGI ) CARGILL INC.
XX
XX Liao HH, Gokarn RR, Gort SJ, Jessen HT, Selifonova O;
XX
XX WPI; 2003-646066/61.
XX
XX New cell, comprising alanine 2,3-aminomutase activity, useful for
XX producing beta-alanine from alpha-alanine, 1,3-propanediol, pantothenate,
XX CoA, HP or 1,3-propanediol.
XX
XX Example 10; SEQ ID NO 19; 119pp; English.
XX
XX The present invention describes a cell, comprising alanine 2,3-
XX aminomutase activity, and which produces beta-alanine from alpha-alanine.
XX Also described: (1) a polypeptide comprising alanine 2,3-aminomutase
XX activity; (2) an isolated nucleic acid comprising a sequence that encodes
XX the polypeptide; (3) a vector comprising the isolated nucleic acid; (4) a
XX recombinant nucleic acid comprising the isolated nucleic acid; (5) a cell
XX transformed with the recombinant nucleic acid; (6) a non-human transgenic
XX animal comprising the recombinant nucleic acid; (7) a transformed cell
XX comprising at least exogenous nucleic acid molecule, which encodes the
XX polypeptide; (8) a specific binding agent that specifically binds to the
XX polypeptide; (9) a method of producing the polypeptide; (10) a method of
XX making beta-alanine from alpha-alanine; (11) a method of identifying a
XX cell comprising alanine 2,3-aminomutase activity; (12) a method for
XX making 1,3-propanediol, pantothenate, CoA, 3-hydroxypropionic acid (HP);
XX (13) a method for making 1,3-propanediol from 3-HP; and (14) a transgenic
XX plant comprising the recombinant nucleic acid. The cell is useful for
XX producing beta-alanine from alpha-alanine, 1,3-propanediol, pantothenate,
XX CoA, HP or 1,3-propanediol. The present sequence represents a PCR primer
XX which is used in the exemplification of the present invention.
XX
XX Sequence 27 BP; 5 A; 5 C; 11 G; 6 T; 0 U; 0 Other;
SQ
Query Match 77.0%; Score 15.4; DB 10; Length 27;
Best Local Similarity 94.1%; Pred. No. 5.7e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 ACGAGGGCGAGCAGCGC 19
DB 6 ACGAGGGCGAGCAGCGC 22
```

```
RESULT 5
ADP85110/c
ID ADP85110 standard; DNA; 51 BP.
XX
XX ADB85110;
XX
XX 23-SEP-2004 (first entry)
XX
XX
```

```
XX
XX PCR primer used to amplify human RAMOS RA-1 VHS leader gDNA.
DE
XX hypermutating cell; in vivo nucleic acid evolution; diversity;
XX RAMOS RA-1 cell; human; VHS leader; ss; PCR; primer.
XX
XX Homo sapiens.
OS
XX WO2004055182-A1.
XX
XX 01-JUL-2004.
XX
XX 18-DEC-2003; 2003WO-AU001697.
XX
XX 18-DEC-2002; 2002AU-00953381.
XX
XX (DIAT-) DIATECH PTY LTD.
XX
XX Irving RA, Hudson PJ, Mustafa H, Mark K, Abregu ME;
XX
XX WPI; 2004-488066/46.
XX
XX Producing and selecting a gene product with desired characteristics by
XX introducing into a hypermutating cell a target nucleic acid molecule
XX encoding a gene product, useful in the field of evolution of nucleic
XX acids in vivo.
XX
XX Example 1; SEQ ID NO 117; 143pp; English.
XX
XX The invention relates to a novel method for producing and selecting a
XX gene product with desired characteristics. The method comprises
XX introducing into a hypermutating cell, a target nucleic acid molecule
XX encoding a gene product, such that the molecule is integrated into an
XX immunoglobulin locus of the genome of the hypermutating cell, culturing
XX the hypermutating cell so the molecule undergoes hypermutation during DNA
XX and/or RNA synthesis giving rise to a population of cells expressing
XX mutant gene products and selecting a mutant gene product with desired
XX characteristics. The compositions and methods of the invention may be
XX useful in the field of evolution of nucleic acids in vivo and for
XX introducing diversity into gene products. The current sequence is that of
XX a PCR primer which was used in the exemplification of the invention.
XX
XX Sequence 51 BP; 6 A; 22 C; 10 G; 13 T; 0 U; 0 Other;
SQ
Query Match 76.0%; Score 15.2; DB 12; Length 51;
Best Local Similarity 85.0%; Pred. No. 6.5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GGAGGAGGGCGAGCAGCGCG 20
DB 40 GGAGGAGGGCGAGGATGCGC 21
```

```
RESULT 6
AAQ42957/c
ID AAQ42957 standard; DNA; 95 BP.
XX
XX AAQ42957;
XX
XX 25-MAR-2003 (revised)
XX 07-SEP-1993 (first entry)
XX
XX Encodes 8 Arg C-terminal extension of G-CSF.
XX
XX Granulocyte Colony Stimulating Factor; Cell-homing factor;
XX fusion protein; targeting; gene therapy; de.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
XX FH 63..86
XX FT misc_feature
XX
XX /tag= a
XX /note= "8 Arg codons - there is a 4-nucleotide overhang
XX
```

at the 5' end of the coding strand and a 4-nt overhang (5'-AGCT-3') at the 5' end of the complementary strand"

EP544292-A2.
02-JUN-1993.
26-NOV-1992; 92EP-00120205.
27-NOV-1991; 91DE-04139001.
(BOEF) BOEHRINGER MANNHEIM GMBH.
Stern A, Hagemann I, Ziegler-Landesberger D;
WPI; 1993-177078/22.
Cell introduction of cell homing factor-polycation-nucleic acid complex -
of linear genetic cell homing factor-polycation fusion having ionic
interaction with nucleic acid, the polycation part having at least three
lysine and arginine.
Example 2; Page 6; 17pp; German.
This sequence codes for the C-terminal region of G-CSF fused to 8
Arginine residues and a proline residue. The basic nature of the
extension ("polycation chain") results in ionic interaction of the
protein with DNA to form a complex. The G-CSF acts to target the complex
to e.g. NFS60 cells where the associated DNA can be taken up by those
cells at a much higher rate than when the basic extension is not present.
(Updated on 25-MAR-2003 to correct PN field.)

Sequence 95 BP; 12 A; 35 C; 26 G; 22 T; 0 U; 0 Other;
Query Match 76.0%; Score 15.2; DB 2; Length 95;
Best Local Similarity 85.0%; Pred. No. 6.2e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 GGACGAGGGCGACGACGCGC 20
88 GGACGAGCGCGCGACGCGCG 69

RESULT 7
ACD78116
ID ACD78116 standard; DNA; 100 BP.
ACD78116;
19-SEP-2003 (first entry)
E. coli K12 MG1655 biochip probe SEQ ID 9392.
Biochip; gene expression; gut; diagnostic; detection; probe; ss.
Escherichia coli.
EP1260592-A1.
27-NOV-2002.
17-MAY-2001; 2001EP-00112179.
17-MAY-2001; 2001EP-00112179.
(MMGB-) MMG-BIOTECH AG.
Donner H, Drescher B, Huber A, Weber J;
WPI; 2003-241155/24.
Biochip containing probes complementary with open reading frames in
Escherichia coli K12, useful for detecting gene expression and expression

patterns.
Claim 3; Page 1465; 2004pp; German.
This invention describes a novel biochip comprising probe spots, each
containing many identical probes. The probes are nucleotide sequences of
30-80 bases, are prepared ex situ from synthetic oligonucleotides and at
least one includes a segment of at least 20 bases identical with, or
complementary to, a segment of an open reading frame (orf) of Escherichia
coli K12. The biochip is used for specific detection of gene expression
in K12 and for determining the gene expression pattern, e.g. for
diagnostic determination of which E. coli strains are present in the gut,
and to determine the effects of e.g. growth media on gene expression. The
biochip provides as comprehensive as possible detection of the K12
genome, with simultaneous analysis of many different genes with a single
device, and comparison of gene expression between K12 and its mutants or
other E. coli strains in a single experiment. Apart from qualitative and
quantitative information about gene expression, it also allows
measurements of population densities for the various strains. The use of
synthetic oligonucleotides for preparation of probes allows free
variation in probe length and ensures high purity (and thus selectivity,
reactivity and reproducibility); also synthetic probes are generally
shorter than probes prepared by polymerase chain reaction. ACD6731 to
ACD81540 represent oligonucleotide probes used with the biochip described
in the invention

Sequence 100 BP; 29 A; 21 C; 27 G; 23 T; 0 U; 0 Other;
Query Match 74.0%; Score 14.8; DB 8; Length 100;
Best Local Similarity 88.9%; Pred. No. 9e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2 GACGAGGGCGACGACGCGC 19
15 GACGAGGACGACGACGCGC 32

RESULT 8
ACD78117
ID ACD78117 standard; DNA; 100 BP.
ACD78117;
19-SEP-2003 (first entry)
E. coli K12 MG1655 biochip probe SEQ ID 9393.
Biochip; gene expression; gut; diagnostic; detection; probe; ss.
Escherichia coli.
EP1260592-A1.
27-NOV-2002.
17-MAY-2001; 2001EP-00112179.
17-MAY-2001; 2001EP-00112179.
(MMGB-) MMG-BIOTECH AG.
Donner H, Drescher B, Huber A, Weber J;
WPI; 2003-241155/24.
Biochip containing probes complementary with open reading frames in
Escherichia coli K12, useful for detecting gene expression and expression
patterns.
Claim 3; Page 1465; 2004pp; German.
This invention describes a novel biochip comprising probe spots, each
containing many identical probes. The probes are nucleotide sequences of

CC 30-80 bases, are prepared ex situ from synthetic oligonucleotides and at
 CC least one includes a segment of at least 20 bases identical with, or
 CC complementary to, a segment of an open reading frame (or) of Escherichia
 CC coli K12. The biochip is used for specific detection of gene expression
 CC in K12 and for determining the gene expression pattern, e.g. for
 CC diagnostic determination of which E. coli strains are present in the gut,
 CC and to determine the effects of e.g. growth media on gene expression. The
 CC biochip provides as comprehensive as possible detection of the K12
 CC genome, with simultaneous analysis of many different genes with a single
 CC device, and comparison of gene expression between K12 and its mutants or
 CC other E. coli strains in a single experiment. Apart from qualitative and
 CC quantitative information about gene expression, it also allows
 CC measurements of population densities for the various strains. The use of
 CC synthetic oligonucleotides for preparation of probes allows free
 CC variation in probe length and ensures high purity (and thus selectivity,
 CC reactivity and reproducibility); also synthetic probes are generally
 CC shorter than probes prepared by polymerase chain reaction. ACD68731 to
 CC ACD81540 represent oligonucleotide probes used with the biochip described
 CC in the invention

SO Sequence 100 BP; 23 A; 21 C; 27 G; 29 T; 0 U; 0 Other;

Query Match 74.0%; Score 14.8; DB 8; Length 100;
 Best Local Similarity 88.9%; Pred. No. 9e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GACGAGCGGACACGCGC 19
 DB 79 GACGAGGACGACGACGCGC 96

RESULT 9

AAD06342/C
 ID AAD06342 standard; DNA; 26 BP.

AC AAD06342;

DT 10-AUG-2001 (first entry)

DE Sorghum dwarfing gene, Dw3 allele amplifying PCR primer #1.

KM Sorghum; dwarfing gene; Dw3; P-glycoprotein; transgenic plant;

KM plant growth; pathogen resistance; plant breeding; PCR primer; ss.

OS Sorghum bicolor.

PN WO200134818-A2.

PD 17-MAY-2001.

PF 10-NOV-2000; 2000WO-US030816.

PR 12-NOV-1999; 99US-0165176P.

PA (JOHA/) JOHAL G S.

PA (MUT/) MUTANI D S.

PI Johal GS, Mutani DS;

DR WPI; 2001-329088/34.

PT Novel sorghum dwarfing genes useful for modifying the growth of the
 PT organisms, particularly plants, such as maize, wheat, Basmati rice,
 PT rye, millet and barley and for enhancing resistance to pathogens.

PS Example 1; Page 63; 76pp; English.

CC The present sequence is a PCR primer used for amplifying sorghum dwarfing
 CC gene, Dw3 allele. The primer is derived from the nucleotide sequence of
 CC maize Bz2 gene. Dw3 DNA is useful for modifying the growth of an
 CC organism, especially reducing the height of monocotyledon plants, such as
 CC maize, wheat, rice, Basmati rice, sorghum, rye, millet and barley. Dw3
 CC DNA is useful for producing transgenic monocotyledon and dicotyledon

CC plants like soybean, sunflower, safflower, alfalfa, cotton, Brassica sp.,
 CC peanuts or fruit trees. The Dw3 DNA is also useful for isolating the
 CC nucleotide homologue molecules that encode P-glycoproteins, enhancing the
 CC resistance of plants to pathogens, including bacteria, fungi, viruses,
 CC nematodes and insects, as probes for the isolation of other P-
 CC glycoprotein-like genes and as molecular markers. Identifying plants that
 CC possess a mutant allele is useful in agriculture, particularly in
 CC breeding dwarf crop plants, particularly dwarf sorghum plants

SO Sequence 26 BP; 0 A; 12 C; 6 G; 8 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 4; Length 26;
 Best Local Similarity 84.2%; Pred. No. 1.7e+04;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GACGAGCGGACACGCGC 20
 DB 24 GACGAGCGGACACGCGC 6

RESULT 10

AAZ98666/C
 ID AAZ98666 standard; DNA; 30 BP.

AC AAZ98666;

DT 05-JUN-2000 (first entry)

DE Escherichia coli K12 DNAJ gene fragment probe sequence.

KM Specific binding assay; DNAJ; analyte determination; antigen; hapten;
 KM drug; cancer marker; pesticide; chemiluminescent compound; pollutant;
 KM probe; ss.

OS Escherichia coli.

PN EP984282-A2.

PD 08-MAR-2000.

PF 21-MAY-1992; 99EP-00121551.

PR 22-MAY-1991; 91US-00704569.

PR 20-JUN-1991; 91US-00718490.

PR 21-MAY-1992; 92EP-00304630.

PA (DADE-) DADE BEHRING MARBURG GMBH.

PI Ullman EF, Kirakosian H, Pease JS, Wagner DB, Deniloff Y;

DR WPI; 2000-225922/20.

PT Particles containing a chemiluminescent donor and a fluorescent acceptor
 PT are useful in specific binding assays to determine antigens, haptens,
 PT enzymes, hormones, cancer markers or nutritional markers.

PS Example 5; Page 66; 79pp; English.

CC This sequence represents a probe for a fragment of the Escherichia coli
 CC DNAJ gene. The fragment is used as an example target sequence in a method
 CC for determining analyte in a sample using the particles of the invention.
 CC The invention relates to particles (I) containing a compound (II) and a
 CC fluorescent compound (III). Compound II reacts with singlet oxygen to
 CC form a metastable intermediate that can decompose with simultaneous or
 CC subsequent emission of light. The fluorescent compound (III) is excited
 CC by activated compound (II) and emits at a wavelength longer than the
 CC emission wavelength of compound (II). The particles are useful in
 CC specific binding assays. The assays can be used to determine antigens or
 CC haptens, e.g. blood group or HLA antigens or bacterial, fungal, protozoal
 CC or viral antigens, other proteins e.g. immunoglobulins, cytokines,
 CC enzymes, hormones, cancer markers or nutritional markers, microorganisms,
 CC drugs, metabolites, pesticides, pollutants or polynucleotides. The longer
 CC emission wavelength of (III) eliminates interference from serum

CC components when the particles are used in specific binding assays in the
CC presence of such components
XX
SQ Sequence 30 BP; 2 A; 14 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 3; Length 30;
Best Local Similarity 84.2%; Pred. No. 1.7e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GACGAGGCGGACGCGG 20
DB 28 GAAGCGGCGGACGCGG 10

RESULT 11

AA298642/C
ID AA298642 standard; DNA; 30 BP.

XX AA298642;

XX 05-JUN-2000 (first entry)

DE Probe for E. coli DNAJ gene fragment target sequence.

XX Homogeneous specific binding assay; DNAJ gene; analyte determination;
KW antigen; hapten; drug; cancer marker; pesticide; pollutant;
KW photochemically activatable chemiluminescent compound; probe; ss.

XX Escherichia coli.

XX EP984281-A2.

XX 08-MAR-2000.

XX 21-MAY-1992; 99EP-00121547.

XX 22-MAY-1991; 91US-00704569.

XX 20-JUN-1991; 91US-00718490.

XX 21-MAY-1992; 92EP-00304630.

XX (DADE-) DADE BEHRING MARBURG GMBH.

XX Ullman EF, Klrakossian H, Pease JS, Wagner DB, Daniloff Y;

XX WPI; 2000-197307/18.

PT Homogeneous specific binding assay, e.g. for proteins or nucleic acids,
PT uses photochemically activatable chemiluminescent compound.
XX
XX Example 5; Page 66; 78pp; English.

CC This sequence represents a probe for a fragment of the Escherichia coli
CC K12 DNAJ gene, used as an example of a target sequence in a homogeneous
CC assay. The invention relates to a homogeneous assay for determining an
CC analyte, comprising combining medium suspected of containing an analyte
CC with a label reagent, and intrinsically metastable species, and
CC determining the reaction. The label reagent comprises a suspended
CC particle and a specific binding pair (sbp) member associated with a
CC photochemically activatable chemiluminescent compound (PACC), the sbp is
CC capable of binding to a second sbp or to the analyte, the second sbp
CC being capable of binding to the analyte. The metastable species is
CC PACC, when brought into close proximity by the presence or absence of the
CC analyte. The method can be used to determine antigens or haptens, e.g.
CC blood group or HLA antigens or bacterial, fungal, protozoal or viral
CC antigens, other proteins e.g. immunoglobulins, cytokines, enzymes,
CC hormones, cancer markers or nutritional markers, microorganisms, drugs,
CC metabolites, pesticides, pollutants or polynucleotides. The method is a
CC homogeneous assay and does not require a separation step
XX
SQ Sequence 30 BP; 2 A; 14 C; 8 G; 6 T; 0 U; 0 Other;

Query Match

71.0%; Score 14.2; DB 3; Length 30;

Best Local Similarity 84.2%; Pred. No. 1.7e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GACGAGGCGGACGCGG 20
DB 28 GAAGCGGCGGACGCGG 10

RESULT 12

ABN84043/C
ID ABN84043 standard; DNA; 40 BP.

XX ABN84043;

XX 23-SEP-2002 (first entry)

DE Single chain Class II MHC, I-Ag7 mutagenic primer 4.

XX Major histocompatibility complex; MHC; combinatorial library; I-Ag7;
KW insulin-dependent diabetes mellitus; autoimmune disease; antidiabetic;
KW diagnosis; mutagenesis; PCR; primer; ss.

XX Synthetic.

XX WO200246400-A2.

XX 13-JUN-2002.

XX 10-DEC-2001; 2001WO-US047830.

XX 08-DEC-2000; 2000US-0254248P.

XX (UNIT I) UNIT ILLINOIS FOUND.

XX Krantz DM, Starwalt S, Bluestone JA;

XX WPI; 2002-537566/57.

PT Novel isolated mutant major histocompatibility complex class II chimeric
PT protein displayed on recombinant yeast cell surface has improved
PT stability or T-cell receptor binding, useful for treating autoimmune
PT disease.
XX
XX Example 3; Page 27; 66pp; English.

XX The present sequence is mutagenic primer 3 for positions beta-56 and beta
CC -57 of a single chain (sc) Class II major histocompatibility complex
CC (MHC) haplotype I-Ag7 construct. A site-directed mutagenesis strategy
CC involving PCR sewing and yeast homologous recombination was used to
CC mutate residues beta-56 and -57. Mutant libraries of sc MHC Class II
CC protein were generated and displayed on the cell surface of recombinant
CC yeast cells, and stabilised I-Ag7 proteins were identified. Haplotype I-
CC Ag7 is associated with the development of insulin-dependent diabetes
CC mellitus (IDDM) in the non-obese (NOD) mouse model of IDDM. The present
CC invention allows the creation and isolation of stabilised variants of
CC Class II peptide-MHC complexes. Stabilised variants of single chain I-
CC Ag7, in association with each of 3 peptides of interest (BDC2.5(A)),
CC GAD65(78-95) and B9-23 (insulin), have been produced. These can be used in
CC diagnostic tests of IDDM, in imaging tests, and in the treatment or
CC prevention of IDDM
XX
SQ Sequence 40 BP; 4 A; 19 C; 12 G; 5 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 6; Length 40;
Best Local Similarity 84.2%; Pred. No. 1.7e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GACGAGGCGGACGCGG 20
DB 39 GACGCGGCGGACTACCGG 21

RESULT 13

```

AAD06100
ID AAD06100 standard; DNA; 45 BP.
XX
AC AAD06100;
XX
DT 31-JUL-2001 (first entry)
XX
DE Drosophila Ecr coding region amplifying primer, (Aec1)-Ecr.
XX
KW Fusion protein; nucleotide-binding domain; NBD; ligand-binding domain;
KW LBD; transcription regulating domain; TRD; zinc finger protein; ZFP;
KW ligand-activated transcriptional regulator; gene regulation;
KW gene therapy; cell proliferative disorder; cancer; psoriasis;
KW pemphigus vulgaris; Behcet's syndrome; lipid histiocytosis; Ecr;
KW PCR primer; ecdysone receptor; ss.
XX
OS Drosophila sp.
XX
PN WO200130843-A1.
XX
PD 03-MAY-2001.
XX
PF 23-OCT-2000; 2000WO-EP010430.
XX
PR 25-OCT-1999; 99US-00433042.
XX
PR 02-JUN-2000; 2000US-00586625.
XX
PA (NOVS ) NOVARTIS AG.
XX
PA (SCRI ) SCRIPPS RES INST.
XX
PI Barbas CF, Kadan M, Beerli R;
XX
DR WPI; 2001-308618/32.
XX
PT New fusion protein containing nucleotide-binding and ligand-binding
PT domains, useful e.g. in gene therapy of cancer, provides ligand-activated
PT control of gene expression.
XX
XX
PS Example 12; Page 110; 218pp; English.
XX
CC The invention relates to fusion protein comprising a nucleotide-binding
CC domain (NBD), a ligand-binding domain (LBD) of an intracellular receptor
CC (ICR) and a transcription regulating domain (TRD). NBD is a polydactyl
CC zinc finger protein, or a modular part of it, that interacts specifically
CC with a contiguous sequence of at least 3 nucleotides. The fusion protein
CC functions as a ligand-activated transcriptional regulator. The fusion
CC protein and the nucleic acid encoding it, are used to regulate gene
CC expression, particularly in gene therapy for treating malignant cell
CC proliferative diseases (e.g. colon cancer, prostate cancer, renal-cell
CC carcinoma) and non-malignant cell proliferative diseases (e.g. psoriasis,
CC pemphigus vulgaris, Behcet's syndrome and lipid histiocytosis). The
CC fusion protein and its DNA are also useful for treating diseases caused
CC by viruses in humans/plants, genetic and/or acquired diseases. The fusion
CC protein can be designed to target any selected gene (endogenous or
CC exogenous), and can be made to have different selectivity or specificity
CC for endogenous or exogenous ligands. The present sequence is Drosophila
CC ecdysone receptor (Ecr) coding region amplifying primer, (Aec1)-Ecr. This
CC primer is used to obtain LBD which is used to construct fusion protein of
CC the invention
XX
SQ Sequence 45 BP; 9 A; 14 C; 17 G; 5 T; 0 U; 0 Other;
XX
Query Match 71.0%; Score 14.2; DB 4; Length 45;
Best Local Similarity 84.2%; Pred. No. 1.7e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 1 GGACGAGGGCGAGCAGGC 19
Db 3 GGAGGAGGGCGCGCCCGGC 21

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```

ID AAI72470 standard; DNA; 45 BP.
XX
AC AAI72470;
XX
DT 16-MAY-2002 (first entry)
XX
DE D. melanogaster ecdysone receptor LBD primer, EcRasc-B.
XX
KW Polymerase chain reaction; primer; amplify; PCR; reporter;
KW polypeptide gene switch; ligand binding domain; LBD; transcription;
KW nuclear hormone receptor; gene therapy; regulation; expression; ss.
XX
OS Synthetic.
XX
PN WO200206463-A2.
XX
PD 24-JAN-2002.
XX
PF 16-JUL-2001; 2001WO-EP008190.
XX
PR 18-JUL-2000; 2000US-00619063.
XX
PA (NOVS ) NOVARTIS AG.
XX
PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GRS MBH.
XX
PA (SCRI ) SCRIPPS RES INST.
XX
PI Beerli R, Schopfer U, Barbas CF;
XX
DR WPI; 2002-179793/23.
XX
PT Single chain, monomeric polypeptide gene switches for regulating gene
PT function, comprise two ligand binding domains derived from nuclear
PT hormone receptors operatively linked to one functional domain.
XX
XX
PS Example 1; Page 31; 63pp; English.
XX
CC The sequences given in AAI72463-72 are primers which were used in the
CC generation of single chain switch which could be used in the construction
CC of a non-naturally occurring polypeptide gene switch comprising two
CC ligand binding domains (LBds) derived from nuclear hormone receptors
CC operatively linked to a first functional domain. The gene switch is
CC useful for regulating the function of a target nucleotide that contains a
CC defined sequence, by exposing the target nucleotide to the polypeptide
CC gene switch in the presence of a ligand that binds one of the LBds of the
CC polypeptide, where the DNA binding domain of the polypeptide binds the
CC defined sequence, or the functional domain of the polypeptide alters the
CC function of the target nucleotide. The gene switch is also useful in the
CC field of gene therapy and as a regulator of gene expression or
CC transcription. The advantage of the gene switches of the invention over
CC existing gene switches is the need for only a single molecular switch and
CC a single expression vector for production of that switch
XX
SQ Sequence 45 BP; 9 A; 14 C; 17 G; 5 T; 0 U; 0 Other;
XX
Query Match 71.0%; Score 14.2; DB 6; Length 45;
Best Local Similarity 84.2%; Pred. No. 1.7e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 1 GGACGAGGGCGAGCAGGC 19
Db 3 GGAGGAGGGCGCGCCCGGC 21

```

RESULT 14
AAI72470

RESULT 15
ID AAI72470 standard; DNA; 45 BP.
AC AAI72470;
DT 16-MAY-2002 (first entry)
DE D. melanogaster ecdysone receptor LBD amplification primer EcRasc-B.
XX

```

KM Ecdysone receptor; ligand binding domain; LBD; PCR; primer; ss;
KW gene switch; gene regulation; fruit fly.
XX
OS Drosophila melanogaster.
OS Synthetic.
XX
PN US2002168714-A1.
XX
PD 14-NOV-2002.
XX
PF 18-JUL-2001; 2001US-00908153.
XX
PR 18-JUL-2000; 2000US-00325747.
XX
PA (SCRI ) SCRIPPS RES INST.
XX
PI Barbas CF, Beerli R, Schopfer U;
XX
DR WPI; 2003-328405/31.
XX
PT Novel polypeptide gene switch useful for regulating gene function,
PT comprises two ligand binding domains derived from nuclear hormone
PT receptors operatively linked to a functional domain.
XX
PS Example 1; Page 11; 33pp; English.
XX
CC The invention relates to a non-naturally occurring polypeptide (or
CC polypeptide gene switch) comprising two ligand binding domains derived
CC from nuclear hormone receptors operatively linked to a first functional
CC domain. The polypeptide is useful for regulating the function of a target
CC nucleotide that contains a defined sequence, by exposing the target
CC nucleotide to the polypeptide in the presence of a ligand that binds one
CC of the ligand binding domains of the polypeptide, where the DNA binding
CC domain of the polypeptide binds the defined sequence or alters the
CC function of the target nucleotide. The gene switches can be produced
CC using a single molecular switch and a single expression vector. The
CC present sequence represents a Drosophila melanogaster ecdysone receptor
CC ligand binding domain amplification primer
XX
SQ Sequence 45 BP; 9 A; 14 C; 17 G; 5 T; 0 U; 0 Other;

```

Query Match 71.0%; Score 14.2; DB 8; Length 45;
 Best Local Similarity 84.2%; Pred. No. 1.7e+04;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

QY 1 GGACGAGGGCGGACGCGC 19
   ||| ||||| ||| |||
Db 3 GGAGGAGGGCGGCGCCGCGC 21

```

Search completed: December 24, 2005, 12:28:53
 Job time : 172.4 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 10:37:31 ; Search time 1572 Seconds

(without alignments)
595.256 Million cell updates/sec

Title: US-09-296-264-3

Perfect score: 20

Sequence: 1 ggcagcggcgagcagcagcgcg 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 2339354128 residues

Total number of hits satisfying chosen parameters: 768474

Minimum DB seq length: 20

Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :
EST:
1: gb_ests1:
2: gb_ests2:
3: gb_ests3:
4: gb_ests4:
5: gb_ests5:
6: gb_ests6:
7: gb_ests7:
8: gb_ests8:
9: gb_ests9:
10: gb_ests10:
11: gb_ests11:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	15.8	79.0	88	10	C2293884 P078A09 G
2	15.2	76.0	79	1	A1000040
3	15.2	76.0	88	10	C2914888
4	14.8	74.0	84	9	CC796892
5	14.8	74.0	87	1	AM064096
6	14.8	74.0	91	9	A2919805
7	14.8	74.0	91	9	BH218633
8	14.4	72.0	64	1	A1900558
9	14.4	72.0	84	9	BH226921
10	14.4	71.0	57	8	DT018411
11	14.2	71.0	63	10	CG601030
12	14.2	71.0	80	1	AV920979
13	14.2	71.0	82	10	CM049484
14	14.2	71.0	83	1	A1430740
15	14.2	71.0	89	2	BE264581
16	14.2	71.0	90	11	TA178C01P
17	14.2	71.0	93	6	CF640238
18	14.2	71.0	97	10	CM054847
19	14.2	71.0	99	11	BX906358
20	14.2	71.0	99	11	BAF098E10
21	14.2	71.0	100	7	CF961070
22	14.2	71.0	100	10	CM364834

C 23	13.8	69.0	55	10	CM412671
C 24	13.8	69.0	66	10	C2906735
C 25	13.8	69.0	67	10	CG807832
C 26	13.8	69.0	79	9	BH407770
C 27	13.8	69.0	80	2	BF022188
C 28	13.8	69.0	85	3	BI855354
C 29	13.8	69.0	93	9	AZ848413
C 30	13.8	69.0	96	9	BH416254
C 31	13.6	68.0	43	1	AA663711
C 32	13.6	68.0	49	6	CB212499
C 33	13.6	68.0	49	9	BH802890
C 34	13.6	68.0	50	1	AU103161
C 35	13.6	68.0	50	1	AU103162
C 36	13.6	68.0	50	1	AU103170
C 37	13.6	68.0	50	1	AU103171
C 38	13.6	68.0	50	1	AU103175
C 39	13.6	68.0	50	1	AU103176
C 40	13.6	68.0	50	1	AU103180
C 41	13.6	68.0	58	6	CA913849
C 42	13.6	68.0	59	10	CG733240
C 43	13.6	68.0	61	2	BI109390
C 44	13.6	68.0	63	10	CM882812
C 45	13.6	68.0	67	1	AW246906

ALIGNMENTS

RESULT 1
LOCUS C2293884/C
DEFINITION P078A09 GGTG Gene Trap Library GV09C04 Mus musculus CDNA clone
ACCESSION C2293884
VERSION C2293884.1 GI:61681634
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Hansen, J., Flores, T., van Sloun, P., Fuchtbauer, E.M., Vauti, F., Arnold, H.H., Schutgen, F., Wurst, W., Von Melchner, H. and Ruiz, P. A large-scale, gene-driven mutagenesis approach for the functional analysis of the mouse genome
Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)
Contact: GGTG
German Genetrap Consortium (GGTC)
Email: info@genetrap.de
rf1p@rosabeteo.de
Additional sequence information can be found at:
'http://genetrap.gsf.de/project/web_new/database/result_clone.html?clone_id=P078A09', ES cell line harboring insertion mutation of target gene is available at:
'http://genetrap.gsf.de/project/web_new/order_clones/howtoorder.htm 1', Inhouse Sequence Identifier: 25293
Class: Gene Trap.

FEATURES
SOURCE location/Qualifiers

1. 88
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 Sv"
/db_xref="taxon:10090"
/clone="P078A09"
/sex="Male"
/cell_type="Embryonic stem cell"
/cell_line="ES cells 129S2 (formerly 129/SvPae)"
/clone_lib="GGTC Gene Trap Library GV09C04"
/notes="Vector: rf1p@rosabeteo"

ORIGIN

Query Match 79.0%; Score 15.8; DB 10; Length 88;
Best Local Similarity 89.5%; Pred. No. 1.9e+04;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GACGAGGCGACGACGCGC 20
|||||
43 GACGCGGCGACGACTGCG 25

Db 43 GACGCGGCGACGACTGCG 25

RESULT 2
AI000040
LOCUS AI000040 79 bp mRNA linear EST 05-JUN-1998
DEFINITION os46c07.s1 NCI CGAP Br2 Homo sapiens CDNA clone IMAGE:1608396 3'
similar to TR:O15551 O15551 RAT VENTRAL PROSTATE.1 HOMOLOG.
; contains TAR1.b1 MSRI repetitive element ;, mRNA sequence.
ACCESSION AI000040.1 GI:3190594
KEYWORDS EST.
SOURCE Homo sapiens
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 79)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation by: Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html

FEATURES
source
Trace considered overall poor quality
Seq primer: -40m3 fwd. ET from Amerham
High quality sequence stop: 1.
Location/Qualifiers
1..79
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1608396"
/sex="female, pooled"
/tissue_type="breast"
/lab_host="DH10B"
/clone_lib="NCI CGAP Br2"
/note="Vector: pTR73D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from pooled bulk
breast tumor tissue, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pTR73
vector. This library is the normalized version of
NCI CGAP Br1.1. Library was constructed by Bento Soares
and M. Fatima Bonaldo."

ORIGIN
Query Match 76.0%; Score 15.2; DB 1; Length 79;
Best Local Similarity 85.0%; Pred. No. 3.4e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGACGAGGCGACGACGCGC 20
|||||
52 GGACGAGGCGACGACGCGC 71

Db 52 GGACGAGGCGACGACGCGC 71

RESULT 3

C2914888
LOCUS C2914888 88 bp DNA linear GSS 08-AUG-2005
DEFINITION 4013009A12.x1 4013 - RescueMu Grid O Zea mays genomic, genomic
survey sequence.
ACCESSION C2914888
VERSION C2914888.1 GI:71931823
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 88)
Walbot, V.
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 4013009 row: 40
Class: transposon-tagged.

FEATURES
source
Location/Qualifiers
1..88
/organism="Zea mays"
/mol_type="genomic DNA"
/cultiivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="4013 - RescueMu Grid O"
/note="Organ: leaf; Vector: RescueMu (engineered from
pBluescript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site "<http://www.mutransposon.org/project/RescueMu/>". Grid
O was grown at Stanford in 2001. DNA was extracted from
leaf strips, double digested using BamHI and BglII, and
ligated to form circular plasmids. DH10B cells were
transformed and then screened on LB plates with
ampicillin."

ORIGIN
Query Match 76.0%; Score 15.2; DB 10; Length 88;
Best Local Similarity 85.0%; Pred. No. 3.4e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGACGAGGCGACGACGCGC 20
|||||
57 GGACGAGGCGACGACGCGC 76

Db 57 GGACGAGGCGACGACGCGC 76

RESULT 4
CC796892
LOCUS CC796892 84 bp DNA linear GSS 01-JUL-2003
DEFINITION SALK_144200.16.65.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_144200.16.65.x, genomic
survey sequence.
ACCESSION CC796892
VERSION CC796892.1 GI:32392115
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 84)

AUTHORS

Alonso, J.M., Leisbe, T.J., Barajas, P., Chen, H., Cheuk, R.,
Gadlinb, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
Shim, P., Zimmerman, J., and Ecker, J.R.

TITLE

A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome

JOURNAL
COMMENT

Unpublished (2001)
Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu

This is single pass sequence recovered from the left border of
TDNA. This sequence lies within 300 bases of the 3' end of
At5g05530 and 300 bases of the 5' end of At5g05540.
Class: TDNA tagged.

FEATURES
source

Location/Qualifiers
1..84
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_14200.16.65.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 74.0%; Score 14.8; DB 9; Length 84;
Best Local Similarity 88.9%; Pred. No. 5e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ACGAGGCGGACGCGG 20
|||||
56 ACGAGGCGGACGCGG 73

Db

RESULT 5

AM064096/c

LOCUS AM064096 87 bp mRNA linear EST 07-DEC-2000
DEFINITION SP0522 KRIIB Human CD4 intrathymic T-cell cDNA library Homo sapiens
CDNA 3', mRNA sequence.

ACCESSION AM064096

VERSION AM064096.1 GI:8888033

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE

1 (bases 1 to 87)
Goh, S.-H., Park, J.-H., Lee, Y.-J., Lee, H.-G., Yoo, H.-S., Lee, I.-C.,
Park, V.-H., Kim, Y.-S., and Lee, C.-C.

Gene expression profile and identification of differentially
expressed transcripts during human intrathymic T-cell development
by cDNA sequencing analysis

Genomics 70 (1), 1-18 (2000)

JOURNAL PUBMED

11087656

Contact: Sung-Ho Goh

Genome Research Center

Korea Research Institute of Bioscience and Biotechnology

On-dong 52, Yu Sung-Gu, Daejeon 305-333, Republic of Korea

Tel: 82-42-860-4473

Fax: 82-42-860-4479

Email: gohsh@mail.kribb.re.kr

Seq primer: 77

High quality sequence stop: 87

FEATURES

source

Location/Qualifiers
1..87

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/tissue_type="Thymus"

/cell_type="Intrathymic T-cell"

/dev_stage="CD3+4+8- single positive stage"

/clone_lib="KRIIB Human CD4 intrathymic T-cell cDNA
library"

/note="Vector: pGEM-T; cDNA was made from total
cytoplasmic RNA of sorted human intrathymic CD3+4+8-
T-cell, adaptor ligated, amplified with PCR, and cloned
into pGEM-T vector."

ORIGIN

Query Match 74.0%; Score 14.8; DB 1; Length 87;
Best Local Similarity 88.9%; Pred. No. 5e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ACGAGGCGGACGCGG 20
|||||
38 ACGAGGCGGACGCGG 21

Db

RESULT 6

AZ919805/c

LOCUS AZ919805 91 bp DNA linear GSS 17-DEC-2001
DEFINITION 1006016G03.Y1 1006 - Rescuemu Grid G Zea mays genomic, genomic
survey sequence.

ACCESSION AZ919805

VERSION AZ919805.1 GI:13389882

KEYWORDS GSS.

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 91)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 1006016 row: 41

Class: transposon-tagged.

Location/Qualifiers

1..91

/organism="Zea mays"

/mol_type="genomic DNA"

/cultivar="mixed background W23/A188/B73"

/db_xref="taxon:4577"

/tissue_type="leaf"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="1006 - Rescuemu Grid G"

/note="Organ: leaf; Vector: Rescuemu (engineered from
pBluescript backbone); Site_1: BamHI; Site_2: BglII;
Rescuemu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on Rescuemu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'Rescuemu'. Grid G was grown at Stanford in 2000. DNA was
extracted from leaf punches, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."

ORIGIN

Query Match 74.0%; Score 14.8; DB 9; Length 91;
 Best Local Similarity 88.9%; Pred. No. 5e+04;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGACGAGGCGGACGACG 18
 |||||
 Db 34 GCACGAGGCGGACGACG 17

RESULT 7
 BH218633 91 bp DNA linear GSS 08-NOV-2001
 LOCUS 1006080D10.x1 1006 - Rescuemu Grid G Zea mays genomic, genomic
 DEFINITION survey sequence.
 ACCESSION BH218633
 VERSION BH218633.1 GI:16811673
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 91)
 Walbot, V.
 Maize genomic sequences found using engineered Rescuemu transposon
 Unpublished (2001)
 CONTACT: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 1006080 row: 28
 Class: transposon-tagged.
 Location/Qualifiers
 1..91
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /cultivar="mixed Background W23/A188/B73"
 /db_xref="taxon:4577"
 /tissue_type="leaf"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="1006 - Rescuemu Grid G"
 /note="Organ: leaf; Vector: Rescuemu (engineered from
 pBluescript backbone); Site 1: BamHI; Site 2: BglII;
 Rescuemu is a 4.9 kb, modified maize Mu transposon
 designed to allow plasmid rescue from total genomic DNA.
 Mu elements insert preferentially into transcription
 units. For more information on Rescuemu, go to the web
 site 'www.zmdb.iastate.edu' and follow the links for
 'Rescuemu.' Grid G was grown at Stanford in 2000. DNA was
 extracted from leaf punches, double digested using BamHI
 and BglII, and ligated to form circular plasmids. DH10B
 cells were transformed and then screened on LB plates with
 ampicillin."

ORIGIN

Query Match 74.0%; Score 14.8; DB 9; Length 91;
 Best Local Similarity 88.9%; Pred. No. 5e+04;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GACGAGGCGGACGACGCG 19
 |||||
 Db 77 GACGAGGCGGACGACGAC 60

RESULT 8
 A1900558/c 64 bp mRNA linear EST 12-JUL-2004
 LOCUS A1900558

DEFINITION
 sc07g10.y1 Gm-cl012 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
 Gm-cl012-1531 5' similar to SW:PSAF FLATR P46486 PHOTOSYSTEM I
 REACTION CENTRE SUBUNIT III PRECURSOR ;, mRNA sequence.
 A1900558
 A1900558.1 GI:5606404
 EST.

ACCESSION
 VERSION A1900558
 KEYWORDS
 SOURCE
 ORGANISM
 Glycine max (soybean)
 Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseolae;
 Glycine.
 1 (bases 1 to 64)
 Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V.,
 Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
 Beck, C., Wylie, T., Underwood, K., Streptoc, M., Theising, B., Allen, M.,
 Bowers, Y., Person, B., Swaller, T., Gibbons, M., Page, D., Harvey, N.,
 Schurk, R., Riltter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
 McCann, R., Waterston, R. and Wilson, R.
 Public Soybean EST Project
 Unpublished (1999)
 TITLE
 JOURNAL
 COMMENT
 CONTACT: Shoemaker R/Public Soybean EST Project
 Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 When it has been determined, an EST from the other end of this
 clone is listed in the 'Other ESTs on clone' field. Trace
 considered overall poor quality possible reversed clone: similarity
 on wrong strand This clone is available through: Biogenetic
 Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423
 4163; email: info@biogeneticservices.com)
 Seq primer: -40RP from Gibco
 High quality sequence scop: 1.
 Location/Qualifiers
 1..64
 /organism="Glycine max"
 /mol_type="mRNA"
 /cultivar="Williams"
 /db_xref="taxon:3847"
 /clone="GENOME SYSTEMS CLONE ID: Gm-cl012-1531"
 /tissue_type="Apical shoot tips, 9-10 day old etiolated
 seedlings"
 /lab_host="XLI0-Gold"
 /clone_lib="Gm-cl012"
 /note="Vector: pBluescript II Xr; Site 1: EcoRI, Site 2:
 XhoI; This cDNA library was constructed from mRNA isolated
 from the apical shoots of 9 to 10 day old etiolated
 seedlings. The shoot tips including any emerged leaves
 were harvested for mRNA isolation. The cDNA library was
 prepared using the Stratagene pBluescript II Xr cDNA
 library construction kit. Complementary DNA was
 synthesized from mRNA using a primer consisting of a poly
 (dT) sequence with a XhoI restriction site. EcoRI adapters
 were ligated to the blunt-ended cDNA fragments followed by
 XhoI digestion. The cDNA fragments were directionally
 cloned into the EcoRI-XhoI restriction site of the
 pBluescript vector. The ligated cDNA fragments were
 transformed into XLI0-Gold host cells. This library was
 constructed by Dr. Randy Shoemaker and Dr. John
 Erpelting."

ORIGIN

Query Match 72.0%; Score 14.4; DB 1; Length 64;
 Best Local Similarity 93.8%; Pred. No. 7.6e+04;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GAGGGCGGACGCGGCG 20
 |||||
 Db 34 GAGGGCGGACGCGGCG 19

RESULT 9
BH226921/c 84 bp DNA linear GSS 08-NOV-2001
LOCUS 1006135G08.2EL_Y1 1006 - RescuemU Grid G Zea mays genomic, genomic
DEFINITION survey sequence.
ACCESSION BH226921
VERSION BH226921.1 GI:16826390
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 84)
Walbot, V.
Maize genomic sequences found using engineered RescuemU transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1006135 Column: 32
Class: transposon-tagged.
Location/Qualifiers
1..84
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1006 - RescuemU Grid G"
/note="Organ: leaf; Vector: RescuemU (engineered from
pBluescript backbone); Site 1: BamHI; Site 2: BglII;
RescuemU is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescuemU, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescuemU'. Grid G was grown at Stanford in 2000. DNA was
extracted from leaf punches, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."

ORIGIN
Query Match 72.0%; Score 14.4; DB 9; Length 84;
Best Local Similarity 93.8%; Pred. No. 7.5e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GACGAGGGCGGACG 17
|||
D6 69 GACGAGGGCGGACG 54
|||

RESULT 10
DT018411/c 57 bp mRNA linear EST 05-AUG-2005
LOCUS VV1024A01.586662 CabSau Flower Stage 12 (FlOu0012) Vitis vinifera
DEFINITION cDNA clone VV1024A01 5, mRNA sequence.
ACCESSION DT018411
VERSION DT018411.1 GI:71869356
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE
AUTHORS Iocco, P., Hua, C., Davies, C. and Thomas, M.R.
TITLE Expressed sequence tags from the grapevine cultivar Cabernet Sauvignon
JOURNAL Unpublished (2003)
COMMENT Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR Primers
FORWARD: T7 20mer (forward)
BACKWARD: Sp6 18mer
Plate: 024 row: A column: 01
Seq primer: T7 20mer (forward)
High quality sequence stop: 57.
Location/Qualifiers
1..57
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="VV1024A01"
/sex="Hermaphrodite"
/dev_stage="12 - modified E-L system"
/clone_lib="CabSau Flower Stage 12 (FlOu0012)"
/note="Organ: Inflorescence including flowers; Vector:
pZL; A cDNA library from immature inflorescences at stage
12 of the modified E-L system. Tissue collected from
field grown plants. A description of the modified E-L
system can be found in the paper by B. G. Coombe
'Adoption of a system for identifying grapevine growth
stages' (1995) Aust. J. Grape and Wine Res. 1: 104-110."

ORIGIN
Query Match 71.0%; Score 14.2; DB 8; Length 57;
Best Local Similarity 84.2%; Pred. No. 9.3e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GACGAGGGCGGACG 19
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D6 41 GACGAGGGCGGACG 23
|||

RESULT 11
CG601030/c 63 bp mRNA linear GSS 02-OCT-2003
LOCUS OST271917 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST271917,
DEFINITION mRNA sequence.
ACCESSION CG601030
VERSION CG601030.1 GI:37419251
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 63)
Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,
Fridde, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jasing, C.,
Key, B.W., Jr., Kipp, P., Kohlhauff, B., Ma, Z.-O., Markesich, D.,
Payne, R., Potter, D.G., Qian, N., Shaw, J., Schick, J., Shi, Z.-Z.,
Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,
Zhu, Q., Person, C. and Sands, A.T.
Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
14610273

COMMENT Contact: Zambrowicz BP
OmiBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature, 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.

FEATURES
source 1. 63
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST271917"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"

ORIGIN
Query Match 71.0%; Score 14.2; DB 10; Length 63;
Best Local Similarity 80.0%; Pred. No. 9.2e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GACGAGGCGGACGACGCG 20
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44 GGTCCGGGCGGAGNAGCG 25

Db

RESULT 12
AV920979/c
LOCUS AV920979 K. Sato unpublished cDNA library, cv. Haruna NiJo
DEFINITION germination shootc Hordeum vulgare subsp. vulgare cDNA clone
bag916f09 3', mRNA sequence.
ACCESSION AV920979
VERSION AV920979.1 GI:18216758
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Hordeum.
1 (bases 1 to 80)
Sato, K., Saitoh, D. and Takeda, K.
Barley EST sequencing project in NIG and Okayama Univ
Unpublished (2002)
Contact: Tadao Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.

FEATURES
source 1. 80
Location/Qualifiers
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="Haruna NiJo"
/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="bag916f09"
/tissue_type="shoots"
/dev_stage="germination"
/clone_lib="K. Sato unpublished cDNA library, cv. Haruna
NiJo germination shootc"

ORIGIN
Query Match 71.0%; Score 14.2; DB 1; Length 80;
Best Local Similarity 84.2%; Pred. No. 9.1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GACGAGGCGGACGACGCG 20
|||||
|||||

Db 48 GACGAGGCGGACGAGCGCG 30

RESULT 13
CM049484/c
LOCUS CM049484 82 bp DNA linear GSS 28-OCT-2004
DEFINITION 104_288_10514054_115_30199 Sorghum methylation filtered library
(LibID: 104) Sorghum bicolor genomic clone 10514054, genomic survey
sequence.

ACCESSION CM049484
VERSION CM049484.1 GI:54726214
KEYWORDS GSS.
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 82)
Bedell, J. A., Budiman, M. A., Nunberg, A., Citek, R. W., Robbins, D.,
Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K.,
McKenamy, J., Smith, M., Holman, H., Roe, B. A., Wiley, G., Korff, I. F.,
Rabinowicz, P. D., Lakey, N., McCombie, W. R., Jeddeloh, J. A. and
Martensen, R. A.
Sorghum genome sequencing by methylation filtration
Plos Biol. 3 (1), e13 (2005)
15660154
Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 288 row: m column: 12
Seq primer: M13/pUC Reverse
Class: methylation filtered
High quality sequence stop: 82.
Location/Qualifiers

FEATURES
source 1. 82
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="RTx623"
/db_xref="taxon:4558"
/clone="10514054"
/clone_lib="Sorghum methylation filtered library (LibID:
104)"
/note="Organ: leaf; Vector: pBCSK(-); Site 1: HincII; DNA
prepared from purified nuclei was randomly sheared,
end-repaired, size fractionated to enrich for the 0.5 to 5
kb fraction, ligated into HincII-digested pBCSK(-) vector
and electroporated into E. coli cells. This is a
methylation filtered library."

ORIGIN
Query Match 71.0%; Score 14.2; DB 10; Length 82;
Best Local Similarity 84.2%; Pred. No. 9.1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GACGAGGCGGACGACGCG 20
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75 GACGAGCGCGGAGCAGCGG 57

Db

RESULT 14
AT430740/c
LOCUS AT430740 83 bp mRNA linear EST 09-MAR-1999
DEFINITION ths1e05.x1 Soares mouse placenta 4NBp13.5 14.5 Mus musculus cDNA
clone IMAGE:446048 3', mRNA sequence.
ACCESSION AT430740
VERSION AT430740.1 GI:4276576
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 11:34:25 : Search time 48.1 Seconds
(without alignments)
739.111 Million cell updates/sec

Title: US-09-296-264-3

Perfect score: 20

Sequence: 1 GAGCAGGCGGAGCAGCGCG 20

Scoring table: IDENTITY_NUC

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1134872

Minimum DB seq length: 20
Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.2	71.0	26	3	US-09-711-619-5
2	14.2	71.0	30	2	US-07-718-490-2
3	14.2	71.0	50	2	US-07-718-490-1
4	14.2	71.0	65	2	US-08-479-743-5
5	14.2	71.0	65	6	PCT-US94-09705-5
6	14.2	71.0	66	2	US-08-479-743-3
7	14.2	71.0	66	6	PCT-US94-09705-3
8	13.8	69.0	50	3	US-10-131-827-3240
9	13.8	69.0	50	3	US-10-131-827-4792
10	13.8	69.0	60	2	US-08-484-192-151
11	13.6	68.0	30	2	US-08-428-370A-12
12	13.6	68.0	30	2	US-08-600-764-12
13	13.4	67.0	50	3	US-09-907-794A-89
14	13.4	67.0	50	3	US-09-905-125A-89
15	13.4	67.0	50	3	US-09-902-775A-89
16	13.4	67.0	50	3	US-09-906-700-89
17	13.4	67.0	50	3	US-09-903-603A-89
18	13.4	67.0	50	3	US-09-904-920A-89
19	13.4	67.0	50	3	US-09-909-064-89
20	13.4	67.0	50	3	US-09-905-381A-89
21	13.4	67.0	50	3	US-09-906-618-89
22	13.4	67.0	50	3	US-09-906-646-89
23	13.4	67.0	50	3	US-09-904-462-89
24	13.4	67.0	50	3	US-09-902-736A-89

25	13.4	67.0	50	3	US-09-906-722A-89	Sequence 89, Appl
26	13.2	66.0	21	2	US-08-816-105A-3	Sequence 3, Appl
27	13.2	66.0	31	3	US-09-657-453A-6	Sequence 6, Appl
28	13.2	66.0	59	3	US-09-270-767-26314	Sequence 26314, A
29	13.2	66.0	60	2	US-08-484-192-150	Sequence 150, App
30	13.2	66.0	81	3	US-09-621-976-7854	Sequence 7854, Ap
31	13.2	66.0	84	3	US-09-513-999C-34413	Sequence 34413, A
32	13.2	65.0	37	3	US-09-344-888A-19	Sequence 19, Appl
33	12.6	63.0	23	2	US-08-064-271-8	Sequence 8, Appl
34	12.6	63.0	23	3	US-08-930-589A-8	Sequence 8, Appl
35	12.6	63.0	23	3	US-09-599-781-8	Sequence 8, Appl
36	12.6	63.0	23	3	US-10-027-961A-8	Sequence 8, Appl
37	12.6	63.0	24	3	US-09-182-450-15	Sequence 15, Appl
38	12.6	63.0	25	3	US-09-323-873A-30	Sequence 30, Appl
39	12.6	63.0	25	3	US-09-702-114A-11	Sequence 11, Appl
40	12.6	63.0	25	3	US-09-638-203-19	Sequence 19, Appl
41	12.6	63.0	25	3	US-09-409-938-17	Sequence 17, Appl
42	12.6	63.0	25	3	US-09-680-728-29	Sequence 29, Appl
43	12.6	63.0	25	3	US-10-017-066A-29	Sequence 29, Appl
44	12.6	63.0	25	3	US-09-935-430-669	Sequence 669, App
45	12.6	63.0	25	3	US-10-010-667A-30	Sequence 30, Appl

ALIGNMENTS

```
RESULT 1
US-09-711-619-5/c
; Sequence 5, Application US/09711619
; Patent No. 6750380
; GENERAL INFORMATION:
; APPLICANT: Johal, Gurmukh S
; TITLE OF INVENTION: SORGHUM DWARFING GENES AND METHODS OF USE
; FILE REFERENCE: 5718-100 (035718/205458)
; CURRENT APPLICATION NUMBER: US/09/711,619
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: 60/165,176
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
US-09-711-619-5

Query Match      71.0%; Score 14.2; DB 3; Length 26;
Best Local Similarity 84.2%; Pred. No. 6.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy      2 GAGCAGGCGGAGCAGCGCG 20
Db      24 GACGAGCGGAGAACACGCGC 6

RESULT 2
US-07-718-490-2/c
; Sequence 2, Application US/07718490
; Patent No. 5340716
; GENERAL INFORMATION:
; APPLICANT: Ullman, Edwin F.
; APPLICANT: Kirakossian, Hrair
; APPLICANT: Pease, John S.
; APPLICANT: Daniloff, Yuri
; APPLICANT: Wagner, Daniel B.
; TITLE OF INVENTION: Assay Method Utilizing Photoactivated
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
```

```
/ ADDRESSER: Syntex (U.S.A.) Inc.
/ STREET: 3401 Hillview Avenue
/ CITY: Palo Alto
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/718,490
/ FILING DATE: 19910620
/ CLASSIFICATION: 436
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Leitberg, Theodore J.
/ REGISTRATION NUMBER: 28,319
/ REFERENCE/DOCKET NUMBER: 27340/ DO-1557
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 852-1091
/ TELEFAX: (415) 496-3529
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 30 base pairs
/ TYPE: NUCLEIC ACID
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ FRAGMENT TYPE: Internal
/ ORIGINAL SOURCE:
/ ORGANISM: Escherichia coli
/ STRAIN: K12 DNAJ
/ INDIVIDUAL ISOLATE: Synthetic
/ US-07-718-490-2

Query Match          71.0%; Score 14.2; DB 2; Length 30;
Best Local Similarity 84.2%; Pred. No. 6.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 GACGAGCGCGACGCGCG 20
Db      28 GAAGCGCGCGACGATGCGC 10

RESULT 3
US-07-718-490-1
/ Sequence 1, Application US/07718490
/ Patent No. 5340716
/ GENERAL INFORMATION:
/ APPLICANT: Ullman, Edwin F.
/ APPLICANT: Kirakosian, Hrair
/ APPLICANT: Pease, John S.
/ APPLICANT: Daniloff, Yuri
/ APPLICANT: Wagner, Daniel B.
/ TITLE OF INVENTION: Assay Method Utilizing Photoactivated
/ TITLE OF INVENTION: Chemiluminescent Label
/ NUMBER OF SEQUENCES: 2
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Syntex (U.S.A.) Inc.
/ STREET: 3401 Hillview Avenue
/ CITY: Palo Alto
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
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/ APPLICATION NUMBER: US/07/718,490
/ FILING DATE: 19910620
/ CLASSIFICATION: 436
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Leitberg, Theodore J.
/ REGISTRATION NUMBER: 28,319
/ REFERENCE/DOCKET NUMBER: 27340/ DO-1557
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 852-1091
/ TELEFAX: (415) 496-3529
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 50 base pairs
/ TYPE: NUCLEIC ACID
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)T
/ ANTI-SENSE: NO
/ FRAGMENT TYPE: Internal
/ ORIGINAL SOURCE:
/ ORGANISM: Escherichia coli
/ STRAIN: K12 DNAJ
/ INDIVIDUAL ISOLATE: Synthetic
/ US-07-718-490-1

Query Match          71.0%; Score 14.2; DB 2; Length 50;
Best Local Similarity 84.2%; Pred. No. 6.3e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 GACGAGCGCGACGCGCG 20
Db      13 GAAGCGCGCGACGATGCGC 31

RESULT 4
US-08-479-743-5
/ Sequence 5, Application US/08479743
/ Patent No. 5807675
/ GENERAL INFORMATION:
/ APPLICANT: Davalian, Darlush
/ APPLICANT: Singh, Rajendra
/ APPLICANT: Ullman, Edwin F.
/ TITLE OF INVENTION: Fluorescent Oxygen Channeling Assays
/ NUMBER OF SEQUENCES: 5
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Syntex (U.S.A.) Inc.
/ STREET: 3401 Hillview Avenue
/ CITY: Palo Alto
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/479,743
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/117,365
/ FILING DATE: 03-SEP-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Roth, Carol J.
/ REGISTRATION NUMBER: 32,783
/ REFERENCE/DOCKET NUMBER: 27870
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 852-1698
/ TELEFAX: (415) 496-3529
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 65 base pairs
```

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: synthetic
US-08-479-743-5

Query Match 71.0%; Score 14.2; DB 2; Length 65;
Best Local Similarity 84.2%; Pred. No. 6.2e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 GACGAGGGCGAGCAGCGCG 20
DB 3 GAAGCGGGCGAGCATGGCG 21

RESULT 5

PCT-US94-09705-5
Sequence 5, Application PC/TUS9409705
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: FLUORESCENT OXYGEN CHANNELLING IMMUNOASSAYS
NUMBER OF SEQUENCES: 5
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09705
FILING DATE: 29-AUG-1994
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 65 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: synthetic
PCT-US94-09705-5

Query Match 71.0%; Score 14.2; DB 6; Length 65;
Best Local Similarity 84.2%; Pred. No. 6.2e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 GACGAGGGCGAGCAGCGCG 20
DB 3 GAAGCGGGCGAGCATGGCG 21

RESULT 6

US-08-479-743-3/C
Sequence 3, Application US/08479743
Patent No. 5807675
GENERAL INFORMATION:
APPLICANT: Davalian, Darlush
APPLICANT: Singh, Rajendra
APPLICANT: Ullman, Edwin F.
TITLE OF INVENTION: Fluorescent Oxygen Channeling Assays
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Syntex (U.S.A.) Inc.
STREET: 3401 Hillview Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,743
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117,365
FILING DATE: 03-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Roth, Carol J.
REGISTRATION NUMBER: 32,783
REFERENCE/DOCKET NUMBER: 27870
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 852-1698
TELEFAX: (415) 496-3529
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 66 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: synthetic
US-08-479-743-3

Query Match 71.0%; Score 14.2; DB 2; Length 66;
Best Local Similarity 84.2%; Pred. No. 6.2e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 GACGAGGGCGAGCAGCGCG 20
DB 28 GAAGCGGGCGAGCATGGCG 10

RESULT 7

PCT-US94-09705-3/C
Sequence 3, Application PC/TUS9409705
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: FLUORESCENT OXYGEN CHANNELLING IMMUNOASSAYS
NUMBER OF SEQUENCES: 5
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09705
FILING DATE: 29-AUG-1994
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 66 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: synthetic
PCT-US94-09705-3

Query Match 71.0%; Score 14.2; DB 6; Length 66;
Best Local Similarity 84.2%; Pred. No. 6.2e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CITY: Buffalo
STATE: New York
COUNTRY: United States
ZIP: 14203-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS/ Microsoft Windows
SOFTWARE: Wordperfect for windows 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,370A
FILING DATE: 25/04/95
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Nelson, M. Bud
REGISTRATION NUMBER: 35,300
REFERENCE/DOCKET NUMBER: 03551.0015
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716)856-4000
TELEFAX: 716-849-0349
INFORMATION FOR SEQ. ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single-stranded
TOPOLOGY: linear
ORIGINAL SOURCE:
ORGANISM: Herpes simplex virus 2
FEATURE:
LOCATION: Polymerase gene sequence bases 2268-2297
US-08-428-370A-12

Query Match 68.0%; Score 13.6; DB 2; Length 30;
Best Local Similarity 80.0%; Pred. No. 1.1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 GGACGAGGCGACGACGCGG 20
DB 1 GGACGAGGCGACGACGCGG 20

RESULT 12
US-08-600-764-12
Sequence 12, Application US/08600764
Patent No. 5846706
GENERAL INFORMATION:
APPLICANT: Greenberg, Steven J.
APPLICANT: Evans, Mary Jo
TITLE OF INVENTION: Rapid and Sensitive Detection of
TITLE OF INVENTION: Herpesviruses
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
STREET: 1800 One M&T Plaza
CITY: Buffalo
STATE: New York
COUNTRY: United States
ZIP: 14203-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS/ Microsoft Windows
SOFTWARE: Wordperfect for windows 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/600,764
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/428,370
FILING DATE: 25/04/95
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Nelson, M. Bud

REGISTRATION NUMBER: 35,300
REFERENCE/DOCKET NUMBER: 03551.0016
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716)856-4000
TELEFAX: 716-849-0349
INFORMATION FOR SEQ. ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single-stranded
TOPOLOGY: linear
ORIGINAL SOURCE:
ORGANISM: Herpes simplex virus 2
FEATURE:
LOCATION: Polymerase gene sequence bases 2268-2297
US-08-600-764-12

Query Match 68.0%; Score 13.6; DB 2; Length 30;
Best Local Similarity 80.0%; Pred. No. 1.1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 GGACGAGGCGACGACGCGG 20
DB 1 GGACGAGGCGACGACGCGG 20

RESULT 13
US-09-907-794A-89
Sequence 89, Application US/09907794A
Patent No. 6635468
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Deans, Luc
APPLICANT: Eason, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,794A
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13

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/ PRIOR APPLICATION NUMBER: PCT/US99/21090
/ PRIOR FILING DATE: 1999-09-15
/ PRIOR APPLICATION NUMBER: PCT/US99/21547
/ PRIOR FILING DATE: 1999-09-15
/ PRIOR APPLICATION NUMBER: PCT/US99/23089
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: PCT/US99/28214
/ PRIOR FILING DATE: 1999-11-29
/ PRIOR APPLICATION NUMBER: PCT/US99/28313
/ PRIOR FILING DATE: 1999-11-30
/ PRIOR APPLICATION NUMBER: PCT/US99/28564
/ PRIOR FILING DATE: 1999-12-02
/ PRIOR APPLICATION NUMBER: PCT/US99/28565
/ PRIOR FILING DATE: 1999-12-02
/ PRIOR APPLICATION NUMBER: PCT/US99/30095
/ PRIOR FILING DATE: 1999-12-16
/ PRIOR APPLICATION NUMBER: PCT/US99/30911
/ PRIOR FILING DATE: 1999-12-20
/ PRIOR APPLICATION NUMBER: PCT/US99/30999
/ PRIOR FILING DATE: 1999-12-20
/ PRIOR APPLICATION NUMBER: PCT/US00/00219
/ PRIOR FILING DATE: 2000-01-05
/ NUMBER OF SEQ ID NOS: 423
/ SEQ ID NO 89
/ LENGTH: 50
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ OTHER INFORMATION: oligonucleotide probe
US-09-907-794A-89
```

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Query Match      67.0%; Score 13.4; DB 3; Length 50;
Best Local Similarity 93.3%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY      2 GACGAGGCGGAGCAGC 16
        |||||
Db      10 GACGAGGCGGAGTAC 24
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RESULT 14
US-09-905-125A-89
/ Sequence 89, Application US/09905125A
/ Patent No. 6664376
/ GENERAL INFORMATION:
/ APPLICANT: Genentech, Inc.
/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Baton, Dan L.
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Geritsen, Mary E.
/ APPLICANT: Goddard, A.
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, Christopher J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth, J.
/ APPLICANT: Kljavin, Ivar J.
/ APPLICANT: Mather, Jennie P.
/ APPLICANT: Pan, James
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William, I.
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ TITLE OF INVENTION: Acids Encoding the Same
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/ FILE REFERENCE: 10466-14
/ CURRENT APPLICATION NUMBER: US/09/905,125A
/ CURRENT FILING DATE: 2001-07-12
/ PRIOR APPLICATION NUMBER: PCT/US00/04414
/ PRIOR FILING DATE: 2000-02-22
/ PRIOR APPLICATION NUMBER: US 60/143,048
/ PRIOR FILING DATE: 1999-07-07
/ PRIOR APPLICATION NUMBER: US 60/145,698
/ PRIOR FILING DATE: 1999-07-26
/ PRIOR APPLICATION NUMBER: US 60/146,222
/ PRIOR FILING DATE: 1999-07-28
/ PRIOR APPLICATION NUMBER: PCT/US99/20594
/ PRIOR FILING DATE: 1999-09-08
/ PRIOR APPLICATION NUMBER: PCT/US99/20944
/ PRIOR FILING DATE: 1999-09-13
/ PRIOR APPLICATION NUMBER: PCT/US99/21090
/ PRIOR FILING DATE: 1999-09-15
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/ PRIOR FILING DATE: 1999-11-29
/ PRIOR APPLICATION NUMBER: PCT/US99/28313
/ PRIOR FILING DATE: 1999-11-30
/ PRIOR APPLICATION NUMBER: PCT/US99/28564
/ PRIOR FILING DATE: 1999-12-02
/ PRIOR APPLICATION NUMBER: PCT/US99/28565
/ PRIOR FILING DATE: 1999-12-02
/ PRIOR APPLICATION NUMBER: PCT/US99/30095
/ PRIOR FILING DATE: 1999-12-16
/ PRIOR APPLICATION NUMBER: PCT/US99/30911
/ PRIOR FILING DATE: 1999-12-20
/ PRIOR APPLICATION NUMBER: PCT/US99/30999
/ PRIOR FILING DATE: 1999-12-20
/ PRIOR APPLICATION NUMBER: PCT/US00/00219
/ PRIOR FILING DATE: 2000-01-05
/ NUMBER OF SEQ ID NOS: 423
/ SEQ ID NO 89
/ LENGTH: 50
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ OTHER INFORMATION: oligonucleotide probe
US-09-905-125A-89
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Query Match      67.0%; Score 13.4; DB 3; Length 50;
Best Local Similarity 93.3%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      2 GACGAGGCGGAGCAGC 16
        |||||
Db      10 GACGAGGCGGAGTAC 24
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```
RESULT 15
US-09-902-775A-89
/ Sequence 89, Application US/09902775A
/ Patent No. 6686451
/ GENERAL INFORMATION:
/ APPLICANT: Genentech, Inc.
/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Baton, Dan L.
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Geritsen, Mary E.
/ APPLICANT: Goddard, A.
```

```

; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,775A
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
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; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
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; PRIOR APPLICATION NUMBER: PCT/US99/26214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 89
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide probe
us-09-902-775A-69

Query Match      67.0%; Score 13.4; DB 3; Length 50;
Best Local Similarity 93.3%; Pred. No. 1.3e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      2 GACGAGGGCGAGCAC 16
        |||||||||
Db      10 GACGAGGGCGAGTAC 24
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Search completed: December 24, 2005, 18:36:27
Job time : 56.1 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 14:06:30 : Search time 337.6 seconds
(without alignments)
489.892 Million cell updates/sec

Title: US-09-296-264-3

Perfect score: 20

Sequence: 1 ggcagagggcgagcagcgcg 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 9887334

Minimum DB seq length: 20
Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Listing: First 45 summaries

Database : Published Applications NA Main:

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3: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
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10: /cgn2_6/ptodata/1/pubpna/US16_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3	US-09-296-264-3
2	15.8	79.0	25	8	US-10-719-900-385716
3	15.4	77.0	27	9	US-10-502-040-19
4	15.2	76.0	25	10	US-11-036-317-781803
5	14.4	72.0	25	10	US-11-036-317-876911
6	14.4	72.0	25	10	US-11-036-317-812288
7	14.4	72.0	25	10	US-11-036-317-955941
8	14.2	71.0	25	8	US-10-719-900-385715
9	14.2	71.0	25	8	US-10-719-900-776619
10	14.2	71.0	25	10	US-11-036-317-149338
11	14.2	71.0	26	7	US-10-795-931-5
12	14.2	71.0	40	5	US-10-015-536-13
13	14.2	71.0	45	3	US-09-908-153B-26
14	14.2	71.0	45	6	US-10-422-934-62
15	14.2	71.0	60	3	US-09-815-242-1169
16	14.2	71.0	60	3	US-09-815-242-1192
17	14.2	71.0	60	7	US-10-282-122A-3511
18	14.2	71.0	60	7	US-10-282-122A-3511
19	13.8	69.0	25	7	US-10-719-956-287366
20	13.8	69.0	27	9	US-10-502-040-27
21	13.8	69.0	33	9	US-10-965-607-3
22	13.8	69.0	50	6	US-10-131-827-3240
23	13.8	69.0	50	6	US-10-131-827-4792

24	13.6	68.0	25	10	US-11-036-317-248373	Sequence 248373,
25	13.6	68.0	25	10	US-11-036-317-259912	Sequence 259912,
26	13.6	68.0	25	10	US-11-036-317-321489	Sequence 321489,
27	13.6	68.0	25	10	US-11-036-317-781802	Sequence 781802,
28	13.6	68.0	31	7	US-10-375-404-4	Sequence 4, Appl1
29	13.6	68.0	31	7	US-10-375-404-3	Sequence 12, Appl1
30	13.6	68.0	32	7	US-10-375-404-5	Sequence 3, Appl1
31	13.6	68.0	32	7	US-10-375-404-7	Sequence 5, Appl1
32	13.6	68.0	32	7	US-10-375-404-6	Sequence 6, Appl1
33	13.6	68.0	35	7	US-10-375-404-8	Sequence 8, Appl1
34	13.6	68.0	35	7	US-10-375-404-8	Sequence 29, Appl1
35	13.6	68.0	37	3	US-09-894-633A-29	Sequence 989, App
36	13.6	68.0	40	9	US-10-477-173-988	Sequence 426, App
37	13.6	68.0	40	9	US-10-477-173-989	Sequence 320, App
38	13.6	68.0	86	7	US-10-220-481-426	Sequence 26864,
39	13.6	68.0	90	7	US-10-220-481-320	Sequence 876909,
40	13.4	67.0	25	9	US-10-956-157-268664	Sequence 89, Appl1
41	13.4	67.0	25	10	US-11-036-317-876909	Sequence 89, Appl1
42	13.4	67.0	50	3	US-09-909-320-89	Sequence 89, Appl1
43	13.4	67.0	50	3	US-09-909-088B-89	Sequence 89, Appl1
44	13.4	67.0	50	3	US-09-905-281A-89	Sequence 89, Appl1
45	13.4	67.0	50	3	US-09-902-853-89	Sequence 89, Appl1

ALIGNMENTS

```
RESULT 1
US-09-296-264-3
; Sequence 3, Application US/09296264
; Publication No. US20030083274A1
; GENERAL INFORMATION:
; APPLICANT: WRIGHT, Jim A.
; APPLICANT: YOUNG, Aiping H.
; TITLE OF INVENTION: NEUROPILIN ANTISENSE OLIGONUCLEOTIDE SEQUENCES AND
; TITLE OF INVENTION: METHODS OF USING SAME TO MODULATE CELL GROWTH
; FILE REFERENCE: 032396-043
; CURRENT APPLICATION NUMBER: US/09/296,264
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 60/082,791
; EARLIER FILING DATE: 1998-04-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-09-296-264-3

Query Match      100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 GGACGAGGGCGAGCAGCGCG 20
Db 1 GGACGAGGGCGAGCAGCGCG 20

RESULT 2
US-10-719-900-385716
; Sequence 385716, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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SEQ ID NO 385716
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-10-719-900-385716

Query Match 79.0%; Score 15.8; DB 8; Length 25;
Best Local Similarity 89.5%; Pred. No. 1.2e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGACGAGCGCGACGACGCG 19
|||||
Db 3 GGACGAGCGCGACGACGCG 21

RESULT 3
US-10-502-040-19
Sequence 19, Application US/10502040
Publication No. US2005021466A1
GENERAL INFORMATION:
APPLICANT: Liao et al.
TITLE OF INVENTION: ALANINE 2,3-AMINOMUTASE
FILE REFERENCE: 63358-09
CURRENT APPLICATION NUMBER: US/10/502,040
CURRENT FILING DATE: 2004-07-19
PRIOR APPLICATION NUMBER: PCT/US03/01635
PRIOR FILING DATE: 2003-01-17
PRIOR APPLICATION NUMBER: US 60/350,727
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/375,785
PRIOR FILING DATE: 2002-04-25
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.1
SEQ ID NO 19
LENGTH: 27
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PCR primer
US-10-502-040-19

Query Match 77.0%; Score 15.4; DB 9; Length 27;
Best Local Similarity 94.1%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ACGAGGCGGACGACGCG 19
|||||
Db 6 ACGAGGCGGACGACGCG 22

RESULT 4
US-11-036-317-781803/C
Sequence 781803, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 781803
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-781803

Query Match 76.0%; Score 15.2; DB 10; Length 25;
Best Local Similarity 85.0%; Pred. No. 2.3e+03;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GGACGAGCGCGACGACGCG 20
|||||
Db 24 GCACCGGCGCGACGACGCG 5

RESULT 5
US-11-036-317-876911
Sequence 876911, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 876911
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-876911

Query Match 72.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%; Pred. No. 5.4e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CGAGGCGGACGACGCG 19
|||||
Db 7 CGAGGCGGACGACGCG 22

RESULT 6
US-11-036-317-912288
Sequence 912288, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 912288
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-912288

Query Match 72.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%; Pred. No. 5.4e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CGAGGCGGACGACGCG 19
|||||
Db 10 CGAGGCGGACGACGCG 25

RESULT 7
US-11-036-317-955941
Sequence 955941, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan

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; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 955941
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-955941

Query Match
Best Local Similarity 72.0%; Score 14.4; DB 10; Length 25;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 4 GGAGGCGGCGAGCGGC 19
Db 9 GGAGGCGGCGAGCGGC 24

RESULT 8
US-10-719-900-385715
; Sequence 385715, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 385715
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-385715

Query Match
Best Local Similarity 71.0%; Score 14.2; DB 8; Length 25;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 GGACGAGGCGGCGAGCGGC 19
Db 3 GGACGAGGCGGCGAGCGGC 21

RESULT 9
US-10-719-900-776619
; Sequence 776619, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 776619
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-776619
```

```

Query Match
Best Local Similarity 71.0%; Score 14.2; DB 8; Length 25;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 GGACGAGGCGGCGAGCGGC 19
Db 3 GGACGAGGCGGCGAGCGGC 21

RESULT 10
US-11-036-317-149338/c
; Sequence 149338, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 149338
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-149338

Query Match
Best Local Similarity 71.0%; Score 14.2; DB 10; Length 25;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 GGACGAGGCGGCGAGCGGC 19
Db 24 GGACCACTGGGAGGAGCGGC 6

RESULT 11
US-10-795-931-5/c
; Sequence 5, Application US/10795931
; Publication No. US20040148652A1
; GENERAL INFORMATION:
; APPLICANT: Jomai, Gurmukh S
; APPLICANT: Multani, Dilbag S
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING THE DW3
; TITLE OF INVENTION: P-GLYCOPROTEIN OF SORGHUM AND METHODS OF MODIFYING
; FILE REFERENCE: 035718/275561
; CURRENT APPLICATION NUMBER: US/10/795,931
; CURRENT FILING DATE: 2004-03-08
; PRIOR APPLICATION NUMBER: 60/165,176
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 09/711,619
; PRIOR FILING DATE: 2000-11-13
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: oligonucleotide
; OTHER INFORMATION: primer designed from sequence of Zea mays Br2 gene
US-10-795-931-5

Query Match
Best Local Similarity 71.0%; Score 14.2; DB 7; Length 26;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 GACGAGGCGGCGAGCGGC 20
```

Db 24 GACGAGCGGAGACACGGCG 6

RESULT 12

US-10-015-536-13/c
; Sequence 13, Application US/10015536
; Publication No. US20020165149A1
; GENERAL INFORMATION:
; APPLICANT: Kranz, David M.
; APPLICANT: Starwalt, David
; APPLICANT: Bluestone, Jeffrey A.
; TITLE OF INVENTION: Mutated Class II Major Histocompatibility Proteins
; FILE REFERENCE: 103-00
; CURRENT APPLICATION NUMBER: US/10/015,536
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 60/254,248
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-015-536-13

Query Match 71.0%; Score 14.2; DB 5; Length 40;

Best Local Similarity 84.2%; Pred. No. 6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GACGAGCGGAGACACGGCG 20
DB 39 GACGTGGCGAGTACCGCG 21

RESULT 13

US-09-908-153B-26
; Sequence 26, Application US/09908153B
; Patent No. US2002016871A1
; GENERAL INFORMATION:
; APPLICANT: Barbas, Carlos F.
; APPLICANT: Beerli, Roger
; APPLICANT: Schodfer, Ulrich
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION USING
; TITLE OF INVENTION: SINGLE-CHAIN, MONOMERIC, LIGAND DEPENDENT POLYPEPTIDE
; FILE REFERENCE: TSRI 725.1
; CURRENT APPLICATION NUMBER: US/09/908,153B
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 09/619,063
; PRIOR FILING DATE: 2000-07-18
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Synthesized
US-09-908-153B-26

Query Match 71.0%; Score 14.2; DB 3; Length 45;

Best Local Similarity 84.2%; Pred. No. 5.9e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGACGAGGCGGAGACACGGC 19
DB 3 GGAGGAGGCGCGCCCGCGC 21

RESULT 14

US-10-422-934-62

; Sequence 62, Application US/10422934
; Publication No. US20030186841A1
; GENERAL INFORMATION:
; APPLICANT: Barbas, Carlos F., III
; APPLICANT: Kadan, Michael
; APPLICANT: Beerli, Roger
; TITLE OF INVENTION: LIGAND ACTIVATED TRANSCRIPTIONAL REGULATOR PROTEINS
; FILE REFERENCE: 22908-1227C
; CURRENT APPLICATION NUMBER: US/10/422,934
; CURRENT FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 09/586,625
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: 09/433,042
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Recombinant
US-10-422-934-62

Query Match 71.0%; Score 14.2; DB 6; Length 45;

Best Local Similarity 84.2%; Pred. No. 5.9e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGACGAGGCGGAGACACGGC 19
DB 3 GGAGGAGGCGCGCCCGCGC 21

RESULT 15

US-09-815-242-1169/c
; Sequence 1169, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1169
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa

US-09-815-242-1169

Query Match 71.0%; Score 14.2; DB 3; Length 60;

Best Local Similarity 84.2%; Pred. No. 5.5e+03;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGACGAGGGCGACGCGC 19

Db 47 GGACCGAGGGCGACGCGC 29

Search completed: December 25, 2005, 04:14:20
Job time : 337.6 secs

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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 18:29:07 ; Search time 135.3 seconds
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76.712 Million cell updates/sec

Title: US-09-296-264-3

Perfect score: 20
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 416828 seqs, 259477437 residues

Total number of hits satisfying chosen parameters: 1608458

Minimum DB seq length: 20
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA New:

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10: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	14.8	74.0	25	US-11-121-849-468072	Sequence 468072, A
2	14.4	72.0	25	US-11-121-849-154619	Sequence 154619, A
3	13.6	68.0	25	US-11-121-849-52835	Sequence 52835, A
4	13.6	68.0	25	US-11-121-849-52836	Sequence 52836, A
5	13.6	68.0	25	US-11-121-849-52837	Sequence 52837, A
6	13.6	68.0	25	US-11-121-849-52838	Sequence 52838, A
7	13.6	68.0	25	US-11-121-849-52839	Sequence 52839, A
8	13.6	68.0	25	US-11-121-849-52840	Sequence 52840, A
9	13.6	68.0	25	US-11-121-849-52841	Sequence 52841, A
10	13.6	68.0	25	US-11-121-849-52842	Sequence 52842, A
11	13.6	68.0	25	US-11-121-849-52843	Sequence 52843, A
12	13.6	68.0	25	US-11-121-849-52844	Sequence 52844, A
13	13.6	68.0	25	US-11-121-849-52845	Sequence 52845, A
14	13.6	68.0	25	US-11-121-849-52846	Sequence 52846, A
15	13.6	68.0	25	US-11-121-849-52847	Sequence 52847, A
16	13.6	68.0	25	US-11-121-849-52848	Sequence 52848, A
17	13.6	68.0	25	US-11-121-849-52849	Sequence 52849, A
18	13.6	68.0	25	US-11-121-849-52850	Sequence 52850, A
19	13.6	68.0	25	US-11-121-849-52851	Sequence 52851, A
20	13.6	68.0	25	US-11-121-849-52852	Sequence 52852, A
21	13.6	68.0	25	US-11-121-849-52853	Sequence 52853, A
22	13.6	68.0	25	US-11-121-849-52854	Sequence 52854, A
23	13.6	68.0	25	US-11-121-849-52855	Sequence 52855, A

24	12.6	63.0	38	US-11-092-988-45	Sequence 45, Appl
25	12.4	62.0	21	US-11-112-882-53	Sequence 53, Appl
26	12.4	62.0	25	US-11-121-849-22698	Sequence 22698, A
27	12.4	62.0	25	US-11-121-849-46961	Sequence 46961, A
C 28	12.4	62.0	32	US-10-939-294A-16788	Sequence 16788, A
C 29	12.4	62.0	32	US-10-939-294A-16792	Sequence 16792, A
C 30	12.4	62.0	32	US-10-939-294A-17186	Sequence 17186, A
C 31	12.4	62.0	32	US-10-939-294A-18059	Sequence 18059, A
C 32	12.4	62.0	32	US-10-939-294A-18119	Sequence 18119, A
C 33	12.2	61.0	25	US-11-121-849-31702	Sequence 31702, A
C 34	12.2	61.0	25	US-11-121-849-32295	Sequence 32295, A
C 35	12.2	61.0	25	US-11-121-849-51406	Sequence 51406, A
C 36	12.2	61.0	25	US-11-121-849-490705	Sequence 490705, A
C 37	12.2	61.0	25	US-11-121-849-632887	Sequence 632887, A
C 38	12.2	61.0	25	US-11-121-849-640971	Sequence 640971, A
C 39	12.2	61.0	25	US-11-121-849-640972	Sequence 640972, A
C 40	12.2	61.0	28	US-11-046-456-145	Sequence 145, App
C 41	12.2	61.0	28	US-11-046-644-145	Sequence 145, App
C 42	12.2	61.0	58	US-11-013-247A-44	Sequence 44, Appl
C 43	12.2	60.0	25	US-11-121-849-138726	Sequence 138726, A
C 44	12.2	60.0	32	US-10-939-294A-15268	Sequence 15268, A
C 45	12.2	60.0	32	US-10-939-294A-15327	Sequence 15327, A

ALIGNMENTS

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RESULT 1
US-11-121-849-468072/c
; Sequence 468072, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121, 849
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567, 949
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 468072
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-468072

Query Match      74.0% Score 14.8; DB 7; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy      2 GACGAGGCGGACGCGC 19
Db      23 GACGTGGCGGACGCGC 6

RESULT 2
US-11-121-849-154619
; Sequence 154619, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121, 849
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567, 949
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 154619

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LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-154619

Query Match 72.0%; Score 14.4; DB 7; Length 25;
Best Local Similarity 93.8%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGAGGCGGACGACCGCG 19
|||||
DB 5 GGAGGCGGACGACCGCG 20

RESULT 3
US-11-121-849-52835

Sequence 52835, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:

APPLICANT: John Palma

TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S

FILE REFERENCE: 3684.1

CURRENT APPLICATION NUMBER: US/11/121,849

CURRENT FILING DATE: 2005-05-03

PRIOR APPLICATION NUMBER: 60/567,949

PRIOR FILING DATE: 2004-05-03

NUMBER OF SEQ ID NOS: 673904

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 52835

LENGTH: 25

TYPE: DNA

ORGANISM: Homo sapien

US-11-121-849-52835

Query Match 68.0%; Score 13.6; DB 7; Length 25;
Best Local Similarity 80.0%; Pred. No. 5.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGAGGCGGCGGACGACCGCG 20
|||||
DB 6 GGAGGCGGCGGACGACCGCG 25

RESULT 4
US-11-121-849-52836

Sequence 52836, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:

APPLICANT: John Palma

TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S

FILE REFERENCE: 3684.1

CURRENT APPLICATION NUMBER: US/11/121,849

CURRENT FILING DATE: 2005-05-03

PRIOR APPLICATION NUMBER: 60/567,949

PRIOR FILING DATE: 2004-05-03

NUMBER OF SEQ ID NOS: 673904

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 52836

LENGTH: 25

TYPE: DNA

ORGANISM: Homo sapien

US-11-121-849-52836

Query Match 68.0%; Score 13.6; DB 7; Length 25;
Best Local Similarity 80.0%; Pred. No. 5.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGAGGCGGCGGACGACCGCG 20
|||||
DB 5 GGAGGCGGCGGACGACCGCG 24

RESULT 5
US-11-121-849-52837

Sequence 52837, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:

APPLICANT: John Palma

TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S

FILE REFERENCE: 3684.1

CURRENT APPLICATION NUMBER: US/11/121,849

CURRENT FILING DATE: 2005-05-03

PRIOR APPLICATION NUMBER: 60/567,949

PRIOR FILING DATE: 2004-05-03

NUMBER OF SEQ ID NOS: 673904

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 52837

LENGTH: 25

TYPE: DNA

ORGANISM: Homo sapien

US-11-121-849-52837

Query Match 68.0%; Score 13.6; DB 7; Length 25;
Best Local Similarity 80.0%; Pred. No. 5.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGAGGCGGCGGACGACCGCG 20
|||||
DB 3 GGAGGCGGCGGACGACCGCG 22

RESULT 6
US-11-121-849-52838

Sequence 52838, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:

APPLICANT: John Palma

TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S

FILE REFERENCE: 3684.1

CURRENT APPLICATION NUMBER: US/11/121,849

CURRENT FILING DATE: 2005-05-03

PRIOR APPLICATION NUMBER: 60/567,949

PRIOR FILING DATE: 2004-05-03

NUMBER OF SEQ ID NOS: 673904

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 52838

LENGTH: 25

TYPE: DNA

ORGANISM: Homo sapien

US-11-121-849-52838

Query Match 68.0%; Score 13.6; DB 7; Length 25;
Best Local Similarity 80.0%; Pred. No. 5.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGAGGCGGCGGACGACCGCG 20
|||||
DB 1 GGAGGCGGCGGACGACCGCG 20

RESULT 7
US-11-121-849-53223

Sequence 53223, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:

APPLICANT: John Palma

TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S

FILE REFERENCE: 3684.1

CURRENT APPLICATION NUMBER: US/11/121,849

CURRENT FILING DATE: 2005-05-03

PRIOR APPLICATION NUMBER: 60/567,949

PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 53223
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-53223

Query Match 68.0%; Score 13.6; DB 7; Length 25;
Best Local Similarity 80.0%; Pred. No. 5.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GGACGAGGGCGAGCAGCGCG 20
DB 5 GGACTACTGCGAGCAGCGCG 24

RESULT 8
US-11-121-849-53224
Sequence 53224, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121.849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 53224
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-53224

Query Match 68.0%; Score 13.6; DB 7; Length 25;
Best Local Similarity 80.0%; Pred. No. 5.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GGACGAGGGCGAGCAGCGCG 20
DB 1 GGACTACTGCGAGCAGCGCG 20

RESULT 9
US-11-121-849-364778
Sequence 364778, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121.849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 364778
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-364778

Query Match 68.0%; Score 13.6; DB 7; Length 25;
Best Local Similarity 80.0%; Pred. No. 5.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GGACGAGGGCGAGCAGCGCG 20
DB 2 GGACCCGGGCGAGCGCGCG 21

RESULT 10
US-11-121-849-365185
Sequence 365185, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121.849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 365185
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-365185

Query Match 68.0%; Score 13.6; DB 7; Length 25;
Best Local Similarity 80.0%; Pred. No. 5.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GGACGAGGGCGAGCAGCGCG 20
DB 2 GGACCCGGGCGAGCGCGCG 21

RESULT 11
US-10-939-294A-16208
Sequence 16208, Application US/10939294A
Publication No. US20050266417A1
GENERAL INFORMATION:
APPLICANT: Barney, Francis
APPLICANT: Turner, Daniel
APPLICANT: Pingle, Maneesh
APPLICANT: Pincas, Hanna
TITLE OF INVENTION: Methods for identifying target nucleic acid molecules
FILE REFERENCE: 19603/4121 (CRF D-2995-02)
CURRENT APPLICATION NUMBER: US/10/939.294A
CURRENT FILING DATE: 2004-09-10
PRIOR APPLICATION NUMBER: US 60/502/731
PRIOR FILING DATE: 2003-09-12
NUMBER OF SEQ ID NOS: 38895
SOFTWARE: PatentIn version 3.3
SEQ ID NO 16208
LENGTH: 32
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: oligonucleotide probe
US-10-939-294A-16208

Query Match 68.0%; Score 13.6; DB 6; Length 32;
Best Local Similarity 80.0%; Pred. No. 4.9e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GGACGAGGGCGAGCAGCGCG 20
DB 10 GGACGAGGAGCAGCGCAGCG 29

RESULT 12
US-10-939-294A-16756
Sequence 16756, Application US/10939294A
Publication No. US20050266417A1

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; GENERAL INFORMATION:
; APPLICANT: Barany, Francis
; APPLICANT: Turner, Daniel
; APPLICANT: Pingel, Maneesh
; APPLICANT: Pincas, Hanna
; TITLE OF INVENTION: Methods for identifying target nucleic acid molecules
; FILE REFERENCE: 19603/4121 (CRF D-2995-02)
; CURRENT APPLICATION NUMBER: US/10/939,294A
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: US 60/502/731
; PRIOR FILING DATE: 2003-09-12
; NUMBER OF SEQ ID NOS: 38895
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16756
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: oligonucleotide probe
US-10-939-294A-16756
```

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Query Match          68.0%; Score 13.6; DB 6; Length 32;
Best Local Similarity 80.0%; Pred. No. 4.9e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Qy      1  GGACGAGGCGCGACGCGG 20
         |||||
Db      4  GCACCGCGCGACGCGG 23
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```
RESULT 13
US-10-939-294A-16816
; Sequence 16816, Application US/10939294A
; Publication No. US20050266417A1
; GENERAL INFORMATION:
; APPLICANT: Barany, Francis
; APPLICANT: Turner, Daniel
; APPLICANT: Pingel, Maneesh
; APPLICANT: Pincas, Hanna
; TITLE OF INVENTION: Methods for identifying target nucleic acid molecules
; FILE REFERENCE: 19603/4121 (CRF D-2995-02)
; CURRENT APPLICATION NUMBER: US/10/939,294A
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: US 60/502/731
; PRIOR FILING DATE: 2003-09-12
; NUMBER OF SEQ ID NOS: 38895
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16816
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: oligonucleotide probe
US-10-939-294A-16816
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Query Match          68.0%; Score 13.6; DB 6; Length 32;
Best Local Similarity 80.0%; Pred. No. 4.9e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Qy      1  GGACGAGGCGCGACGCGG 20
         |||||
Db      4  GCACCGCGCGACGCGG 23
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RESULT 14
US-10-770-726-16681
; Sequence 16681, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
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; TITLE OF INVENTION: CANCERS
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16681
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi
US-10-770-726-16681
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Query Match          64.0%; Score 12.8; DB 6; Length 21;
Best Local Similarity 87.5%; Pred. No. 1.1e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy      2  GACGAGGCGCGACGACG 17
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Db      3  GACGAGGCGCGACGACG 18
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RESULT 15
US-11-121-849-322231/C
; Sequence 322231, Application US/1121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 322231
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-322231
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Query Match          64.0%; Score 12.8; DB 7; Length 25;
Best Local Similarity 87.5%; Pred. No. 1e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy      1  GGACGAGGCGCGACGAC 16
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Db      16  GGACGAGGAGGAGGAC 1
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Job time : 135.3 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 10:28:41 ; Search time 582 Seconds
(without alignments)
1953.383 Million cell updates/sec

Title: US-09-296-264-5

Perfect score: 20

Sequence: 1 ttcttcagggaatccg9599 20

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 1658228

Minimum DB seq length: 20

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_scs:*
11: gb_sy:*
12: gb_un:*
13: gb_vl:*
14: gb_hlg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	BD211662	BD211662 Antisense
2	15.4	77.0	25	AX609775	AX609775 Sequence
3	14.2	71.0	25	CQ428968	CQ428968 Sequence
4	14.2	71.0	52	TCUMIRO3	AP154453 Toxostoma
5	13.8	69.0	25	AX609773	AX609773 Sequence
6	13.8	69.0	25	AX612836	AX612836 Sequence
7	13.8	69.0	53	TCIMIRO3	AP154459 Toxostoma
8	13.8	69.0	72	AY604622	AY604622 Sus scrofa
9	13.8	69.0	86	AJ840678	AJ840678 Arabidops
10	13.6	68.0	37	AX698174	AX698174 Sequence
11	13.6	68.0	50	AX160046	AX160046 Sequence
12	13.6	68.0	51	AX160045	AX160045 Sequence
13	13.6	68.0	54	TOIMIRO3	AP154447 Toxostoma
14	13.6	68.0	65	CQ559452	CQ559452 Sequence
15	13.6	68.0	72	AX653469	AX653469 Sequence
16	13.6	68.0	73	ARS20567	ARS20567 Sequence
17	13.6	68.0	97	AL772837	AL772837 Arabidops
18	13.6	68.0	100	AX93510	AX93510 Sequence

19	13.4	67.0	21	6	AR020977	AR020977 Sequence
20	13.4	67.0	21	6	AR020978	AR020978 Sequence
21	13.4	67.0	21	6	AR043392	AR043392 Sequence
22	13.4	67.0	21	6	AR043393	AR043393 Sequence
23	13.4	67.0	21	6	AR062307	AR062307 Sequence
24	13.4	67.0	21	6	AR062308	AR062308 Sequence
25	13.4	67.0	21	6	BD078760	BD078760 Recombine
26	13.4	67.0	21	6	BD078761	BD078761 Recombine
27	13.4	67.0	21	6	BD085587	BD085587 Recombina
28	13.4	67.0	21	6	BD085588	BD085588 Recombina
29	13.4	67.0	21	6	AR183766	AR183766 Sequence
30	13.4	67.0	21	6	AR183767	AR183767 Sequence
31	13.4	67.0	21	6	AR221165	AR221165 Sequence
32	13.4	67.0	21	6	AR221166	AR221166 Sequence
33	13.4	67.0	21	6	AR230592	AR230592 Sequence
34	13.4	67.0	21	6	AR230593	AR230593 Sequence
35	13.4	67.0	21	6	AR234066	AR234066 Sequence
36	13.4	67.0	21	6	AR234067	AR234067 Sequence
37	13.4	67.0	21	6	AR237676	AR237676 Sequence
38	13.4	67.0	21	6	AR237677	AR237677 Sequence
39	13.4	67.0	21	6	AR353186	AR353186 Sequence
40	13.4	67.0	21	6	AR353187	AR353187 Sequence
41	13.4	67.0	21	6	AR368149	AR368149 Sequence
42	13.4	67.0	21	6	AR368150	AR368150 Sequence
43	13.4	67.0	80	6	AX656204	AX656204 Sequence
44	13.4	67.0	100	6	AX99486	AX99486 Sequence
45	13.2	66.0	25	6	CQ862079	CQ862079 Sequence

ALIGNMENTS

RESULT 1
LOCUS BD211662
DEFINITION Antisense oligonucleotide sequence of neuropilin and method of using the same for controlling cell proliferation.
ACCESSION BD211662.1 GI:33021432
VERSION JP 2002512793-A/5.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 20)
AUTHORS Wright,J.A., Young,A.H. and Lee,Y.S.
TITLE Antisense oligonucleotide sequence of neuropilin and method of using the same for controlling cell proliferation
JOURNAL Patent: JP 2002512793-A 5 08-MAY-2002;
GENESENSE TECHNOLOGIES INC
COMMENT OS Homo sapiens (human)
PD JP 2002512793-A/5
PN 08-MAY-2002
PF 23-APR-1999 JP 2000545999
PR 23-APR-1998 US 60/082791
PT JIM A WRIGHT, AIPING H YOUNG, YOON S LEE
PC C12N15/09,A61K31/711,A61K48/00,A61P35/00,C12N15/00 CC
Antisense oligonucleotide sequence of neuropilin and method of using the same for controlling cell proliferation
CC same for controlling cell proliferation
FH key Location/Qualifiers
FT source 1..20
FT Location/Qualifiers
FEATURES
source 1..20
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTTCAGGAAATCCGGG 20
Db 1 TTTTCAGGAAATCCGGG 20

RESULT 2
AX609775
LOCUS AX609775 25 bp DNA linear PAT 17-FEB-2003
DEFINITION Sequence 800 from Patent WO02072882.
ACCESSION AX609775
VERSION AX609775.1 GI:28405204
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE
AUTHORS Cullen, P. and Seedorf, U.
TITLE Coronary chip
JOURNAL Patent: WO 02072882-A 800 19-SEP-2002;
OGHAM GmbH (DE)
FEATURES
source 1..25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 77.0%; Score 15.4; DB 6; Length 25;
Best Local Similarity 94.1%; Pred. No. 9.2e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTTTCAGGAAATCCGG 17
2 TTTTCAGGAAATCTGG 18
Db 2 TTTTCAGGAAATCTGG 18

RESULT 3
LOCUS CQ428968 25 bp DNA linear PAT 28-JAN-2004
DEFINITION Sequence 14002 from Patent WO0151628.
ACCESSION CQ428968
VERSION CQ428968.1 GI:41381197
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE
AUTHORS Lillie, J., Xu, Y., Wang, Y. and Steinmann, K.
TITLE Novel genes, compositions, kits, and methods for identification,
assessment, prevention, and therapy of breast cancer
JOURNAL Patent: WO 0151628-A 14002 19-JUL-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
source 1..25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 71.0%; Score 14.2; DB 6; Length 25;
Best Local Similarity 84.2%; Pred. No. 4e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TTTTCAGGAAATCCGGG 19
19 TTTTCAGGAAATCCGGT 1
Db 19 TTTTCAGGAAATCCGGT 1

RESULT 4
TCUMIT03/C
LOCUS TCUMIT03 52 bp DNA linear VRT 23-SEP-1999
DEFINITION Toxostoma curvirostre isolate C87H6TX cRNA-Glu gene, partial
sequence; mitochondrial gene for mitochondrial product.
ACCESSION AF154453
VERSION AF154453.1 GI:5918791
KEYWORDS
SEGMENT 3 of 6
SOURCE mitochondrion Toxostoma curvirostre
ORGANISM Toxostoma curvirostre
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Passeriformes; Mimidae; Toxostoma.
1 (bases 1 to 52)
Zink, R.M., Dittmann, D.L., Klicka, J. and Blackwell-Rago, R.C.
Evolutionary patterns of morphometrics, allozymes and mitochondrial
DNA in thrashers (Toxostoma)
The Auk (1999) In press
2 (bases 1 to 52)
Zink, R.M., Dittmann, D.L., Klicka, J. and Blackwell-Rago, R.C.
Direct Submission
Submitted (26-MAY-1999) Bell Museum, University of Minnesota, 100
Ecology Bldg, 1987 Upper Buford Circle, St Paul, MN 55108, USA
FEATURES
source 1..52
/organism="Toxostoma curvirostre"
/organelle="mitochondrion"
/mol_type="genomic DNA"
/isolate="C87H6TX"
/specimen_voucher="RMZ 2951, ISU Museum of Zoology"
/db_xref="taxon:99878"
/sex="male"
/country="USA:Texas, 10 miles SSE of Charlotte"
/note="Isolated May 26, 1992"
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/product="cRNA-Glu"

ORIGIN
Query Match 71.0%; Score 14.2; DB 5; Length 52;
Best Local Similarity 84.2%; Pred. No. 3.7e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TTTTCAGGAAATCCGGG 20
32 TTTTCAGGAAATCTGG 14
Db 32 TTTTCAGGAAATCTGG 14

RESULT 5
AX609773
LOCUS AX609773 25 bp DNA linear PAT 17-FEB-2003
DEFINITION Sequence 798 from Patent WO02072882.
ACCESSION AX609773
VERSION AX609773.1 GI:28405202
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE
AUTHORS Cullen, P. and Seedorf, U.
TITLE Coronary chip
JOURNAL Patent: WO 02072882-A 798 19-SEP-2002;
OGHAM GmbH (DE)
FEATURES
source 1..25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 69.0%; Score 13.8; DB 6; Length 25;

Best Local Similarity 88.2%; Pred. No. 6.6e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TTTTCAGGGAATCCGG 17
|||||
2 TTTTCAGGGAATCTCG 18

/sex="female"
/country="Mexico:Baja California, 3 km. west of Camalu"
/note="isolated November 10, 1983"
<1..>53
/product="tRNA-Glu"

ORIGIN

RESULT 6
LOCUS AK612836 25 bp DNA linear PAT 17-FEB-2003

DEFINITION Sequence 3861 from Patent WO02072882.

ACCESSION AK612836

VERSION AK612836.1 GI:28408265

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

REFERENCE
AUTHORS Homo sapiens
TITLE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
JOURNAL Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE

AUTHORS Cullen, P. and Seedorf, U.

TITLE Coronary chip

JOURNAL Patent: WO 02072882-A 3861 19-SEP-2002;

OGHAM GmbH (DE)

FEATURES
SOURCE location/Qualifiers

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/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 69.0%; Score 13.8; DB 6; Length 25;
Best Local Similarity 88.2%; Pred. No. 6.6e+04;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TTTTCAGGGAATCCGG 17
|||||
7 TTTTCAGGGAATCTCG 23

Db

RESULT 7
LOCUS TCIMT03 53 bp DNA linear VRT 23-SEP-1999

DEFINITION Toxostoma cinereum isolate GRTH4BN tRNA-Glu gene, partial sequence;

ACCESSION AF154459

VERSION AF154459.1 GI:5918797

KEYWORDS

SEGMENT

SOURCE

ORGANISM 3 of 6
mitochondrion Toxostoma cinereum

Toxostoma cinereum

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Passeriformes; Mimidae; Toxostoma.

1 (bases 1 to 53)

Zink, R.M., Dittmann, D.L., Klicka, J. and Blackwell-Rago, R.C.

Evolutionary patterns of morphometrics, allozymes and mitochondrial

DNA in thrashers (Toxostoma)

The Auk (1999) in press

2 (bases 1 to 53)

Zink, R.M., Dittmann, D.L., Klicka, J. and Blackwell-Rago, R.C.

Direct Submission

Submitted (26-MAY-1999) Bell Museum, University of Minnesota, 100

Ecology Bldg, 1987 Upper Buford Circle, St Paul, MN 55108, USA

location/Qualifiers

1..53

/organism="Toxostoma cinereum"

/organelle="mitochondrion"

/mol_type="genomic DNA"

/isolate="GRTH4BN"

/specimen_voucher="B16587, LSU Museum of Zoology"

/specimen_voucher="RMZ 2165, American Museum, New York"

/db_xref="taxon:99877"

/sex="female"
/country="Mexico:Baja California, 3 km. west of Camalu"
/note="isolated November 10, 1983"
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/product="tRNA-Glu"

ORIGIN

Query Match 69.0%; Score 13.8; DB 5; Length 53;
Best Local Similarity 88.2%; Pred. No. 6.1e+04;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTTTCAGGGAATCCGG 18
|||||

33 TTTTCAGGGAATCTCG 17

Db

RESULT 8
LOCUS AY604622

DEFINITION AY604622 72 bp mRNA linear MAM 09-JUN-2004

(TCRD) mRNA, partial cds.

AY604622

VERSION AY604622.1 GI:48249542

KEYWORDS

SOURCE

ORGANISM Sus scrofa (pig)

Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;

Sus.

1 (bases 1 to 72)

Holtmeier, W., Geisel, W., Bernert, K., Butler, J.E., Sinkora, M.,

Rehakova, Z., Sinkora, J. and Caspar, W.F. delta repertoire: Dominant

prenatal development of the porcine TCR delta repertoire: Dominant

expression of an invariant T cell receptor Vdelta3-Jdelta3 chain

Eur. J. Immunol. (2004) in press

2 (bases 1 to 72)

Holtmeier, W., Geisel, W., Bernert, K., Butler, J.E., Sinkora, M.,

Rehakova, Z., Sinkora, J. and Caspar, W.F.

Direct Submission

Submitted (22-APR-2004) Medizinische Klinik II, Department of

Gastroenterology, Johann Wolfgang Goethe-Universität,

Theodor-Stern-Kai 7, Frankfurt am Main 60590, Germany

location/Qualifiers

1..72

/organism="Sus scrofa"

/mol_type="mRNA"

/db_xref="taxon:9823"

/clone="8401-10"

/dev_stage="fetal"

<1..>72

/gene="TCRD"

/note="TRD"

<1..>72

/gene="TCRD"

/note="TRDVTJ1"

/product="T-cell receptor delta chain CDR3 region"

/protein_id="AA141020.1"

/db_xref="GI:48249543"

/translation="ADSAHYFCAFMESWDTDLIFGKG"

ORIGIN

Query Match 69.0%; Score 13.8; DB 4; Length 72;

Best Local Similarity 88.2%; Pred. No. 5.9e+04;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TTTTCAGGGAATCCGG 19
|||||

27 TTTTCAGGGAATCTCG 43

Db

RESULT 9

AJ840678

LOCUS AJ840678 86 bp DNA linear PLN 22-SEP-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, right border, clone 605E05
ACCESSION AJ840678
VERSION AJ840678.1 GI:52544884
KEYWORDS right border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; eudicotyledons; core eudicotyledons; rosids; eustrodi II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
AUTHORS 1 Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechthold, N., Cruaud, C., Derose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.
TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
REFERENCE
PUBMED 12446565
2 (bases 1 to 86)
AUTHORS Balzergue, S.
TITLE Direct Submission
JOURNAL Submitted (21-SEP-2004) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment (s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'genoplante' (<http://www.genoplante.com> and <http://genoplante.info.inbio.gen.fr>).
FEATURES
source 1..86
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="605E05"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Massilewska"
misc_feature 1..86
/note="T-DNA flanking sequence
right border"
ORIGIN
Query Match 69.0%; Score 13.8; DB 15; Length 86;
Best Local Similarity 88.2%; Pred. No. 5.8e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 TTTTTCAGGGAATCCGG 17
|||||
19 TTTTTCAGGGAATCAG 35
Db 19 TTTTTCAGGGAATCAG 35
RESULT 10
AX16045
LOCUS AX16045 51 bp DNA linear PAT 02-APR-2003
DEFINITION Sequence 23 from Patent WO03010332.
ACCESSION AX16045
VERSION AX16045.1 GI:29499183
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.
REFERENCE
AUTHORS 1 Volkenlofer-Schrumpf, S., Schlinker, M. and Fraenzl, G.
TITLE Test-kit for detecting enterohemorrhagic _E. coli strains (ehec)
JOURNAL Patent: WO 03010332-A 23 06-FEB-2003;
Sy-Lab GmbH (AT)

FEATURES
source Location/Qualifiers
1..37
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Random oligonucleotide"
ORIGIN
Query Match 68.0%; Score 13.6; DB 6; Length 37;
Best Local Similarity 80.0%; Pred. No. 8.1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 TTTTTCAGGGAATCCGGGG 20
|||||
9 TTTTCCGGTAGTCCGGGG 28
Db 9 TTTTCCGGTAGTCCGGGG 28
RESULT 11
AX160046
LOCUS AX160046 50 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 3374 from Patent WO0140521.
ACCESSION AX160046
VERSION AX160046.1 GI:14541377
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS 1 Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0140521-A 3374 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source 1..50
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 25..26
/note="Nucleotide deleted between bases 25 and 26
Accession number cg43253001"
misc_feature 26
/note="2 of 2 allelic variants (3373 is other entry)"
ORIGIN
Query Match 68.0%; Score 13.6; DB 6; Length 50;
Best Local Similarity 80.0%; Pred. No. 7.8e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 TTTTTCAGGGAATCCGGGG 20
|||||
4 TGTCTCGGGGAATCCGGGG 23
Db 4 TGTCTCGGGGAATCCGGGG 23
RESULT 12
AX160045
LOCUS AX160045 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 3373 from Patent WO0140521.
ACCESSION AX160045
VERSION AX160045.1 GI:14541376
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS 1 Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0140521-A 3373 07-JUN-2001;

FEATURES	Curegen Corporation (US)
SOURCE	Location/Qualifiers 1..51
misc_feature	/organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606" 26
ORIGIN	/note="1 of 2 allelic variants (3374 is other entry) Accession number C943253001"
Query Match	68.0%; Score 13.6; DB 6; Length 51;
Best Local Similarity	80.0%; Pred. No. 7.8e+04;
Matches	16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY	1 TTTTTCAGGGAATCCGGGG 20 4 TGTCTCGGGGAAGCCGGGG 23
Db	
RESULT 13	
TO1MITO3/C	
LOCUS	54 bp DNA linear VRT 23-SEP-1999
DEFINITION	Toxostoma ocellatum isolate OCH2MX tRNA-Glu gene, partial
ACCESSION	AF154447
VERSION	AF154447.1 GI:5918785
KEYWORDS	
SEGMENT	
SOURCE	3 of 6
ORGANISM	mitochondrion Toxostoma ocellatum
REFERENCE	Toxostoma ocellatum
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Passeriformes; Mimidae; Toxostoma.
TITLE	1 (bases 1 to 54)
DESCRIPTION	Zink, R.M., Dittmann, D.L., Klicka, J. and Blackwell-Rago, R.C. Evolutionary patterns of morphometrics, allozymes and mitochondrial DNA in thrashers (Toxostoma) The Auk (1999) In press
JOURNAL	2 (bases 1 to 54)
REFERENCE	Zink, R.M., Dittmann, D.L., Klicka, J. and Blackwell-Rago, R.C. Direct Submission
AUTHORS	Submitted (26-MAY-1999) Bell Museum, University of Minnesota, 100 Ecology Bldg, 1997 Upper Buford Circle, St Paul, MN 55108, USA
JOURNAL	Location/Qualifiers
FEATURES	1..54
SOURCE	/organism="Toxostoma ocellatum" /organelle="mitochondrion" /mol_type="genomic DNA" /isolate="OCH2MX" /specimen_voucher="RMZ 2190, American Museum, New York" /specimen_voucher="B16570, LSU Museum of Zoology" /db_xref="taxon:99881" /sex="male" /country="Mexico;Oaxaca, 5 km SE of Matatlan" /note="Isolated November 18, 1993" <1..>54 /product="cRNA-Glu"
ORIGIN	
Query Match	68.0%; Score 13.6; DB 5; Length 54;
Best Local Similarity	80.0%; Pred. No. 7.7e+04;
Matches	16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY	1 TTTTTCAGGGAATCCGGGG 20 34 TTTTTCAGGGAATCCTGAG 15
Db	
RESULT 14	
LOCUS	65 bp DNA linear PAT 30-JAN-2004
DEFINITION	COS59452
SEQUENCE	29087 from Patent WO0210449.
ACCESSION	COS59452

```

VERSION      CQ559452.1  GI:41525879
KEYWORDS
SOURCE
ORGANISM     Mus musculus (house mouse)
              Mus musculus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
              Sciurognathi; Muridae; Muridae; Murinae; Mus.

REFERENCE
AUTHORS      Shoshun,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
TITLE        Oligonucleotide library for detecting rna transcripts and splice
              variants that populate a transcritome
JOURNAL      Patent: WO 0210449-A 29087 07-FEB-2002;
              Compugen Inc. (US)

FEATURES
             location/Qualifiers
             source
               1..65
               /organism="Mus musculus"
               /mol_type="unassigned DNA"
               /db_xref="taxon:10090"

ORIGIN
Query Match 68.0%; Score 13.6; DB 6; Length 65;
Best Local Similarity 80.0%; Pred. No. 7.6e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0.

Oy          1 TTTTTCAGGGGATCCGGGG 20
Db          39 TTGTTCCAGGAACTCGTGGG 58

RESULT 15
AX655469          72 bp  DNA  linear  PAT 22-MAR-2003
LOCUS             AX655469
DEFINITION        Sequence 5339 from Patent WO03000898.
ACCESSION          AX655469
VERSION            AX655469.1  GI:29158283
KEYWORDS
SOURCE
ORGANISM           Oryza sativa
                  Oryza sativa
                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                  Eriarthroideae; Oryzaceae; Oryza.
1
REFERENCE
AUTHORS           Chang,H.-S., Chen,W., Cooper,B., Glazebrook,J., Goff,S.A., Hou,Y.M.,
                  Katagiri,F., Quan,S., Tao,Y., Whitman,S., Xie,Z., Zhu,T. and Zou,G.
TITLE             Plant genes involved in defense against pathogens
JOURNAL           Patent: WO 03000898-A 5339 03-JAN-2003;
                  Syngenta Participations AG (CH)
FEATURES
             location/Qualifiers
             source
               1..72
               /organism="Oryza sativa"
               /mol_type="unassigned DNA"
               /db_xref="taxon:4530"

ORIGIN
Query Match 68.0%; Score 13.6; DB 6; Length 72;
Best Local Similarity 72.2%; Pred. No. 7.5e+04;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0.

OY          2 TTTTTCAGGGGATCCGGGG 19
Db          38 TTTTCCGCGARCCCGGK 55

Search completed: December 24, 2005, 14:06:07
Job time : 584 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 01:41:40 : Search time 171.4 Seconds
(without alignments)
777.677 Million cell updates/sec

Title: US-09-296-264-5

Perfect score: 20
Sequence: 1 ttttcagggaatccgsgsg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 3390896

Minimum DB seq length: 20
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_21:*

1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3	AA231435 Human neu
2	20	100.0	20	9	ADA74687 GTI3605 a
3	14.2	71.0	25	4	AA121532 Human bre
4	14.2	71.0	51	10	ACF79352 Upstream
5	14.2	71.0	57	10	ADD94398 Mouse HUI
6	14.2	71.0	57	10	ADD94399 Mouse HUI
7	14	70.0	57	10	ADD94400 Mouse HUI
8	13.8	69.0	21	10	ADG84972 FAM/TAMRA
9	13.8	69.0	24	10	ADF72668
10	13.8	69.0	57	6	ABK36270 HIV DNA e
11	13.8	69.0	57	10	ADD94401 Mouse HUI
12	13.8	69.0	80	12	ADM95446 Rat antic
13	13.6	68.0	33	12	ADM6724 primer 3
14	13.6	68.0	37	8	ABX94733 Negative
15	13.6	68.0	50	4	AA176433 Human sll
16	13.6	68.0	51	4	AA176432 Human sll
17	13.6	68.0	55	10	ADK12084 Breast ca
18	13.6	68.0	65	6	ABN56339 Mouse bpl
19	13.6	68.0	68	14	ACL59655 Human col

20	13.6	68.0	72	8	ADA72014	Ada72014 Rice gene	
C	21	13.6	68.0	88	12	ACH84195	Ach84195 Human gen
22	13.6	68.0	91	2	AAT22379	Aat22379 Human gen	
23	13.6	68.0	100	8	ACD73703	Act73703 E. coli K	
24	13.4	67.0	21	2	AAQ86161	Aaq86161 Sindbis p	
C	25	13.4	67.0	21	2	AAQ86162	Aaq86162 Sindbis p
26	13.4	67.0	21	2	AAT35060	Aat35060 Sindbis v	
C	27	13.4	67.0	21	2	AAT35061	Aat35061 Sindbis v
28	13.4	67.0	21	2	AAT30796	Aat30796 Sindbis g	
C	29	13.4	67.0	21	2	AAT30795	Aat30795 Sindbis g
30	13.4	67.0	21	2	AAx59247	Aax59247 primer 73	
C	31	13.4	67.0	21	2	AAx59246	Aax59246 primer 73
32	13.4	67.0	21	2	AAV42372	Aav42372 PCR prime	
C	33	13.4	67.0	21	2	AAV42373	Aav42373 PCR prime
C	34	13.4	67.0	21	2	AAV60134	Aav60134 PCR prime
35	13.4	67.0	21	2	AAV60133	Aav60133 PCR prime	
C	36	13.4	67.0	21	2	AAV70693	Aav70693 PCR prime
37	13.4	67.0	21	2	AAV70692	Aav70692 PCR prime	
38	13.4	67.0	21	2	AAx58488	Aax58488 primer 73	
C	39	13.4	67.0	21	2	AAx58489	Aax58489 primer 73
C	40	13.4	67.0	21	3	AAZ92901	Aaz92901 Sindbis v
41	13.4	67.0	21	3	AAZ92900	Aaz92900 Sindbis v	
C	42	13.4	67.0	21	3	AAZ92773	Aaz92773 Sindbis v
C	43	13.4	67.0	21	3	AAZ92774	Aaz92774 Sindbis v
C	44	13.4	67.0	21	6	AA138780	Al138780 Alphaviru
C	45	13.4	67.0	21	6	AA138781	Al138781 Alphaviru

ALIGNMENTS

RESULT 1	
AA231435	AA231435 standard; DNA; 20 BP.
ID	AA231435 standard; DNA; 20 BP.
XX	AA231435;
AC	
XX	
DT	07-FEB-2000 (first entry)
XX	
DE	Human neuropilin mRNA specific antisense oligo GTI3605.
XX	
KW	Neuropilin; human; growth; metastasis; tumor; neovascularisation; cancer; papilloma; diabetic retinopathy; antisense; ss.
XX	
OS	Synthetic.
OS	Homo sapiens.
XX	
PN	W0955855-A2.
XX	
PD	04-NOV-1999.
XX	
PF	23-APR-1999; 99WO-CA000324.
XX	
PR	23-APR-1998; 98US-0082791P.
XX	
PA	(GENE-) GENENSENSE TECHNOLOGIES INC.
XX	
PI	Wright JA, Young AH, Lee YS;
XX	
WP	WPI; 2000-023357/02.
PT	Antisense oligonucleotides that inhibit neuropilin expression, useful for treating cancer.
XX	
PS	Claim 4; Page 16; 57pp; English.
CC	Sequences AA231431-460 represent antisense oligonucleotides which inhibit human neuropilin expression. The antisense oligonucleotides can be used to inhibit the growth or metastasis of a mammalian tumor and inhibit neovascularisation. The oligonucleotides may be used to treat various forms of cancers or tumors, such as sarcomas, melanomas, adenomas, carcinomas of solid tissue, hypoxic tumors, squamous cell carcinomas of the mouth, throat, larynx and lung, genitourinary cancers such as

CC cervical and bladder cancer, hematopoietic cancers, colon cancer, breast
CC cancer, pancreatic cancer, renal cancer, brain cancer, skin cancer, liver
CC cancer, head and neck cancers, and nervous system cancers, as well as
CC benign lesions such as papillomas. The methods may be used to treat
CC neovascularisation disorders such as diabetic retinopathy, and
CC retinopathy of prematurity and age related macular degeneration
XX
SQ Sequence 20 BP; 3 A; 3 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTTTCAGGGAATCCGGGG 20
1 TTTTCAGGGAATCCGGGG 20
DB 1 TTTTCAGGGAATCCGGGG 20

RESULT 2
ADA74687
ID ADA74687 standard; DNA; 20 BP.
XX
AC ADA74687;

DT 20-NOV-2003 (first entry)
DE GT13605 antisense oligonucleotide targeted to human neuropilin mRNA.
XX
XX neuropilin; VEGF165R; vascular endothelial growth factor receptor;
KM cytosolic; growth; tumour metastasis; angiogenesis; gene therapy;
KM GT13605; antisense; human; ss.
XX
XX Homo sapiens.

OS
XX
XX US2003083274-A1.
XX
XX 01-MAY-2003.

XX
XX 22-APR-1999; 99US-00296264.
XX
XX 23-APR-1998; 98US-0082791P.

XX
XX (WRIG/) WRIGHT J A.
XX (YOUNG) YOUNG A H.
XX (LEEY/) LEE Y S.

XX
XX PI Wright JA, Young AH, Lee YS;
XX
XX WPI; 2003-576622/54.

XX
XX DR
XX
XX New antisense oligonucleotide that inhibits neuropilin expression, useful
XX for inhibiting growth of mammalian tumor or inhibiting metastasis of a
XX mammalian tumor.

XX
XX PS Claim 1; Page 5; 27pp; English.

XX
XX CC The invention relates to a novel antisense oligonucleotide that inhibits
XX the expression of neuropilin, also known as VEGF165R (vascular
XX endothelial growth factor receptor). The oligonucleotide of the invention
XX demonstrates cytostatic activity and may be useful for inhibiting the
XX growth or metastasis of a mammalian tumour and to inhibit angiogenesis in
XX mammals. Furthermore, the oligonucleotide may be utilised during gene
XX therapy. The current sequence is that of the GT13605 antisense
XX oligonucleotide of the invention which is targeted to human neuropilin
XX mRNA.

XX
XX SQ Sequence 20 BP; 3 A; 3 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTTTCAGGGAATCCGGGG 20

DB 1 TTTTCAGGGAATCCGGGG 20

RESULT 3
AAL21532/c
ID AAL21532 standard; cDNA; 25 BP.
XX
XX AAL21532;

DT 07-DEC-2001 (first entry)

DE Human breast cancer expressed polynucleotide 13989.

XX
XX Human; breast cancer; cell marker; cytosolic; ss.

OS
XX
XX Homo sapiens.

XX
XX PN WO200151628-A2.

XX
XX PD 19-JUL-2001.

XX
XX PF 10-JAN-2001; 2001WO-US000798.

XX
XX PR 14-JAN-2000; 2000US-0176077P.

XX
XX PR 14-MAR-2000; 2000US-0189167P.

XX
XX PR 24-MAR-2000; 2000US-0192099P.

XX
XX PR 29-MAR-2000; 2000US-0193480P.

XX
XX PR 15-MAY-2000; 2000US-0205230P.

XX
XX PR 09-JUN-2000; 2000US-0211315P.

XX
XX PR 25-JUL-2000; 2000US-0220534P.

XX
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX
XX PI Lillie J, Xu Y, Wang Y, Steinmann K;

XX
XX DR WPI; 2001-451856/48.

XX
XX PT New peptide useful as a marker for the diagnosis of breast cancer.

XX
XX PS Claim 1; Page 2494; 3695pp; English.

XX
XX CC The invention relates to human breast cancer expressed polynucleotides
XX (AAL07544-AAL26789) and methods of assessing whether a patient is
XX afflicted with breast cancer by examining the correlation between the
XX expression of certain markers and the cancerous state of breast cells.
XX The polynucleotides and encoded polypeptides are potential markers for
XX detecting, diagnosing, monitoring, characterising, treating and
XX potentially preventing breast cancer. The polynucleotides and encoded
XX polypeptides are also useful for isolating compounds with cytostatic
XX activity

XX
XX SQ Sequence 25 BP; 6 A; 7 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 4; Length 25;
Best Local Similarity 84.2%; Pred. No. 3.9e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 TTTTCAGGGAATCCGGGG 19
1 TTTTCAGGGAATCCGGGG 19
DB 19 TTTTCAGGGAATCCGGGG 1

RESULT 4
ACF79352/c
ID ACF79352 standard; DNA; 51 BP.

XX
XX AC ACF79352;

XX
XX DT 18-DEC-2003 (first entry)

XX
XX DE Upstream primer for construction of pMPDLM-12alpha-E3L.

KW Z-alpha; DLM-1; mouse; E3L; Z-DNA; virucide; vaccine; PCR; primer; ss.
XX Mus sp.
OS
XX WO2003066807-A2.
PN
XX
XX 14-AUG-2003.
PD
XX
XX 19-DEC-2002; 2002WO-US041107.
PF
XX
XX 20-DEC-2001; 2001US-0343028P.
PR 16-DEC-2002; 2002US-00321785.
XX
XX (MASI) MASSACHUSETTS INST TECHNOLOGY.
PA (UYAR-) UNIV ARIZONA.
XX
XX Jacobs BL, Rich A;
PI
XX WPI; 2003-679540/64.
DR
XX
XX Detecting or identifying an inhibitor of binding of a Z-DNA binding
PT ligand to Z-DNA by combining an agent to be tested, Z-DNA and a
PR composition comprising a Z-DNA binding ligand or Z-DNA binding variant.
XX
XX Example 2; Page 44; 105pp; English.
PS
XX
XX The present sequence is an upstream primer used in the construction of
CC plasmid pMFDLM-1alpha-E3L in which nucleotides 61-261 of the vaccinia
CC virus E3L gene (coding for amino acids 1-67) were replaced by nucleotides
CC 116-316 from the Z-alpha domain of the mouse DLM-1 gene. Vaccinia virus
CC E3L and DLM-1 are Z-DNA binding ligands. Domain swapping was performed in
CC order to identify E3L residues responsible for vaccinia virus
CC pathogenicity. The invention relates to methods of identifying inhibitors
CC of binding of a Z-DNA binding ligand to Z-DNA, methods of inhibiting the
CC pathogenicity of a Z-DNA binding agent, and antiviral therapies. The
CC inhibitors are used to treat a poxvirus infection caused by variola
CC virus, vaccinia virus, orf virus, mousepox virus, monkeypox virus,
CC ecromelia virus, yaba-like disease virus, cowpox virus, myxoma virus,
CC rabbit fibroma virus or lumpy skin disease virus (claimed)
XX
XX Sequence 51 BP; 14 A; 14 C; 13 G; 10 T; 0 U; 0 Other;
SQ
Query Match 71.0%; Score 14.2; DB 10; Length 51;
Best Local Similarity 84.2%; Pred. No. 4.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 TTTTCAGGGAATCCGGGG 20
DB 31 TTTTCAGGGAATCCGGGG 13
RESULT 5
ADD94398/C
ID ADD94398 standard; DNA; 57 BP.
XX
XX ADD94398;
AC
XX 29-JAN-2004 (first entry)
DT
XX
XX Mouse HUIV26 antibody mutagenic PCR primer SegID283.
DE
XX
XX grafted antibody; complementarity determining region; CDR; light CDR;
KW heavy CDR; cryptic collagen epitope; solid tumour;
KW new blood vessel growth; angiogenesis; tumour growth; cytostatic;
KW collagen agonist; collagen antagonist; cancer metastasis;
KW anti-cryptic collagen; PCR; primer; ss; mouse; murine; HUIV26; mutagenic.
XX
XX Synthetic.
OS
XX Mus musculus.
XX
XX WO2003046204-A2.
PN
XX
XX 05-JUN-2003.
PD

XX
XX 26-NOV-2002; 2002WO-US038147.
PF
XX
XX 26-NOV-2001; 2001US-00995529.
PR 06-DEC-2001; 2001US-00011250.
XX
XX
XX (CELL-) CELL MATRIX INC.
PA
XX
XX Waking JD, Huse WD, Tang Y, Broek D, Brooks PC;
PI
XX WPI; 2003-513649/48.
DR
XX
XX New cryptic collagen antibody with one or more complementarity
PT determining regions; useful for diagnosing and treating disorders
PR associated with angiogenesis, tumor growth and/or cancer metastasis.
XX
XX
XX Example 2; SEQ ID NO 283; 232pp; English.
PS
XX
XX This invention relates to a novel grafted antibody or its functional
CC fragment comprising one or more complementarity determining regions
CC (CDRs) of a defined light CDR and a heavy CDR with at least one amino
CC acid (aa) substitution where the antibody has specific binding activity
CC for a cryptic collagen epitope. The growth of all solid tumours requires
CC new blood vessel growth, angiogenesis, inhibition of which is an approach
CC to limiting tumor growth. The invention may allow development of
CC therapeutics with a cytostatic activity as a collagen agonist or
CC antagonist. The invention is useful for diagnosing and treating disorders
CC associated with angiogenesis, tumor growth and/or cancer metastasis. The
CC present sequence is that of a mutagenic PCR primer which was used to
CC amplify a region of the sequence encoding the mouse HUIV26 antibody
CC during the exemplification of the invention.
XX
XX Sequence 57 BP; 13 A; 12 C; 18 G; 11 T; 0 U; 3 Other;
SQ
Query Match 71.0%; Score 14.2; DB 10; Length 57;
Best Local Similarity 84.2%; Pred. No. 4.2e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 TTTTCAGGGAATCCGGGG 19
DB 33 TTTTCAGGGAATCCGGGG 15
RESULT 6
ADD94399/C
ID ADD94399 standard; DNA; 57 BP.
XX
XX ADD94399;
AC
XX 29-JAN-2004 (first entry)
DT
XX
XX Mouse HUIV26 antibody mutagenic PCR primer SegID284.
DE
XX
XX grafted antibody; complementarity determining region; CDR; light CDR;
KW heavy CDR; cryptic collagen epitope; solid tumour;
KW new blood vessel growth; angiogenesis; tumour growth; cytostatic;
KW collagen agonist; collagen antagonist; cancer metastasis;
KW anti-cryptic collagen; PCR; primer; ss; mouse; murine; HUIV26; mutagenic.
XX
XX Synthetic.
OS
XX Mus musculus.
XX
XX WO2003046204-A2.
PN
XX
XX 05-JUN-2003.
PD
XX
XX 26-NOV-2002; 2002WO-US038147.
PF
XX
XX 26-NOV-2001; 2001US-00995529.
PR 06-DEC-2001; 2001US-00011250.
XX
XX
XX (CELL-) CELL MATRIX INC.
PA
XX

PI Wackling JD, Huse WD, Tang Y, Broek D, Brooks PC;
 XX WPI; 2003-513649/48.
 DR
 XX
 PT New cryptic collagen antibody with one or more complementarity
 PT determining regions, useful for diagnosing and treating disorders
 PT associated with angiogenesis, tumor growth and/or cancer metastasis.
 XX
 PS Example 2; SEQ ID NO 284; 232pp; English.
 CC This invention relates to a novel grafted antibody or its functional
 CC fragment comprising one or more complementarity determining regions
 CC (CDRs) of a defined light CDR and a heavy CDR with at least one amino
 CC acid (aa) substitution where the antibody has specific binding activity
 CC for a cryptic collagen epitope. The growth of all solid tumours requires
 CC new blood vessel growth, angiogenesis, inhibition of which is an approach
 CC to limiting tumour growth. The invention may allow development of
 CC therapeutics with a cytostatic activity as a collagen agonist or
 CC antagonist. The invention is useful for diagnosing and treating disorders
 CC associated with angiogenesis, tumour growth and/or cancer metastasis. The
 CC present sequence is that of a mutagenic PCR primer which was used to
 CC amplify a region of the sequence encoding the mouse HUIV26 antibody
 CC during the exemplification of the invention.
 CC
 SQ Sequence 57 BP; 13 A; 14 C; 17 G; 10 T; 0 U; 3 Other;
 Query Match 71.0%; Score 14.2; DB 10; Length 57;
 Best Local Similarity 84.2%; Pred. No. 4.2e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 TTTTTCAGGGAATCCGGG 19
 DB 33 TCTACAGGGAATCCGGG 15
 RESULT 7
 ADD94400/C
 ID ADD94400 standard; DNA; 57 BP.
 XX
 AC ADD94400;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Mouse HUIV26 antibody mutagenic PCR primer SeqID285.
 XX
 KW grafted antibody; complementarity determining region; CDR; light CDR;
 KW heavy CDR; cryptic collagen epitope; solid tumour;
 KW new blood vessel growth; angiogenesis; tumour growth; cytostatic;
 KW collagen agonist; collagen antagonist; cancer metastasis;
 KW anti-cryptic collagen; PCR; primer; ss; mouse; murine; HUIV26; mutagenic.
 XX
 OS Synthetic.
 OS Mus musculus.
 XX
 PN WO2003046204-A2.
 XX
 PD 05-JUN-2003.
 XX
 PF 26-NOV-2002; 2002WO-US038147.
 XX
 PR 26-NOV-2001; 2001US-00995529.
 PR 06-DEC-2001; 2001US-00011250.
 XX
 PA (CELL-) CELL MATRIX INC.
 XX
 PI Wackling JD, Huse WD, Tang Y, Broek D, Brooks PC;
 DR WPI; 2003-513649/48.
 XX
 PT New cryptic collagen antibody with one or more complementarity
 PT determining regions, useful for diagnosing and treating disorders
 PT associated with angiogenesis, tumor growth and/or cancer metastasis.
 XX

PS Example 2; SEQ ID NO 285; 232pp; English.
 CC This invention relates to a novel grafted antibody or its functional
 CC fragment comprising one or more complementarity determining regions
 CC (CDRs) of a defined light CDR and a heavy CDR with at least one amino
 CC acid (aa) substitution where the antibody has specific binding activity
 CC for a cryptic collagen epitope. The growth of all solid tumours requires
 CC new blood vessel growth, angiogenesis, inhibition of which is an approach
 CC to limiting tumour growth. The invention may allow development of
 CC therapeutics with a cytostatic activity as a collagen agonist or
 CC antagonist. The invention is useful for diagnosing and treating disorders
 CC associated with angiogenesis, tumour growth and/or cancer metastasis. The
 CC present sequence is that of a mutagenic PCR primer which was used to
 CC amplify a region of the sequence encoding the mouse HUIV26 antibody
 CC during the exemplification of the invention.
 CC
 SQ Sequence 57 BP; 11 A; 15 C; 17 G; 11 T; 0 U; 3 Other;
 Query Match 70.0%; Score 14; DB 10; Length 57;
 Best Local Similarity 100.0%; Pred. No. 5.3e+03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 CAGGGAATCCGGG 19
 DB 28 CAGGGAATCCGGG 15
 RESULT 8
 ADG84972
 ID ADG84972 standard; DNA; 21 BP.
 XX
 AC ADG84972;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE FAM/TAMRA labelled probe #SEQ ID 25.
 XX
 KW Cytostatic; gene therapy; cancer; TDRD1; Tudor Domain Protein 1; probe;
 KW ss.
 XX
 OS Homo sapiens.
 OS
 PN WO2003091690-A2.
 XX
 PD 06-NOV-2003.
 XX
 PF 17-APR-2003; 2003WO-US011933.
 XX
 PR 26-APR-2002; 2002US-0375879P.
 XX
 PA (LUDWIG INST CANCER RES.
 XX
 PI De Smet C, Boon-Falleur T, Lortiot A;
 DR WPI; 2003-865624/80.
 XX
 PT Diagnosing cancer in a subject by obtaining a non-testis biological
 PT sample from the subject and determining the expression in the sample of
 PT one or more cancer-associated nucleic acid molecules.
 XX
 PS Example 5; SEQ ID NO 25; 94pp; English.
 CC The invention relates to a method for diagnosing cancer in a subject,
 CC comprising obtaining a non-testis biological sample from a subject and
 CC determining the expression in the sample of one or more cancer-associated
 CC nucleic acid molecules comprising a sequence having 833-8370 bp. Also
 CC disclosed is a method for selecting a course of treatment of a subject
 CC having or suspected of having cancer, and a kit for diagnosis of cancer
 CC in a subject. The sample comprises tissue or cells. The tissue comprises
 CC lung, bladder, epidermoid, breast, esophageal, renal, prostate, brain,
 CC spleen, blood, bone marrow, epidermis, cutaneous, neuronal, colorectal or
 CC thyroid. The cancer is cutaneous melanomas, sarcomas, lung, bladder,
 CC epidermoid, breast or esophageal carcinomas, renal, prostate, brain,

CC uterine or thyroid tumours, neuroblastomas, colorectal carcinomas,
 CC mesotheliomas, uveal melanomas or myelomas. The method is useful in
 CC diagnosing or treating cancer. The current sequence represents a probe
 CC used in an example from the invention for the detection of the Tudor
 CC Domain Protein 1 gene (TUDRD1).

SQ Sequence 21 BP; 4 A; 6 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 69.0%; Score 13.8; DB 10; Length 21;

Best Local Similarity 88.2%; Pred. No. 6e+03; Mismatches 2; Indels 0; Gaps 0;

OY 3 TTTCAGGGAATCCGGG 19
 DB 3 TTTCAGGGAATCCGGT 19

RESULT 9

ADP72668/C
 ID ADP72668 standard; DNA; 24 BP.

AC ADP72668;

DT 12-FEB-2004 (first entry)

DE E. coli VT1B forward PCR primer SEQ ID NO:1.

KW sb; primer; PCR; contamination; pathogenic microbe; food poisoning.

OS Escherichia coli.

PN JP200325099-A.

PD 12-AUG-2003.

PF 04-FEB-2002; 2002JP-00027106.

PR 04-FEB-2002; 2002JP-00027106.

PA (NITTL) NITTO DENKO CORP.

DR WPI; 2003-868855/81.

PT Detecting target DNA useful for determining contamination of the
 PT foodstuffs, by introducing test sample on absorptive base material
 PT containing labeled RNA probe and measuring signal from labeled RNA probe.

PS Example 1; SEQ ID NO 1; 11pp; Japanese.

CC The invention relates to a novel method for detecting target DNA using a
 CC labelled RNA probe. The method of the invention is useful for detecting
 CC target DNA present in the sample, for determining contamination of
 CC foodstuffs by pathogenic microbes, food poisoning, diagnosing condition
 CC of disease and genotyping of an organism. The present sequence is used in
 CC the exemplification of the invention.

SQ Sequence 24 BP; 12 A; 5 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 69.0%; Score 13.8; DB 10; Length 24;

Best Local Similarity 88.2%; Pred. No. 6.1e+03; Mismatches 2; Indels 0; Gaps 0;

OY 1 TTTCAGGGAATCCGG 17
 DB 17 TTTCATGGAATTCGG 1

RESULT 10

ABK36270/C
 ID ABK36270 standard; DNA; 57 BP.

AC ABK36270;

XX

DT 08-MAY-2002 (first entry)

XX HIV DNA encoding GAG segment 33.

DE Saviene; vaccine; cancer; viral infection; HIV; hepatitis C virus;

KW viral infection; human immunodeficiency virus; melanoma;

KW bacterial infection; Salmonella; Legionella; parasitic infection;

KW Trypanosoma; Toxoplasma; Giardia; da.

OS Human immunodeficiency virus 1.

PN WO200190197-A1.

PD 29-NOV-2001.

PF 25-MAY-2001; 2001WO-AU000622.

PR 26-MAY-2000; 2000AU-00007761.

PA (AUSU) UNIV AUSTRALIAN NAT.

PI Thomson SA, Ramshaw IA;

DR WPI; 2002-147575/19.

DR P-Psdb; AAU84431.

PT New synthetic polypeptides having several different segments of at least
 PT one parent polypeptide linked together differently compared to the
 PT linkage in the parent polypeptide, for inducing immune response against a
 PT pathogen or cancer.

PS Example 1; Fig 12; 364pp; English.

CC The invention relates to a new synthetic polypeptide (I) comprising
 CC several different segments of at least one parent polypeptide linked
 CC together in a different relationship relative to their linkage in the
 CC parent polypeptide to impede, abrogate or otherwise alter at least one
 CC function associated with the parent polypeptide and for inducing an
 CC immune response against a pathogen or cancer. Also included are a
 CC synthetic polynucleotide encoding and a computer system for designing the
 CC synthetic polynucleotides. The synthetic polypeptides and polynucleotides
 CC are referred to as a Savine. The synthetic polypeptide is useful for
 CC modulating immune responses preferably directed against a pathogen or a
 CC cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head
 CC and neck, pancreas, prostate, stomach, bladder, kidney, bone liver,
 CC oesophagus, brain, testicle, uterus), as potentiating agents.
 CC Compositions comprising the polypeptide may be used in the treatment or
 CC prophylaxis against viral (such as infections caused by HIV (human
 CC immunodeficiency virus), hepatitis, influenza, Japanese encephalitis
 CC virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
 CC (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,
 CC Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic
 CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
 CC Trypanosoma, Toxoplasma and Giardia) infections. The present sequence
 CC encodes a peptide derived from a parent protein used to construct a
 CC vaccine of the invention

SQ Sequence 57 BP; 13 A; 22 C; 6 G; 13 T; 0 U; 3 Other;

Query Match 69.0%; Score 13.8; DB 6; Length 57;

Best Local Similarity 78.9%; Pred. No. 6.6e+03; Mismatches 3; Indels 0; Gaps 0;

OY 2 TTTCAGGGAATCCGGGG 20
 DB 28 TTTCAGGGAAGCTTAGGG 10

RESULT 11

ADD94401/C
 ID ADD94401 standard; DNA; 57 BP.

XX

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AC ADD94401;
XX
XX 29-JAN-2004 (first entry)
XX
XX Mouse HUIV26 antibody mutagenic PCR primer SeqID286.
DE
XX
XX grafted antibody; complementarily determining region; CDR, light CDR;
XX heavy CDR; cryptic collagen epitope; solid tumour;
XX new blood vessel growth; angiogenesis; tumour growth; cytostatic;
XX collagen agonist; collagen antagonist; cancer metastasis;
XX anti-cryptic collagen; PCR; primer; ss; mouse; murine; HUIV26; mutagenic.
XX
XX Synthetic.
XX Mus musculus.
XX
XX WO2003046204-A2.
XX
XX 05-JUN-2003.
XX
XX 26-NOV-2002; 2002WO-US038147.
XX
XX 26-NOV-2001; 2001US-00995529.
XX
XX 06-DEC-2001; 2001US-00011250.
XX
XX (CELL-) CELL MATRIX INC.
XX
XX Wacking JD, Huse WD, Tang Y, Broek D, Brooke PC;
XX
XX WPI; 2003-513649/48.
XX
XX New cryptic collagen antibody with one or more complementarity
XX determining regions, useful for diagnosing and treating disorders
XX associated with angiogenesis, tumor growth and/or cancer metastasis.
XX
XX Example 2; SEQ ID NO 286; 232bp; English.
XX
XX This invention relates to a novel grafted antibody or its functional
XX fragment comprising one or more complementarity determining regions
XX (CDRs) of a defined light CDR and a heavy CDR with at least one amino
XX acid (aa) substitution where the antibody has specific binding activity
XX for a cryptic collagen epitope. The growth of all solid tumours requires
XX new blood vessel growth, angiogenesis, inhibition of which is an approach
XX to limiting tumour growth. The invention may allow development of
XX therapeutics with a cytostatic activity as a collagen agonist or
XX antagonist. The invention is useful for diagnosing and treating disorders
XX associated with angiogenesis, tumour growth and/or cancer metastasis. The
XX present sequence is that of a mutagenic PCR primer which was used to
XX amplify a region of the sequence encoding the mouse HUIV26 antibody
XX during the exemplification of the invention.
XX
XX Sequence 57 BP; 13 A; 15 C; 16 G; 10 T; 0 U; 3 Other;
SQ
XX
XX Query Match 69.0%; Score 13.8; DB 10; Length 57;
XX Best Local Similarity 78.9%; Pred. No. 6.6e+03;
XX Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 TTTTCAGGGAATCCGGGG 19
DB 33 TCTNNKAGGGAATCCGGGG 15

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XX transport protein; intracellular signal transduction;
XX transcription factor; DNA-binding protein;
XX cell-cell communication protein; stress response gene;
XX apoptosis related gene; growth factor; chemokine; interleukin;
XX interferon; hormone; neurotransmitter; cell surface antigen;
XX cell adhesion molecule.
XX
XX Rattus sp.
XX
XX US2004072191-A1.
XX
XX 15-APR-2004.
XX
XX 07-MAR-2003; 2003US-00384245.
XX
XX 07-MAR-2002; 2002US-0362823P.
XX
XX (CHEN/) CHENCHIK A.
XX
XX Chenchik A;
XX
XX WPI; 2004-373913/35.
XX
XX New standardizing control for RNA samples to be tested on non-control
XX gene sequences on nucleic acid arrays, useful for producing a population
XX of distinct antisense RNA molecules from an initial population of
XX distinct mRNA molecules.
XX
XX Disclosure; SEQ ID NO 339; 282bp; English.
XX
XX The invention relates to a standardising control for RNA samples to be
XX tested on non-control gene sequences on nucleic acid arrays, comprising a
XX pool of unique tagged synthetic antisense RNA molecules of a known
XX concentration, where any two sequences are unique if their sequences
XX differ. The non-control gene sequences on the nucleic acid array comprise
XX oncogenes, genes encoding tumour suppressors, cell cycle regulators, ion
XX channel proteins, transport proteins, intracellular signal transduction
XX modulator and effector factors, transcription factors, DNA-binding
XX proteins, receptors or cell-cell communication proteins, stress response
XX genes, apoptosis related genes, DNA synthesis/recombination/repair genes
XX and DNA-binding proteins. The genes encoding receptors comprise receptors
XX for growth factors, chemokines, interleukins, interferons, hormones,
XX neurotransmitters, cell surface antigens or cell adhesion molecules. The
XX genes encoding cell-cell communication proteins comprise growth factors,
XX cytokines, chemokines, interleukins, interferons or hormones. The
XX standardising control for RNA samples to be tested on non-control gene
XX sequences on nucleic acid arrays is useful for producing a population of
XX distinct antisense RNA molecules from an initial population of distinct
XX mRNA molecules. This sequence represents an antisense oligonucleotide of
XX the invention.
XX
XX Sequence 80 BP; 17 A; 29 C; 10 G; 24 T; 0 U; 0 Other;
SQ
XX
XX Query Match 69.0%; Score 13.8; DB 12; Length 80;
XX Best Local Similarity 88.2%; Pred. No. 6.8e+03;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 TTTCAAGGGAATCCGGGG 19
DB 50 TTTCAAGGGAATGAGGGG 34

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RESULT 12
ADM95446/C
ID ADM95446 standard; DNA; 80 BP.
XX
XX ADM95446;
XX
XX 01-JUL-2004 (first entry)
XX
XX Rat antisense oligonucleotide #339.
XX
XX Rat; antisense oligonucleotide; ss; antisense RNA production; oncogenes;
XX tumour suppressor; cell cycle regulator; ion channel protein;
KW

```

```

RESULT 13
ADM66724
ID ADM66724 standard; DNA; 33 BP.
XX
XX ADM66724;
XX
XX 03-JUN-2004 (first entry)
XX
XX Primer 3 used to generate B. caldolyticus mutant TLP neutral protease.
XX
XX thermolysin-like protease; TLP; SI' site; gluten degradation; wheat;
KW

```

KW baking industry; beer clarification; brewing; dehairing; skin dewooling;
KW leather; protein hydrolysaate production; artificial sweetener; aspartame;
KW PCR; primer; ss; neutral; mutant.
XX
XX Bacillus caldolyticus.
OS
XX
XX
XX WO2004011619-A2.
PN
XX
XX 05-FEB-2004.
PD
XX
XX 28-JUL-2003; 2003WO-US023726.
PF
XX
XX 26-JUL-2002; 2002US-0398656P.
PR
XX
XX (STRA-) STRATAGEME.
PA
XX
XX Clark DD, Bramean JC;
PI
XX
XX WPI; 2004-143847/14.
DR
XX
XX New thermolysin-like protease with substrate specificity for a basic or
PT an acidic amino acid, useful in biological and biomedical research,
PT identifying therapeutic agents and diagnostic markers, or producing
PT artificial sweeteners.
XX
XX
XX Example 2; SEQ ID NO 16; 82pp; English.
PS
XX
XX The invention relates to a novel thermolysin-like protease (TLP)
CC comprising an S1' site and modified to have a substrate specificity for a
CC basic or an acidic amino acid. The thermolysin-like protease of the
CC invention may be useful in proteolysis applications, biological and
CC biomedical research, identifying therapeutic agents and diagnostic
CC markers, characterizing cells and organisms that have undergone genetic
CC modifications, identifying unknown illnesses, characterizing polypeptides
CC or identifying biological samples. The thermolysin-like protease may also
CC be useful in industrial processes, such as the degradation of gluten from
CC wheat within the baking industry, clarification of beer within the
CC brewing industry, dehairing or dewooling of skins within the leather
CC industry, preparation of protein hydrolysates or production of artificial
CC sweeteners like aspartame. The current sequence is that of a PCR primer
CC of the invention which was used to generate Bacillus caldolyticus mutant
CC TLP neutral protease.
XX
XX
SQ Sequence 33 BP; 6 A; 9 C; 10 G; 8 T; 0 U; 0 Other;
Query Match 68.0%; Score 13.6; DB 12; Length 33;
Best Local Similarity 80.0%; Pred. No. 7.9e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 TTTTTCAGGGAATCCGGGG 20
DB 7 TTTTTCAGGGAATCCGGGG 26
RESULT 14
ABX94733
ID ABX94733 standard; DNA; 37 BP.
XX
XX
XX ABX94733;
AC
XX
XX 07-JUL-2003 (first entry)
DT
XX
XX Negative control probe RAN 3.
DE
XX
XX Probe; detection; EHBC; enterohaemorrhagic Escherichia coli; SLT1; SLT2;
KW rfbB; eaeA; KCMJ9; food testing; contamination; ss.
XX
XX Unidentified.
OS
XX
XX WO2003010332-A2.
PN
XX
XX 06-FEB-2003.
PD

XX
XX 26-JUL-2002; 2002WO-AT000222.
PF
XX
XX 26-JUL-2001; 2001AT-00001172.
PR
XX
XX (SYVE-) SY-LAB VERTRIEBS GMBH.
PA
XX
XX Volkenhofer-Schrumpf S, Schlinkinger M, Fraenzl G;
PI
XX
XX WPI; 2003-248085/24.
DR
XX
XX
XX Test kit for detecting enterohaemorrhagic Escherichia coli, useful for
PT testing foods, comprises primers, capture and detection probes for
PT specific genes.
PT
XX
XX Claim 19; Page 35; 35pp; German.
PS
XX
XX This invention describes a novel test kit for detecting
CC enterohaemorrhagic Escherichia coli strains (EHBC). The kit comprises
CC primers for amplification of at least part of the SLT1, SLT2, rfbE and
CC eaeA genes and a control gene in a single reaction. It also includes
CC capture probes and detection probes for hybridisation to the amplicons at
CC room temperature. All capture probes are immobilised on the same solid
CC surface and detection probes are labeled with a visually detectable
CC label. The kit is used to test foods for contamination by EHBC. The kit
CC provides rapid, simple and reliable detection of EHBC in a single
CC reaction. No specialised apparatus is required (contrast use of
CC microarrays) and the method can be performed in routine laboratories. The
CC combination of capture probe and directly labeled probe provides high
CC specificity (typically 1-10 colony-forming units/25 g of food, after an
CC enrichment stage of only 8 hours) and purification of amplicons and
CC separation of unbound label are not required. This sequence represents a
CC probe used to detect an EHBC E. coli gene used in the product of the
CC invention
XX
XX
SQ Sequence 37 BP; 2 A; 9 C; 12 G; 14 T; 0 U; 0 Other;
Query Match 68.0%; Score 13.6; DB 8; Length 37;
Best Local Similarity 80.0%; Pred. No. 8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 TTTTTCAGGGAATCCGGGG 20
DB 9 TTTTTCAGGGAATCCGGGG 28
RESULT 15
AAI76433
ID AAI76433 standard; DNA; 50 BP.
XX
XX
XX AAI76433;
AC
XX
XX 09-NOV-2001 (first entry)
DT
XX
XX Human silent SNP containing nucleic acid SEQ.3374.
DE
XX
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic; ds.
XX
XX Homo sapiens.
OS
XX
XX WO200140521-A2.
PN
XX
XX 07-JUN-2001.
PD
XX
XX 30-NOV-2000; 2000WO-US032758.
PF
XX
XX 30-NOV-1999; 99US-0168138P.
PR
XX
XX 29-NOV-2000; 2000US-00726173.
PN
XX
XX (CURA-) CURAGEN CORP.
PA
XX

PI Shimkets RA, Leach M;

DR WPI; 2001-356160/37.

PT Polymorphic nucleic acid sequences, useful in genetic testing and therapy.

PS Claim 1; Page 1083; 2653pp; English.

PS Claim 1; Page 1083; 2653pp; English.

CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).

CC sequences (I), which contain single nucleotide polymorphisms (SNPs).

CC AA053114 to AA053329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein

CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases

CC associated with inappropriate expression of polymorphic polypeptides. For
CC example, (I) may be used to treat disorders by rectifying mutations or

CC deletions in a patient's genome that affect the activity of polypeptides
CC by expressing inactive proteins or to supplement the patients own
CC

production of polypeptide. Additionally, (I) and its complementary sequences may also be used as DNA probes in diagnostic assays to detect

CC and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The

polypeptides encoded by (I) may be used as antigens in the production of antibodies specific for polymorphic polypeptides. The antibodies may also

be used to down regulate expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of polymorphic

polypeptides in samples

sq Sequence 50 Bf; 10 A; 12 C; 19 G; 9 T; 0 U; 0 Other;
 Query Match 68.0%; Score 13.6; DB 4; Length 50.

Query Match	68.0%;	score 13.6;	DB 4;	length 50;
Best Local Similarity	80.0%;	Pred. No. 8.2e+03;		
Matches	15;	Mismatches	4;	Indels
				0. Cent

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00: 1 ##### 20
Matches 16; conservative 0; mismatches 4; indels 0; gaps 0

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0y 1 TTTTCAGGGATCCGGGG 20
    | | | | | | | | | |
db 4 TTTTCAGGGATCCGGGG 22
    | | | | | | | | | |

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DB 4 TGCTCGGGGAAAGCCGGGGG 23

Search completed: December 24, 2005, 12:28:56
 Tab time: 174.40000

JOB TIME : 174.4 SECS

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using bw model

Run on: December 24, 2005, 10:37:31 ; Search time 1572 Seconds
(Without alignments)
595.256 Million cell updates/sec

Title: US-09-296-264-5

Perfect score: 20

Sequence: 1 ttttcagggaatccggggg 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 2339354128 residues

Total number of hits satisfying chosen parameters: 768474

Minimum DB seq length: 20

Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15.2	76.0	89	6	CB046782 NISC_gf06
2	14.8	74.0	71	1	AJ665651 AJ665651
3	14.8	74.0	79	1	AI925202 wm9h04.x
4	14.8	74.0	96	8	F26680 HSPD14248.H
5	14.2	71.0	51	11	CR010521 Reverse
6	14.2	71.0	61	10	CG646119 OST191595
7	14.2	71.0	77	10	CG553405 OST165917
8	14.2	71.0	87	10	CG653617 OST19275
9	14.2	71.0	88	10	CG581950 OST222704
10	14.2	71.0	96	8	CX287425 C01009007
11	13.8	69.0	49	1	A1756242 EREStea41
12	13.8	69.0	53	11	CR235685 Reverse
13	13.8	69.0	55	10	C2169440 P020C06.G
14	13.8	69.0	64	8	H41671 yoc6f01.81
15	13.8	69.0	66	9	B2353185 SALK.1198
16	13.8	69.0	73	10	CG648700 OST402480
17	13.8	69.0	73	10	CG658614 OST134889
18	13.8	69.0	90	10	CG650838 OST409692
19	13.6	68.0	33	10	AL945989 Arabidops
20	13.6	68.0	43	9	AZ346730 IM0082A11
21	13.6	68.0	67	1	A1799398 tsw56a01.x
22	13.6	68.0	70	1	A1356377 qz21d04.x

23	13.6	68.0	75	10	BX890679	BX890679 Arabidops
24	13.6	68.0	79	6	CD712552	CD712552 VYB019C09
25	13.6	68.0	84	10	CZ907257	CZ907257 401106C0
26	13.6	68.0	85	1	AA854921	AA854921 aJ78h10.s
27	13.6	68.0	88	5	C01948	C01948 HUMG000395
28	13.6	68.0	89	5	B0585916	B0585916 E012532-0
29	13.6	68.0	89	7	CV306463	CV306463 Cj08f11.b
30	13.6	68.0	89	9	CC480457	CC480457 CH240.307
31	13.6	68.0	90	1	AM102784	AM102784 xD38a06.x
32	13.6	68.0	97	9	CC591487	CC591487 CH240.391
33	13.6	68.0	100	2	BG672884	BG672884 DRNAOH08
34	13.4	67.0	61	10	CG667953	CG667953 OST462938
35	13.4	67.0	63	8	T68724	T68724 YC29d01.81
36	13.4	67.0	64	10	CG587635	CG587635 OST337428
37	13.4	67.0	65	10	CG588816	CG588816 OST240242
38	13.4	67.0	67	10	CG587718	CG587718 OST237588
39	13.4	67.0	69	10	CZ490302	CZ490302 F07553-5P
40	13.4	67.0	73	7	CR428430	CR428430 CR428430
41	13.4	67.0	79	1	AA140294	AA140294 mr83c12.r
42	13.4	67.0	82	10	CG574583	CG574583 OST707590
43	13.2	66.0	50	1	AU107883	AU107883 AU107883
44	13.2	66.0	58	10	CL423647	CL423647 0150726-0
45	13.2	66.0	59	11	CR003993	CR003993 Reverse s

ALIGNMENTS

RESULT 1
CB046782
LOCUS
DEFINITION
NISC_gf06g08.x1 NCI CGAP Kid12 Homo sapiens CDNA clone
IMAGE:3253047.3, mRNA sequence.

ACCESSION
CB046782.1 GI:27785069

VERSION
EST.

KEYWORDS
Homo sapiens (human)

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.

REFERENCE
1 (bases 1 to 89)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

AUTHORS
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL
Unpublished (1997)

COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

CDNA Library Preparation:
CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LNL

DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:

info@image.lnl.gov
Plate: LLMW7960 row: M column: 16
Seq primer: -21M13 forward primer (ABI).

Location/Qualifiers
1..89

FEATURES
source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3253047"
/tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DH10B"
/clone_lib="NCI CGAP Kid12"
/note="Organ: kidney; Vector: p773D-Pac (Pharmacia) with
a modified polylinker; Site:1: Not I; Site:2: Eco RI;
Plasmid DNA from the normalized library NCI CGAP Kids was
prepared, and 96 circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library

ORIGIN (cloneIds 132912-1325831, 1471368-1472903 and 1492104-1493255). Subtraction by Bento Soares and M. Fatima Bernaldo.

Query Match 76.0%; Score 15.2; DB 6; Length 89;
Best Local Similarity 85.0%; Pred. No. 7.5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TTTTTCAGGGAATCCGGGG 20
|||||
Db 27 TTTTTCAGGGAATCCGGGG 46

RESULT 2
AJ665651/c 71 bp mRNA linear EST 28-JUN-2004
LOCUS AJ665651 CSEORAN09 Sus scrofa CDNA clone C0000031_P13, mRNA
DEFINITION sequence.
AJ665651
VERSION AJ665651.1 GI:49350102
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.

REFERENCE 1 (bases 1 to 71)
AUTHORS Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
TITLES Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle
JOURNAL Unpublished (2004)
COMMENT Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -mnscore 20
and -mismatch 12 options. Vector:pluScriptIT(KS+) R. Site 1:
EcoRI R. Site 2: NotI Description: Normalised library constructed
from pooled tissue from day 30 placentas. Clones available from UK
Centre for Functional Genomics in Farm Animals, Roslin Institute,
Roslin, Midlothian, UK, EH25 9PS, www.argenomics.org.

FEATURES
source 1..71
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0000031_P13"
/tissue_type="Placenta"
/note="Vector: pluScriptIT(KS+); Site 1: EcoRI; Site 2:
NotI; Single pass sequencing. Normalised library
constructed from pooled tissue from day 30 placentas."

ORIGIN

Query Match 74.0%; Score 14.8; DB 1; Length 71;
Best Local Similarity 88.9%; Pred. No. 1.2e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TTTTTCAGGGAATCCGGGG 18
|||||
Db 71 TTTTTCAGGGAATCCGGGG 54

RESULT 3
AI925202 79 bp mRNA linear EST 07-MAR-2000
LOCUS AI925202
DEFINITION wmg99H04.X1 NCI CGAP Ut2 Homo sapiens CDNA clone IMAGE:2444119 3'
similar to SW:BAT2_HUMAN P48634 LARGE PROLINE-RICH PROTEIN BAT2 ;,
mRNA sequence.
AI925202
ACCESSION AI925202.1 GI:5661166
VERSION

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE 1 (bases 1 to 79)
AUTHORS NCI-CGAP
TITLES NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)

JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/BLNI at:
www.bio.lnl.gov/bbrp/image/image.html

FEATURES
source 1..79
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:244419"
/tissue_type="moderately-differentiated endometrial
adenocarcinoma, 3 pooled tumors"
/adb_nost="DH10B"
/clone_lib="NCI-CGAP_Ut2"
/note="Organ: uterus; Vector: PCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.85 kb. Life Technologies catalog #: 11539-012"

ORIGIN

Query Match 74.0%; Score 14.8; DB 1; Length 79;
Best Local Similarity 88.9%; Pred. No. 1.2e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TTTTCAGGGAATCCGGGG 20
|||||
Db 10 TTTTCAGGGAATCCGGGG 27

RESULT 4
F26680 96 bp mRNA linear EST 13-MAY-1999
LOCUS HSPD14248 HM3 Homo sapiens CDNA clone s400058G04, mRNA sequence.
DEFINITION F26680
VERSION F26680.1 GI:4812306
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE 1 (bases 1 to 96)
AUTHORS Lanfranchi,G., Muraro,T., Caldara,F., Pacchioni,B., Pallavicini,A.,
Pandolfo,D., Toppo,S., Trevisan,S., Scarso,S. and Valle,G.
TITLES Identification of 4370 expressed sequence tags from a
3'-end-specific cDNA library of human skeletal muscle by DNA
sequencing and filter hybridization
JOURNAL Genome Res. 6 (1), 35-42 (1996)
PUBMED 8681137
COMMENT Contact: Valle G.
CIRIB Biotechnology Centre

University of Padua
Via Trieste 75, 35121 Padua, Italy
ABI Chromatograms and other information are available on WWW at
<http://grip.bio.unipd.it>.

FEATURES

source

1..96
/organism="Homo sapiens"
/mol_type="rRNA"
/db_xref="taxon:9606"
/clone="s400058G04"
/sex="female"
/cisse_type="pectoral muscle (after mastectomy)"
/clone_lib="HM3"
/note="Vector: pCDNA1 (Invitrogen); Site 1: BstXI;
Site 2: NotI; The library is not subcloned nor normalized.
Lanfranchi. This library is not subcloned nor normalized.
The first strand cDNA was primed with a biotinylated
oligo-dT-NotI primer
(5'-biotin-AACCGGCTCGAGCGCGCTTTTCTTTTCTTTT-3'). The
ds cDNA was sonicated and size-selected in the range
350-550 bp. The 3' specific fragments were selected by
streptavidin coated magnetic beads, ligated to
non-palindromic BstXI adapters, NotI digested and
directionally cloned into BstXI-NotI cut pCDNA1 vector."

ORIGIN

Query Match 74.0%; Score 14.8; DB 8; Length 96;
Best Local Similarity 88.9%; Pred. No. 1.2e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTTTCAGGGAATCCGGCG 19
Db 79 TTTTCAGGGAATCCGGCG 96

RESULT 5
LOCUS CR010521 51 bp DNA linear GSS 05-UTL-2004

DEFINITION Reverse strand read from insert in 5'HPRT insertion targeting and
chromosome engineering clone MHPN125K14, genomic survey sequence.

ACCESSION CR010521

VERSION CR010521.1 GI:49743512

KEYWORDS GSS; genome survey sequence; MICR.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 51)
Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
Jonkers,J., Smith,J., Plum,R.W., Taylor,R.G., Nienhijma,I., Yu,Y.,
Rogers,J. and Bradley,A.

TITLE

Direct Submission

JOURNAL
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. <http://www.sanger.ac.uk/MICR>

FEATURES

source

1..51
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPN125K14"
/clone_lib="MHPN"

ORIGIN

Query Match 71.0%; Score 14.2; DB 11; Length 51;
Best Local Similarity 84.2%; Pred. No. 2.3e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TTTTCAGGGAATCCGGCG 19
Db 20 TTTTCAGGGAATCCGGCG 2

RESULT 6
LOCUS CG646119

DEFINITION CG646119 61 bp mRNA linear GSS 02-OCT-2003
OSTJ91595 Mus musculus 129Sv/Ev Mus musculus cDNA clone OSTJ91595,
mRNA sequence.

ACCESSION CG646119

VERSION CG646119.1 GI:37469968

KEYWORDS GSS

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 61)
Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
Piggott,J., Beltranderio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
Fridde,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaijing,C.,
Key,B.W., Jr., Kipp,P., Konhauff,B., Ma,Z.-Q., Markesich,D.,
Payne,R., Porter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
Zhu,Q., Pearson,C. and Sands,A.T.

AUTHORS

TITLE
Mx1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)

COMMENT
Contact: Zambrowicz BP
Omnibank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;352(6676):608-11)
Class: Gene trap.

FEATURES

source

1..61
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/db_xref="taxon:10090"
/clone="OSTJ91595"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"

LOCATION/Qualifiers

ORIGIN

Query Match 71.0%; Score 14.2; DB 10; Length 61;
Best Local Similarity 80.0%; Pred. No. 2.4e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TTTTCAGGGAATCCGGCG 20
Db 1 TTTTCAGGGAATCCGGCG 20

RESULT 7

LOCUS CG553405 77 bp mRNA linear GSS 01-OCT-2003
OSTJ165917 Mus musculus 129Sv/Ev Mus musculus cDNA clone OSTJ165917,
mRNA sequence.

ACCESSION CG553405

VERSION CG553405.1 GI:37339992

KEYWORDS GSS

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 77)
Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
Piggott,J., Beltranderio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
Fridde,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaijing,C.,
Key,B.W., Jr., Kipp,P., Konhauff,B., Ma,Z.-Q., Markesich,D.,
Payne,R., Porter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,

TITLE	Zhu, Q., Person, C. and Sands, A.T.
JOURNAL	Mnk1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention
PUBMED	Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
COMMENT	14610273
	Contact: Zambrowicz BP

Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: material@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):1608-11)
Class: Gene Trap.

FEATURES	SOURCE
location/Qualifiers	1..77
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/strain="129Sv/Ev"	
/db_xref="taxon:10090"	
/clone="OS165917"	
/cell_type="embryonic stem cell"	
/clone_lib="Mus musculus 129Sv/Ev"	
ORIGIN	

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Best Local Similarity	80.0%	Pred. No. 2.4e+04		
Matches	16	Conservative	0	Mismatches 4
				Indels 0
				Gaps 0
Oy	1	TTTTTCAGGGAATCCGGGGG	20	
Db	49	TGTTTCAGGGAATCCTGGGG	30	

RESULT 8	
CG653617	
LOCUS	87 bp mRNA linear GSS 02-OCT-2003
DEFINITION	OST419275 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST419275, mRNA sequence.

ACCESSION VERSION KEYWORDS SOURCE	ORGANISM
CG653617 CG653617.1	GSS.
GI:37477466	Mus musculus (house mouse)
	Mus musculus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciuognathii; Muroidae; Muridae; Murinae; Mus. 1 (bases 1 to 87)
REFERENCE	

REFERENCE	AUTHORS	TITLE	JOURNAL	PUBLISHED	COMMENT
1 (bases 1 to 87)	Zambrowicz, B. P., Abuhin, A., Ramirez-Solis, R., Richier, L. J., Piggett, J., Beltrande-Rio, H., Buxton, E. C., Edwards, J., Finch, R. A., Fridde, C. J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Ising, C., Key, B. W., Jr., Kipp, P., Kohlauf, B., Ma, Z.-Q., Matresich, D., Payne, R., Porter, D. G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z., Sparks, M. J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, Q., Pearson, C., and Sands, A. T.	Mn11 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention	Proc. Natl. Acad. Sci. U.S.A.	100 (24), 14109-14114 (2003)	14610273
	Contact: Zambrowicz BP				

OmniBank
 Lexicon Genetics Incorporated
 4000 Research Forest Drive, The Woodlands, TX 77381, USA
 Email: material@lexgen.com
 Gene trap sequence tag generated by 3' RCE from mouse ES cells as described in Zambrowicz et al (Nature, 1998 Apr 9;392(6676):608-11)
 Class: Gene trap.
 Location/Qualifiers
 1..87

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/strain="129Sv/Ev"  
/db_xref="taxon:10090"  
/clone="OST419275"
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Query Match	71.0%	Score 14.2	DB 10	Length 87
Best Local Similarity	84.2%	Pred. No. 2.5e+04		
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ORIGIN	/cell_type="embryonic stem cell" /clone_lib="Mus musculus 129Sv/Ev"			

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QY      1 TTTTTCAGCGAATCCGGCG 19
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Db      23 TTTTTCGCGAATCCGGAG 41

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RESULT	9
CG581950	
LOCUS	
DEFINITION	CG581950 88 bp mRNA linear GSS 02-OCT-2003 OST2227704 Mus musculus 129Sv/Ev Mus musculus CDNA clone OST222704,
	mRNA sequence.
ACCESSION	CG581950
VERSION	CG581950.1 GI:37379122
KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus

REFERENCE
AUTHORS

1 (bases 1 to 88)
Zambrowicz, B. P., Aubin, A., Ramirez-Solis, R., Richter, L. J.,

TITLE
 Journal
 PubMed
 Comment
 Contact:

What kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention
 Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
 14610273
 Zambronicz BP

```

FEATURES
source      1. .88
            Location/Qualifiers
            OmniBank
            Lexicon Genetics Incorporated
            4000 Research Forest Drive, The Woodlands, TX 77381, USA
            Email: materials@lexgen.com
            Gene trap sequence tag generated by 3' RACE from mouse BS cells as
            described in Zambrowicz et al (Nature. 1998 Apr 9;352(6676):608-11)
            Class: Gene trap.

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/organism="Mus musculus"
/mol_type="mRNA"
/strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST222704"
/cell_type="embryonic stem cell"
/clone_id="Mus musculus 129Sv/Ev"

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[illegible]

RESULT	10
CX287425	
LOCUS	
DEFINITION	CX287425 96 bp mRNA linear EST 06-MAY-2005 C01009D07SK Veg1 Citrus clementina CDNA clone C01009D07, mRNA sequence.
ACCESSION	CX287425
VERSION	CX287425.1 GI:63056124

KEYWORDS
SOURCE EST.
ORGANISM Citrus clementina

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eucosids II; Sapindales; Rutaceae; Citrus.
 1 (bases 1 to 96)
 Forment, J., Gadea, J., Huerta, L., Abizanda, L., Agustí, J., Alamar, S., Aloe, E., Andres, F., Arribas, R., Beltrán, J.P., Berbel, A., Blazquez, M.A., Brumos, J., Canas, L.A., Cercos, M., Colmenero-Flores, J.M., Conesa, A., Establos, B., Gandia, M., Garcia-Martinez, J.L., Gimeno, J., Gisbert, A., Gomez, G., Gonzalez-Candelas, L., Granell, A., Guerri, J., Lafuente, M.T., Madueno, F., Marcos, J.F., Marques, M.C., Martinez, F., Martinez-Godoy, M.A., Miralles, S., Moreno, P., Navarro, L., Pallas, V., Perez-Amador, M.A., Perez-Valle, J., Pons, C., Rodrigo, I., Rodriguez, P.L., Royo, C., Serrano, R., Soler, G., Tadeo, F., Talon, M., Terol, J., Trenor, M., Vaello, L., Vicente, O., Vidal, Ch., Zacarias, L. and Conejero, V.

TITLE
 Development of a citrus genome-wide EST collection and cDNA microarray as resources for genomic studies

JOURNAL
 Plant Mol. Biol. 57 (3), 375-391 (2005)

COMMENT
 Contact: Forment J
 Genomics Laboratory
 Instituto de Biologia Molecular y Celular de Plantas (Universidad Politecnica de Valencia - Consejo Superior de Investigaciones Cientificas)
 Avenida de los Naranjos s/n, 46022 Valencia, Spain
 Email: jforment@bmcp.upv.es.

FEATURES
 source
 1..96
 /organism="Citrus clementina"
 /mol_type="mRNA"
 /cultivar="Clemenules"
 /db_xref="taxon:85681"
 /clone="C0109007"
 /sex="hermaphrodite"
 /dev_stage="adult trees"
 /lab_host="Escherichia coli"
 /note="Organ: leaves, shoots and internodes; Vector: lambda-zap II; cDNA library made from a mixture of equal amounts of poly-A+ RNA from vegetative developing shoots of plants treated with G43 or with paclobutrazol, and leaves and internodes of untreated plants"

ORIGIN
 Query Match 70.0%; Score 14; DB 8; Length 96;
 Beet Local Similarity 100.0%; Pred. No. 3.2e+04;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
 2 TTTTCAGGGAATCC 15
 |||||
 14 TTTTCAGGGAATCC 27

Db
 14 TTTTCAGGGAATCC 27

RESULT 11
 A1756242 49 bp mRNA linear EST 18-JAN-2000
 LOCUS E185441.1.v1 Eimeria S5-2 Sporozoite stage Eimeria tenella cDNA
 DEFINITION 5' similar to SM-U2AG_HUMAN Q01081 SPLICING FACTOR U2AF 35 KD
 SUBUNIT ; mRNA sequence.
 A1756242
 A1756242 GI:5149965

ACCESSION
 A1756242
 A1756242 GI:5149965

VERSION
 A1756242.1 GI:5149965

KEYWORDS
 EST.

SOURCE
 Eimeria tenella

ORGANISM
 Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae; Eimeria.

REFERENCE
 1 (bases 1 to 49)
 Liberators, P., Diaz, C., Tang, K., Marra, M., Hillier, L., Kucaba, T., Martin, J., Wylie, T., Underwood, K., Stepec, M., Theising, B.,

TITLE
 Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurr, R., Ritter, E., Kohn, S., Florence, N., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterson, R., Wilson, R. and Sibley, D.

JOURNAL
 Unpublished (1999)

COMMENT
 Contact: David Sibley, Ph.D.
 WashU-Merck Eimeria tenella project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu
 Contact David Sibley (toxoest@orbcom.wustl.edu) for further information relating to organism, libraries, or clone availability.
 Possible reversed clone: similarity on wrong strand
 Seq primer: -40RP from GlbD
 High quality sequence stop: 1.

FEATURES
 source
 1..49
 /organism="Eimeria tenella"
 /mol_type="mRNA"
 /strain="LS18"
 /db_xref="taxon:5802"
 /dev_stage="Sporozoite"
 /lab_host="SOIR E. coli"
 /clone_lib="Eimeria S5-2 Sporozoite stage"
 /note="Vector: Bluescript SK-; Site 1: EcoRI; Site 2: XhoI; Sporozoites were obtained from in vitro sporulated and excysted oocysts of E. tenella grown in chickens. cDNA was synthesized from poly mRNA using an oligo-dt primer containing a XhoI site. Following second strand synthesis, EcoRI adapters were ligated to the cDNA and products were size selected on Sephacryl S500. cDNAs were digested with EcoRI/XhoI and cloned into lambda ZAP II (Stratagene). Clones were converted to phagemids by mass excision using Exaseist helper phage and SOLR cells (Stratagene). Insert sizes range from 1.2-2.9 kb."

ORIGIN
 Query Match 69.0%; Score 13.8; DB 1; Length 49;
 Beet Local Similarity 88.2%; Pred. No. 3.8e+04;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY
 3 TTTTCAGGGAATCCGCG 19
 |||||
 15 TTTTCAGGGAATCCGCG 31

Db
 15 TTTTCAGGGAATCCGCG 31

RESULT 12
 CR235685 53 bp DNA linear GSS 06-JUN-2004
 LOCUS CR235685/c
 DEFINITION Reverse strand read from insert in 5'HPT insertion targeting and chromosome engineering clone MHPN203d10, genomic survey sequence.
 CR235685
 CR235685 GI:50014534

ACCESSION
 CR235685.1 GI:50014534

KEYWORDS
 GSS; genome survey sequence; MICR.

SOURCE
 Mus musculus
 Mus musculus (house mouse)

ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.

REFERENCE
 1 (bases 1 to 53)
 Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Rogers, J. and Bradley, A.

TITLE
 Direct Submission

JOURNAL
 Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. http://www.sanger.ac.uk/MICR

FEATURES
 source
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 /organism="Mus musculus"
 /mol_type="genomic DNA"

ORIGIN

Query Match 69.0%; Score 13.8; DB 11; Length 53;
Best Local Similarity 88.2%; Pred. No. 3.8e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TTTCAGGGAATCCGGCG 19
|||||
DB 18 TTTCGGGGAATCCGGCG 2

RESULT 13
CZ169440 55 bp mRNA linear GSS 22-MAR-2005
LOCUS P020C06.GGTC Gene Trap Library GV08C05 Mus musculus cDNA clone
DEFINITION P020C06, mRNA sequence.
ACCESSION CZ169440
VERSION CZ169440.2 GI:61684171
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 55)
Hansen, J., Floss, T., van Sloun, P., Fuchtbauer, E.M., Vauti, F.,
Arnold, H.H., Schmutgen, F., Wurtel, W., Von Melchner, H. and Ruiz, P.
A large-scale, gene-driven mutagenesis approach for the functional
analysis of the mouse genome
Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)
12904583
JOURNAL PUBMED
On Mar 22, 2005 this sequence version replaced gi:58224038.
COMMENT Contact: GGTC
German Genetrap Consortium (GGTC)
Email: info@genetrap.de
FliPROSbetageo gene trap. Sequence tag generated by 5'RACE.
Additional sequence information can be found at:
'http://genetrap.gsf.de/project/web_new/database/result_clone.html?clone_id=P020C06'. ES cell line harboring insertion mutation of
target gene is available at:
'http://genetrap.gsf.de/project/web_new/order_clones/howtoorder.htm'
1' Inhouse Sequence Identifier: 20257
Class: Gene Trap.

FEATURES
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 Sv"
/db_xref="taxon:10090"
/clone="P020C06"
/sex="Male"
/cell_type="Embryonic stem cell"
/cell_line="ES cells [C57BL/6J x 129Sv/SvEvTac] Fl"
/clone_lib="GGTC Gene Trap Library GV08C05"
/note="Vector: FliPROSbetageo"

ORIGIN

Query Match 69.0%; Score 13.8; DB 10; Length 55;
Best Local Similarity 88.2%; Pred. No. 3.8e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TTTCAGGGAATCCGGCG 20
|||||
DB 22 TTTCAGTGAATCCGGCG 38

RESULT 14
H41671 64 bp mRNA linear EST 31-JUL-1995
LOCUS H41671
DEFINITION Y006F01.s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone

IMAGE:177145 3' similar to SP:RS9_RAT P29314 40S RIBOSOMAL PROTEIN
; mRNA sequence.
H41671
VERSION H41671.1 GI:9177723
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 64)
Hillier, L., Clark, N., Dubague, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Maira, M.,
Parsons, J., Rifkin, L., Rohlffing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterson, R., Williamson, A., Wohldmann, P. and
Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
CONTACT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1652
Insert length: 1652 Std Error: 0.00
Seg primer: Promega -21m13
High quality sequence stop: 1.
High quality sequence stop: 1.
Location/Qualifiers
1..64
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/mol_type="mRNA"
/db_xref="GDB:3839341"
/db_xref="taxon:9606"
/clone="IMAGE:177145"
/sex="Male"
/dev_stage="55-Year old"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares adult brain N2b5HB55Y"
/note="Organ: Brain; Vector: pT7T3D (pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer (5'
TGTTCACATCTGAGTGGAGCGCGCGCTTTTCTTTTCTTTT 3'),
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 53. Library constructed by Bento
Soares and M.Fatima Bonaldo. The adult brain RNA was
provided by Dr. Donald H. Gilden. Tissue was acquired
17-18 hours after death which occurred in consequence of a
ruptured aortic aneurysm. RNA was prepared from a pool of
tissues representing the following areas of the brain:
frontal, parietal, temporal and occipital cortex from the
left and right hemispheres, subcortical white matter,
basal ganglia, thalamus, cerebellum, midbrain, pons and
medulla."

ORIGIN

Query Match 69.0%; Score 13.8; DB 8; Length 64;
Best Local Similarity 88.2%; Pred. No. 3.9e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TTTCAGGGAATCCGGCG 20
|||||
DB 6 TTTCGGGAATCCAGGGG 22

RESULT 15

B2353185/c

LOCUS SALK_119899.28.80.x Arabidopsis thaliana TDNA insertion lines
 DEFINITION Arabidopsis thaliana genomic clone SALK_119899.28.80.x, genomic
 survey sequence.

ACCESSION B2353185
 B2353185.1 GI:24944047

VERSION GSS.
 KEYWORDS Arabidopsis thaliana (thale cress)

SOURCE Arabidopsis thaliana

ORGANISM

REFERENCE 1 (bases 1 to 66)
 Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
 Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
 Shin, P., Zimmerman, J., and Ecker, J.R.
 A Sequence-indexed Library of Insertion Mutations in the
 Arabidopsis Genome
 Unpublished (2001)

TITLE Arabidopsis Genome
 JOURNAL Unpublished (2001)
 COMMENT Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu

This is single pass sequence recovered from the left border of
 TDNA. This sequence lies within an annotated exon of At2g28150.
 Class: TDNA tagged.

FEATURES

source

Location/Qualifiers

1..66

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone="SALK_119899.28.80.x"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 69.0%; Score 13.8; DB 9; Length 66;

Best Local Similarity 88.2%; Pred.No. 3.9e+04;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TTTTTCAGGCAATCCCG 17

Db 38 TTTTTCAGGCAATCCAG 22

Search completed: December 24, 2005, 18:28:29
 Job time : 1582 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 11:34:25 ; Search time 48.1 Seconds
(without alignments)
739.111 Million cell updates/sec

Title: US-09-296-264-5

Perfect score: 20

Sequence: 1 ttttcagggaatccggg 20

Scoring table: IDENTITY_NUC

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1134872

Minimum DB seq length: 20
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
1: /cgn2_6/ptodata/1/ina/1/COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5/COMB.seq:*
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8: /cgn2_6/ptodata/1/ina/RE/COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.8	74.0	25	3	US-09-396-196G-54618
2	13.6	68.0	25	3	US-09-396-196G-86875
3	13.6	68.0	73	3	US-09-270-767-25527
4	13.4	67.0	21	2	US-08-741-881-9
5	13.4	67.0	21	2	US-08-739-158-9
6	13.4	67.0	21	2	US-08-739-158-10
7	13.4	67.0	21	2	US-08-739-158-9
8	13.4	67.0	21	2	US-08-739-158-10
9	13.4	67.0	21	2	US-08-739-158-9
10	13.4	67.0	21	2	US-08-404-796-9
11	13.4	67.0	21	3	US-08-404-796-10
12	13.4	67.0	21	3	US-08-931-869-9
13	13.4	67.0	21	3	US-08-931-869-10
14	13.4	67.0	21	3	US-09-350-399-9
15	13.4	67.0	21	3	US-09-350-399-10
16	13.4	67.0	21	3	US-09-236-140A-9
17	13.4	67.0	21	3	US-09-236-140A-10
18	13.4	67.0	21	3	US-09-415-784-17
19	13.4	67.0	21	3	US-09-415-784-18
20	13.4	67.0	21	3	US-09-415-785A-17
21	13.4	67.0	21	3	US-09-415-785A-18
22	13.4	67.0	21	3	US-08-944-465-17
23	13.4	67.0	21	3	US-08-944-465-18
24	13.4	67.0	21	3	US-09-415-868-17

c	25	13.4	67.0	21	3	US-09-415-868-18	Sequence 18, Appl
c	26	13.4	67.0	21	3	US-09-415-900-17	Sequence 17, Appl
c	27	13.4	67.0	21	3	US-09-415-900-18	Sequence 18, Appl
c	28	13.4	67.0	21	3	US-09-507-362-17	Sequence 17, Appl
c	29	13.4	67.0	21	3	US-09-507-362-18	Sequence 18, Appl
c	30	13.2	66.0	25	3	US-09-396-196G-49693	Sequence 49693, A
c	31	13.2	66.0	36	2	US-08-486-969-47	Sequence 47, Appl
c	32	13.2	66.0	36	3	US-09-403-752A-14	Sequence 14, Appl
c	33	13.2	66.0	36	3	US-09-622-951-21	Sequence 21, Appl
c	34	13.2	66.0	36	3	US-09-551-151A-14	Sequence 14, Appl
c	35	13.2	66.0	50	3	US-10-131-827-7280	Sequence 7280, Ap
c	36	13	65.0	25	3	US-09-396-196G-54629	Sequence 54629, A
c	37	13	65.0	47	3	US-09-422-978-3512	Sequence 3512, Ap
c	38	12.8	64.0	22	3	US-09-462-606-47	Sequence 47, Appl
c	39	12.8	64.0	25	3	US-09-661-596A-70	Sequence 70, Appl
c	40	12.8	64.0	25	3	US-09-396-196G-48432	Sequence 48432, A
c	41	12.8	64.0	25	3	US-10-288-823-70	Sequence 70, Appl
c	42	12.8	64.0	50	3	US-10-131-827-1528	Sequence 1528, Ap
c	43	12.8	64.0	81	3	US-09-270-767-2645	Sequence 2645, Ap
c	44	12.8	64.0	81	3	US-09-270-767-17927	Sequence 17927, A
c	45	12.6	63.0	23	3	US-09-303-040-40	Sequence 40, Appl

ALIGNMENTS

RESULT 1
US-09-396-196G-54618/c
Sequence 54618, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 54618
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-09-396-196G-54618
Query Match 74.0%; Score 14.8; DB 3; Length 25;
Best Local Similarity 88.9%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 18 TTTTCAGGGAATCCGGG 18
18 TTTTCAGGGAATCCGGG 1
RESULT 2
US-09-396-196G-86875
Sequence 86875, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17

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; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 86875
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-86875

Query Match
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Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TTTTCAGGGAATCCGGGG 20
DB 1 TTTTCAGGGAATCCATGG 20

RESULT 3
US-09-270-767-25527/c
; Sequence 25527, Application US/09270767
; Patent No. 5703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO: 25527
; LENGTH: 73
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-25527

Query Match
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Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TTTTCAGGGAATCCGGGG 20
DB 39 TGTTCAGGGAATCCGGTG 20

RESULT 4
US-08-741-881-9
; Sequence 9, Application US/08741881
; Patent No. 5789245
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/741,881
; FILING DATE: 30-OCT-1996
```

```

; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C6 / 1146.007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-741-881-9

Query Match
Best Local Similarity 67.0%; Score 13.4; DB 2; Length 21;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTTTCAGGGAATCCG 16
DB 3 TTTTCAGGGAATCCG 17

RESULT 5
US-08-741-881-10/c
; Sequence 10, Application US/08741881
; Patent No. 5789245
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/741,881
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C6 / 1146.007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-741-881-10

Query Match
Best Local Similarity 67.0%; Score 13.4; DB 2; Length 21;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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OY 2 TTTTCAGGGAATCCG 16
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Db 19 TTTTCAGGGAATCCG 5

RESULT 6

US-08-739-158-9
Sequence 9, Application US/08739158
Patent No. 5814482
GENERAL INFORMATION:
APPLICANT: Dubensky Jr, Thomas W
APPLICANT: Polo, John M.
APPLICANT: Jolly, Douglas J.
APPLICANT: Driver, David A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/739,158
FILING DATE: 30-OCT-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: McMaisters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423D3 / 1146.012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-739-158-9

Query Match

Best Local Similarity 67.0%; Score 13.4; DB 2; Length 21;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 TTTTCAGGGAATCCG 16
| | | | | | | | | |
Db 3 TTTTCAGGGAATCCG 17

RESULT 7

US-08-739-158-10/c
Sequence 10, Application US/08739158
Patent No. 5814482
GENERAL INFORMATION:
APPLICANT: Dubensky Jr, Thomas W
APPLICANT: Polo, John M.
APPLICANT: Jolly, Douglas J.
APPLICANT: Driver, David A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington

COUNTRY: US

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/739,158

FILING DATE: 30-OCT-1996

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: McMaisters, David D.

REGISTRATION NUMBER: 33,963

REFERENCE/DOCKET NUMBER: 930049.423D3 / 1146.012

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-739-158-10

OY 2 TTTTCAGGGAATCCG 16
| | | | | | | | | |
Db 19 TTTTCAGGGAATCCG 5

Query Match

Best Local Similarity 67.0%; Score 13.4; DB 2; Length 21;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 8

US-08-739-167-9
Sequence 9, Application US/08739167
Patent No. 5843723
GENERAL INFORMATION:
APPLICANT: Dubensky Jr, Thomas W
APPLICANT: Polo, John M.
APPLICANT: Ibanez, Carlos E.
APPLICANT: Chang, Stephen M.W.
APPLICANT: Jolly, Douglas J.
APPLICANT: Driver, David A.
APPLICANT: Belli, Barbara A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS AND ALPHAVIRUS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/739,167
FILING DATE: 30-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McMaisters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423C7 / 1146.008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-739-167-9

Query Match 67.0%; Score 13.4; DB 2; Length 21;
Best Local Similarity 93.3%; Pred. No. 2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTTTCAGGGGATCCG 16
|||||
Db 3 TTTTCAGGGGATCCG 17

RESULT 9
US-08-739-167-10/c
Sequence 10, Application US/08739167
Patent No. 5843723

GENERAL INFORMATION:
APPLICANT: Dubensky Jr, Thomas W
APPLICANT: Polo, John M.
APPLICANT: Ibanez, Carlos E.
APPLICANT: Chang, Stephen M.W.
APPLICANT: Jolly, Douglas J.
APPLICANT: Driver, David A.
APPLICANT: Belli, Barbara A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS AND ALPHAVIRUS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESS: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/739,167
FILING DATE: 30-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McMaesters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423C7 / 1146.008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-739-167-10

Query Match 67.0%; Score 13.4; DB 2; Length 21;
Best Local Similarity 93.3%; Pred. No. 2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTTTCAGGGGATCCG 16
|||||
Db 19 TTTTCAGGGGATCCG 5

RESULT 10
US-08-404-796-9
Sequence 9, Application US/08404796

Patent No. 6015686

GENERAL INFORMATION:
APPLICANT: Dubensky Jr, Thomas W
APPLICANT: Polo, John M.
APPLICANT: Ibanez, Carlos E.
APPLICANT: Chang, Stephen M.W.
APPLICANT: Jolly, Douglas J.
APPLICANT: Driver, David A.
APPLICANT: Belli, Barbara A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESS: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/404,796
FILING DATE: 15-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McMaesters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-404-796-9

Query Match 67.0%; Score 13.4; DB 3; Length 21;
Best Local Similarity 93.3%; Pred. No. 2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTTTCAGGGGATCCG 16
|||||
Db 3 TTTTCAGGGGATCCG 17

RESULT 11
US-08-404-796-10/c
Sequence 10, Application US/08404796
Patent No. 6015686
GENERAL INFORMATION:
APPLICANT: Dubensky Jr, Thomas W
APPLICANT: Polo, John M.
APPLICANT: Ibanez, Carlos E.
APPLICANT: Chang, Stephen M.W.
APPLICANT: Jolly, Douglas J.
APPLICANT: Driver, David A.
APPLICANT: Belli, Barbara A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESS: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/404,796
FILING DATE: 15-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-404-796-10

Query Match
Best Local Similarity 93.3%; Score 13.4; DB 3; Length 21;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTTTCAGGGAATCCG 16
Db 19 TTTTCAGGGAATCCG 5

RESULT 12
US-08-931-869-9
Sequence 9, Application US/08931869
Patent No. 6015694
GENERAL INFORMATION:
APPLICANT: Dubensky Jr, Thomas W
APPLICANT: Polo, John M.
APPLICANT: Ibanez, Carlos E.
APPLICANT: Chang, Stephen M.W.
APPLICANT: Jolly, Douglas J.
APPLICANT: Driver, David A.
APPLICANT: Belli, Barbara A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,869
FILING DATE: 16-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/404,796
FILING DATE: 15-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-931-869-9

Query Match
Best Local Similarity 93.3%; Score 13.4; DB 3; Length 21;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTTTCAGGGAATCCG 16
Db 3 TTTTCAGGGAATCCG 17

RESULT 13
US-08-931-869-10/c
Sequence 10, Application US/08931869
Patent No. 6015694
GENERAL INFORMATION:
APPLICANT: Dubensky Jr, Thomas W
APPLICANT: Polo, John M.
APPLICANT: Ibanez, Carlos E.
APPLICANT: Chang, Stephen M.W.
APPLICANT: Jolly, Douglas J.
APPLICANT: Driver, David A.
APPLICANT: Belli, Barbara A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,869
FILING DATE: 16-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/404,796
FILING DATE: 15-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-931-869-10

Query Match
Best Local Similarity 93.3%; Score 13.4; DB 3; Length 21;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TTTTCAGGGAATCCG 16
Db 19 TTTTCAGGGAATCCG 5

RESULT 14
US-09-350-399-9
Sequence 9, Application US/09350399
Patent No. 6342372
GENERAL INFORMATION:
APPLICANT: Dubensky Jr, Thomas W
Jolly, Douglas J.
Driver, David A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/350,399
FILING DATE: 08-Jul-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-350-399-9
Query Match 67.0%; Score 13.4; DB 3; Length 21;
Best Local Similarity 93.3%; Pred. No. 2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 TTTTCAGGGGATCCG 16
Db 3 TTTTCAGGGGATCCG 17
RESULT 15
US-09-350-399-10/c
Sequence 10, Application US/09350399
Patent No. 6342372
GENERAL INFORMATION:
APPLICANT: Dubensky Jr, Thomas W
Jolly, Douglas J.
Driver, David A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/350,399
FILING DATE: 08-Jul-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-350-399-10
Query Match 67.0%; Score 13.4; DB 3; Length 21;
Best Local Similarity 93.3%; Pred. No. 2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 TTTTCAGGGGATCCG 16
Db 19 TTTTCAGGGGATCCG 5

Search completed: December 24, 2005, 18:36:28
Job time : 49.1 secs

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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 14:06:30 ; Search time 337.6 Seconds
(without alignments)
489.892 Million cell updates/sec

Title: US-09-296-264-5

Perfect score: 20
Sequence: 1 ttttcagggaatccggggg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 9887334

Minimum DB seq length: 20
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA Main:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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3	15.8	79.0	25	10	US-11-036-317-44538
4	14.8	74.0	25	9	US-10-809-189-54618
5	14.4	72.0	25	10	US-11-036-317-425139
6	14.4	72.0	25	10	US-11-036-317-608322
7	14.2	71.0	25	7	US-10-719-956-341263
8	14.2	71.0	51	6	US-10-321-785-20
9	14.2	71.0	57	3	US-09-995-529-283
10	14.2	71.0	57	3	US-09-995-529-284
11	14.2	71.0	57	3	US-09-995-529-283
12	14.2	71.0	57	3	US-09-995-529-284
13	14	70.0	25	10	US-11-036-317-490296
14	14	70.0	25	10	US-11-036-317-832220
15	14	70.0	57	3	US-09-995-529-285
16	14	70.0	57	3	US-09-995-529-285
17	13.8	69.0	21	9	US-10-512-633-25
18	13.8	69.0	25	8	US-10-719-900-795020
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23	13.8	69.0	80	7	US-10-384-245-339

c 24	13.6	68.0	25	7	US-10-719-956-25043	Sequence 25043, A
c 25	13.6	68.0	25	7	US-10-719-956-321181	Sequence 321181, A
c 26	13.6	68.0	25	7	US-10-719-956-681900	Sequence 681900, A
c 27	13.6	68.0	25	7	US-10-719-956-680268	Sequence 680268, A
c 28	13.6	68.0	25	8	US-10-719-900-259080	Sequence 259080, A
c 29	13.6	68.0	25	8	US-10-719-900-980929	Sequence 980929, A
c 30	13.6	68.0	25	8	US-10-719-900-981979	Sequence 981979, A
c 31	13.6	68.0	25	9	US-10-809-189-68875	Sequence 68875, A
c 32	13.6	68.0	25	10	US-11-036-317-759092	Sequence 759092, A
c 33	13.6	68.0	45	9	US-10-973-783-204	Sequence 204, App
c 34	13.6	68.0	65	3	US-09-908-975-29087	Sequence 29087, A
c 35	13.6	68.0	88	6	US-10-029-386-17390	Sequence 17390, A
c 36	13.4	67.0	21	3	US-09-507-362-17	Sequence 17, Appl
c 37	13.4	67.0	21	3	US-09-507-362-18	Sequence 18, Appl
c 38	13.4	67.0	21	6	US-10-346-880-9	Sequence 9, Appl
c 39	13.4	67.0	21	6	US-10-346-880-10	Sequence 10, Appl
c 40	13.4	67.0	21	6	US-10-391-441-17	Sequence 17, Appl
c 41	13.4	67.0	21	6	US-10-391-441-18	Sequence 18, Appl
c 42	13.4	67.0	21	7	US-10-150-407-9	Sequence 9, Appl
c 43	13.4	67.0	21	7	US-10-150-407-10	Sequence 10, Appl
c 44	13.4	67.0	25	5	US-10-215-112-2573	Sequence 2573, Ap
c 45	13.4	67.0	25	7	US-10-719-956-585686	Sequence 585686, A

ALIGNMENTS

```

RESULT 1
US-09-296-264-5
; Sequence 5, Application US/09296264
; Publication No. US20030083274A1
; GENERAL INFORMATION:
; APPLICANT: WRIGHT, Jim A.
; APPLICANT: YOUNG, Aiping H.
; APPLICANT: LEE, Yoon S.
; TITLE OF INVENTION: NEUROPILIN ANTISENSE OLIGONUCLEOTIDE SEQUENCES AND
; FILE REFERENCE: 023396-043
; CURRENT APPLICATION NUMBER: US/09/296,264
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 60/082,791
; EARLIER FILING DATE: 1998-04-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-09-296-264-5

Query Match      100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 TTTTCAGGGAATCCGGGG 20
Db 1 TTTTCAGGGAATCCGGGG 20

RESULT 2
US-10-956-157-293978
; Sequence 293978, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2

```

SEQ ID NO 293978
LENGTH: 25
TYPE: DNA
ORGANISM: Probe Sequence
US-10-956-157-293978

Query Match 79.0%; Score 15.8; DB 9; Length 25;
Best Local Similarity 89.5%; Pred. No. 5.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTTCAGGGAATCCGGG 19
|||||
DB 7 TTTTTCAGGGAATCCAGG 25

RESULT 3
US-11-036-317-44538/c
Sequence 44538, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 44538
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-44538

Query Match 79.0%; Score 15.8; DB 10; Length 25;
Best Local Similarity 89.5%; Pred. No. 5.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTTCAGGGAATCCGGG 19
|||||
DB 22 TTTTCAGGGAATCCGGT 4

RESULT 4
US-10-809-189-54618/c
Sequence 54618, Application US/10809189
Publication No. US20050048531A1
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/10/809,189
CURRENT FILING DATE: 2004-03-25
PRIOR APPLICATION NUMBER: US/09/396,196
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 54618
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-10-809-189-54618

Query Match 74.0%; Score 14.8; DB 9; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTTCAGGGAATCCGG 18
|||||
DB 18 TTTTCAGGGAATGCGG 1

RESULT 5
US-11-036-317-425139/c
Sequence 425139, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 425139
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-425139

Query Match 72.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%; Pred. No. 2.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTTCAGGGAATCCG 16
|||||
DB 16 TTTTCAGGGAATCCG 1

RESULT 6
US-11-036-317-608322/c
Sequence 608322, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 608322
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-608322

Query Match 72.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%; Pred. No. 2.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTTCAGGGAATCCG 16
|||||
DB 16 TTTTCAGGGAATCCG 1

RESULT 7
US-10-719-956-341263/c
Sequence 341263, Application US/10719956
Publication No. US20040146910A1
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat


```
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 341263
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-341263

Query Match      71.0%; Score 14.2; DB 7; Length 25;
Best Local Similarity 84.2%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 TTTTCAGGGAATCCGGGG 20
        |||||
Db      22 TTTTCAGGGAATCCGGGG 4

RESULT 8
US-10-321-785-20/c
; Sequence 20, Application US/10321785
; Publication No. US20030211964A1
; GENERAL INFORMATION:
; APPLICANT: Bertam J. Jacobs
; APPLICANT: Alexander Rich
; TITLE OF INVENTION: METHOD OF INHIBITING PATHOGENICITY OF
; FILE REFERENCE: 0050 2037-001
; CURRENT APPLICATION NUMBER: US/10/321,785
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US 60/343,028
; PRIOR FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer used to amplify Z-DLM nucleic acid molecule
US-10-321-785-20

Query Match      71.0%; Score 14.2; DB 6; Length 51;
Best Local Similarity 84.2%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 TTTTCAGGGAATCCGGGG 20
        |||||
Db      31 TTTTCAGGGAATCCGGGG 13

RESULT 9
US-09-995-529-283/c
; Sequence 283, Application US/0995529
; Publication No. US20030099655A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 283
; LENGTH: 57
; TYPE: DNA
; OTHER INFORMATION: primer
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
; NAME/KEY: misc_feature
; LOCATION: 38, 39
; OTHER INFORMATION: n = A,T,C or G
US-09-995-529-283

Query Match      71.0%; Score 14.2; DB 3; Length 57;
Best Local Similarity 84.2%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 TTTTCAGGGAATCCGGGG 19
        |||||
Db      33 TTTTCAGGGAATCCGGGG 15

RESULT 10
US-09-995-529-284/c
; Sequence 284, Application US/0995529
; Publication No. US20030099655A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 284
; LENGTH: 57
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
; NAME/KEY: misc_feature
; LOCATION: 35, 36
; OTHER INFORMATION: n = A,T,C or G
US-09-995-529-284

Query Match      71.0%; Score 14.2; DB 3; Length 57;
Best Local Similarity 84.2%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 TTTTCAGGGAATCCGGGG 19
        |||||
Db      33 TTTTCAGGGAATCCGGGG 15

RESULT 11
US-09-995-529-283/c
; Sequence 283, Application US/0995529
; Publication No. US20040091482A9
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 283
; LENGTH: 57
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
```

```

; NAME/KEY: misc feature
; LOCATION: 38, 39
; OTHER INFORMATION: n = A,T,C or G
US-09-995-529-283

```

```

Query Match      71.0%; Score 14.2; DB 3; Length 57;
Best Local Similarity 84.2%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY      1 TTTTCAGGGAATCCGGG 19
Db      33 TCTACAGGGAATCCGGG 15

```

```

RESULT 12
US-09-995-529-284/C
; Sequence 284, Application US/09995529
; Publication No. US20040091482A9
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 284
; LENGTH: 57
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
; NAME/KEY: misc_feature
; LOCATION: 35, 36
; OTHER INFORMATION: n = A,T,C or G
US-09-995-529-284

```

```

Query Match      71.0%; Score 14.2; DB 3; Length 57;
Best Local Similarity 84.2%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY      1 TTTTCAGGGAATCCGGG 19
Db      33 TCTACAGGGAATCCGGG 15

```

```

RESULT 13
US-11-036-317-490296/C
; Sequence 490296, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 490296
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-490296

```

```

Query Match      70.0%; Score 14; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2 TTTTCAGGGAATCC 15
      21 TTTTCAGGGAATCC 8
Db

```

```

RESULT 14
US-11-036-317-832220/C
; Sequence 832220, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Blume, John
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 832220
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-832220

```

```

Query Match      70.0%; Score 14; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      2 TTTTCAGGGAATCC 15
Db      21 TTTTCAGGGAATCC 8

```

```

RESULT 15
US-09-995-529-285/C
; Sequence 285, Application US/09995529
; Publication No. US2003009655A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 285
; LENGTH: 57
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
; NAME/KEY: misc_feature
; LOCATION: 32, 33
; OTHER INFORMATION: n = A,T,C or G
US-09-995-529-285

```

```

Query Match      70.0%; Score 14; DB 3; Length 57;
Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      6 CAGGGAATCCGGG 19
Db      28 CAGGGAATCCGGG 15

```

```

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Job time : 338.6 secs

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Tue Jan 3 11:52:56 2006

us-09-296-264-5.sz20-100.rnpbm

Page 5

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 18:29:07 ; Search time 135.3 seconds
(without alignments)
76.712 Million cell updates/sec

Title: US-09-296-264-5

Perfect score: 20

Sequence: 1 ttcttcagggaatccgsgg959 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4168288 seqs, 259477437 residues

Total number of hits satisfying chosen parameters: 1608458

Minimum DB seq length: 20

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA New:

1: /cgn2_6/ptodata/2/pubphn/US06_NEM_PUB.seq.*
2: /cgn2_6/ptodata/2/pubphn/US06_NEM_PUB.seq.*
3: /cgn2_6/ptodata/2/pubphn/US07_NEM_PUB.seq.*
4: /cgn2_6/ptodata/2/pubphn/US07_NEM_PUB.seq.*
5: /cgn2_6/ptodata/2/pubphn/US09_NEM_PUB.seq.*
6: /cgn2_6/ptodata/2/pubphn/US10_NEM_PUB.seq.*
7: /cgn2_6/ptodata/2/pubphn/US11_NEM_PUB.seq.*
8: /cgn2_6/ptodata/2/pubphn/US11_NEM_PUB.seq.*
9: /cgn2_6/ptodata/2/pubphn/US11_NEM_PUB.seq.*
10: /cgn2_6/ptodata/2/pubphn/US11_NEM_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	13.8	69.0	25	US-11-121-849-240361	Sequence 240361, A
C 2	13.6	68.0	25	US-11-121-849-22867	Sequence 22867, A
C 3	13.2	66.0	25	US-11-121-849-181142	Sequence 181142, A
C 4	13.2	66.0	25	US-11-121-849-338152	Sequence 338152, A
C 5	13.2	66.0	25	US-11-121-849-497393	Sequence 497393, A
C 6	13.2	66.0	25	US-11-121-849-600267	Sequence 600267, A
C 7	13.2	66.0	25	US-11-121-849-600268	Sequence 600268, A
C 8	13.2	66.0	32	US-10-864-079-8	Sequence 8, Appl1
C 9	13.2	66.0	36	US-10-893-584-14	Sequence 14, Appl1
C 10	13	65.0	23	US-10-750-185-15044	Sequence 15044, A
C 11	13	65.0	25	US-11-121-849-383597	Sequence 383597, A
C 12	12.8	64.0	25	US-11-121-849-90190	Sequence 90190, A
C 13	12.8	64.0	25	US-11-121-849-90416	Sequence 90416, A
C 14	12.8	64.0	25	US-11-121-849-249360	Sequence 249360, A
C 15	12.8	64.0	25	US-11-121-849-466854	Sequence 466854, A
C 16	12.8	64.0	25	US-11-121-849-552041	Sequence 552041, A
C 17	12.8	64.0	25	US-11-121-849-552700	Sequence 552700, A
C 18	12.8	64.0	25	US-11-121-849-539135	Sequence 539135, A
C 19	12.6	63.0	25	US-11-121-849-24779	Sequence 24779, A
C 20	12.6	63.0	25	US-11-121-849-32312	Sequence 32312, A
C 21	12.6	63.0	25	US-11-121-849-33918	Sequence 33918, A
C 22	12.6	63.0	25	US-11-121-849-124009	Sequence 124009, A
C 23	12.6	63.0	25	US-11-121-849-148217	Sequence 148217, A

24	12.6	63.0	25	US-11-121-849-194169	Sequence 194169, A
25	12.6	63.0	25	US-11-121-849-296434	Sequence 296434, A
C 26	12.6	63.0	25	US-11-121-849-307950	Sequence 307950, A
27	12.6	63.0	25	US-11-121-849-310010	Sequence 310010, A
28	12.6	63.0	25	US-11-121-849-310627	Sequence 310627, A
29	12.6	63.0	25	US-11-121-849-398509	Sequence 398509, A
30	12.6	63.0	25	US-11-121-849-399245	Sequence 399245, A
31	12.6	63.0	25	US-11-121-849-399246	Sequence 399246, A
C 32	12.6	63.0	25	US-11-121-849-449121	Sequence 449121, A
C 33	12.6	63.0	25	US-11-121-849-579858	Sequence 579858, A
C 34	12.6	63.0	72	US-10-469-561-12	Sequence 12, Appl1
C 35	12.4	62.0	25	US-11-121-849-95142	Sequence 95142, A
C 36	12.4	62.0	25	US-11-121-849-95144	Sequence 95144, A
C 37	12.4	62.0	25	US-11-121-849-95145	Sequence 95145, A
C 38	12.4	62.0	25	US-11-121-849-162004	Sequence 162004, A
C 39	12.4	62.0	25	US-11-121-849-192387	Sequence 192387, A
40	12.4	62.0	25	US-11-121-849-420287	Sequence 420287, A
41	12.4	62.0	25	US-11-121-849-422053	Sequence 422053, A
42	12.4	62.0	25	US-11-121-849-581733	Sequence 581733, A
C 43	12.4	62.0	25	US-11-121-849-661763	Sequence 661763, A
C 44	12.2	61.0	25	US-11-121-849-24805	Sequence 24805, A
C 45	12.2	61.0	25	US-11-121-849-25566	Sequence 25566, A

ALIGNMENTS

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RESULT 1
US-11-121-849-240361/c
; Sequence 240361, Application US//11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121.849
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 240361
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
; US-11-121-849-240361

Query Match      69.0% Score 13.8; DB 7; Length 25;
Best Local Similarity 88.2%; Pred. NO. 2.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 TTTTTCAGGATCCCG 17
        |||||
Db       25 TTTTTCAGGATCCCG 9

RESULT 2
US-11-121-849-22867
; Sequence 22867, Application US//11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121.849
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 22867

```

```

; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-22867
```

```
Query Match          68.0%; Score 13.6; DB 7; Length 25;
Best Local Similarity 80.0%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1 TTTTCAGGGAATCCGGGG 20
    ||||| ||||| |||||
Db 6 TTTTCAGGGAATCTAAGG 25
```

```
RESULT 3
US-11-121-849-181142/C
; Sequence 181142, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
```

```

; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 181142
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-181142
```

```
Query Match          66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 5.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 3 TTTTCAGGGAATCCGGGG 20
    ||||| ||||| |||||
Db 24 TTTTCAGGAATCCTGTGG 7
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```
RESULT 4
US-11-121-849-338152
; Sequence 338152, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
```

```

; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 338152
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-338152
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```
Query Match          66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 5.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 TTTTCAGGGAATCCGGG 18
    ||||| ||||| |||||
Db 1 TTTTACATGGAACCGGG 18
```

```
RESULT 5
US-11-121-849-497393
; Sequence 497393, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
```

```

; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 497393
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-497393
```

```
Query Match          66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 5.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 2 TTTTCAGGGAATCCGGGG 19
    ||||| ||||| |||||
Db 6 TTTTCAGGGAATTCAGGG 23
```

```
RESULT 6
US-11-121-849-600267
; Sequence 600267, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
```

```

; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 600267
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-600267
```

```
Query Match          66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 5.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 TTTTCAGGGAATCCGGG 18
    ||||| ||||| |||||
Db 5 TTTTCATAGAAATCCAGG 22
```

```
RESULT 7
US-11-121-849-600268
; Sequence 600268, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
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; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
```

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; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 600268
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-600268

Query Match      66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 5.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 TTTTCAGGGAATCCGGG 18
    |||||
Db 2 TTTTCATGAAATCCAGG 19

RESULT 8
US-10-864-079-8/c
; Sequence 8, Application US/10864079
; Publication No. US20050277607A1
; GENERAL INFORMATION:
; APPLICANT: DINMAN, JONATHAN D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATING
; FILE REFERENCE: 4010.3005US
; CURRENT APPLICATION NUMBER: US/10/864,079
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-864-079-8

Query Match      66.0%; Score 13.2; DB 6; Length 32;
Best Local Similarity 83.3%; Pred. No. 5.7e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 TTTTCAGGGAATCCGGG 19
    |||||
Db 18 TTGTAGGGGATCCGGG 1

RESULT 9
US-10-893-584-14
; Sequence 14, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Adam
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; PRIOR FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 36
```

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: P.falciparum-B linker regions of pAP-225
US-10-893-584-14

Query Match      66.0%; Score 13.2; DB 6; Length 36;
Best Local Similarity 83.3%; Pred. No. 5.8e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 TTTTCAGGGAATCCGGG 19
    |||||
Db 8 TTTTCGGGGAATCCGAG 25

RESULT 10
US-10-750-185-15044/c
; Sequence 15044, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMT GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: PANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15044
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Forward Primer
US-10-750-185-15044

Query Match      65.0%; Score 13; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTTTCAGGGAAT 13
    |||||
Db 16 TTTTCAGGGAAT 4

RESULT 11
US-11-121-849-383597
; Sequence 383597, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 2005-07,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 383597
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-383597
```

Query Match 65.0%; Score 13; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTCAGGAATCCG 16
|||||
DB 7 TTCAGGAATCCG 19

RESULT 12
US-11-121-849-90190/c
; Sequence 90190, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 90190
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-90190

Query Match 64.0%; Score 12.8; DB 7; Length 25;
Best Local Similarity 87.5%; Pred. No. 8.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTTTCAGGGAATCCG 17
|||||
DB 21 TTTTCAGGGAATCCG 6

RESULT 13
US-11-121-849-90416
; Sequence 90416, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 90416
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-90416

Query Match 64.0%; Score 12.8; DB 7; Length 25;
Best Local Similarity 87.5%; Pred. No. 8.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 TCAGGGAATCCGCGG 20
|||||
DB 5 TCAGGGAATCCGCGG 20

RESULT 14
US-11-121-849-249360/c
; Sequence 249360, Application US/11121849
; Publication No. US20050272080A1

; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 249360
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-249360

Query Match 64.0%; Score 12.8; DB 7; Length 25;
Best Local Similarity 87.5%; Pred. No. 8.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 TCAGGGAATCCGCGG 20
|||||
DB 16 TCAGGGAATCCGTAG 1

RESULT 15
US-11-121-849-466854
; Sequence 466854, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 466854
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-466854

Query Match 64.0%; Score 12.8; DB 7; Length 25;
Best Local Similarity 87.5%; Pred. No. 8.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTTTCAGGGAATCCG 17
|||||
DB 7 TATTCAGGGAATCCG 22

Search completed: December 25, 2005, 04:37:02
Job time : 135.3 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 10:28:41 : Search time 582 Seconds
(without alignments)
1953.383 Million cell updates/sec

Title: US-09-296-264-6

Perfect score: 20

Sequence: 1 gggtagtcagcgcgagcg 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 1858228

Minimum DB seq length: 20

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_strs:*
11: gb_by:*
12: gb_un:*
13: gb_vl:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6	BD211663 Antisense
2	20	100.0	20	6	BD211668 Antisense
3	15.2	76.0	100	6	AX990338 Sequence
4	14.8	74.0	100	6	CQ000292 Sequence
5	14.2	71.0	51	6	AX158137 Sequence
6	14.2	71.0	57	6	BD080430 Bicompleu
7	14.2	71.0	65	6	COS55988 Sequence
8	14.2	71.0	75	1	ECCTRNAV
9	14.2	71.0	95	6	AX088789 Sequence
10	14.2	71.0	27	6	AX088790 Sequence
11	13.6	68.0	27	6	CQ973172 Sequence
12	13.6	68.0	38	6	CQ973152 Sequence
13	13.6	68.0	63	6	E27556
14	13.6	68.0	76	1	ECOTRNAPHE
15	13.6	68.0	88	6	BD033603 Sequence
16	13.6	68.0	88	6	AX898070 Sequence
17	13.4	67.0	42	6	AR104424 Sequence
18	13.4	67.0	42	6	BD062184 Bacterici

19	13.4	67.0	63	6	AR127588 Sequence
20	13.4	67.0	63	6	I75257 Sequence 6
21	13.4	67.0	73	6	I13478 Sequence 12
22	13.2	66.0	28	6	I67871 Sequence 7
23	13.2	66.0	33	6	BD234609 Thymidine
24	13.2	66.0	33	6	AR230205 Sequence
25	13.2	66.0	51	6	AX199369 Sequence
26	13.2	66.0	51	6	AX199370 Sequence
27	13.2	66.0	60	6	CQ540119 Sequence
28	13.2	66.0	60	6	CQ553070 Sequence
29	13.2	66.0	65	6	CQ532735 Sequence
30	13.2	66.0	65	6	CQ559822 Sequence
31	13.2	66.0	75	6	BD054182 Sequence
32	13.2	66.0	75	6	AX918649 Sequence
33	13.2	66.0	97	6	BD037478 Sequence
34	13.2	66.0	97	6	AX901945 Sequence
35	13.2	66.0	100	6	CQ824802 Sequence
36	12.8	64.0	21	6	AR148748 Sequence
37	12.8	64.0	40	6	AR279477 Sequence
38	12.8	64.0	40	6	AX025223 Sequence
39	12.8	64.0	48	6	AR031652 Sequence
40	12.8	64.0	48	6	I90270 Sequence 11
41	12.8	64.0	60	6	BD247649 A method
42	12.8	64.0	60	6	CQ755289 Sequence
43	12.8	64.0	60	6	AR345118 Sequence
44	12.8	64.0	65	6	CQ556456 Sequence
45	12.8	64.0	74	6	AX662284 Sequence

ALIGNMENTS

RESULT 1
LOCUS BD211663 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Antisense oligonucleotide sequence of neuropilin and method of using the same for controlling cell proliferation.

ACCESSION BD211663.1 GI:33021433
VERSION JP 2002512793-A/6.

KEYWORDS Homo sapiens (human)
SOURCE

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homnidae; Homo.
REFERENCE 1 (bases 1 to 20)

AUTHORS Wright,J.A., Young,A.H. and Lee,Y.S.
TITLE Antisense oligonucleotide sequence of neuropilin and method of using the same for controlling cell proliferation

JOURNAL Patent: JP 2002512793-A 6 08-MAY-2002;
GENENSENSE TECHNOLOGIES INC

COMMENT OS Homo sapiens (human)
PN JP 2002512793-A/6

PD 08-MAY-2002
PF 23-APR-1999 JP 2000545999

PR 23-APR-1998 US 60/082791
PT JIM A WRIGHT,ALPING H YOUNG,YOON S LEE

PC C12N15/09,A61K13/711,A61K48/00,A61P35/00,C12N15/00 CC
Antisense oligonucleotide sequence of neuropilin and method of

CC using the
FH name for controlling cell proliferation

FT source
Location/Qualifiers

FEATURES
source 1..20 /organism='Homo sapiens (human)'.
Location/Qualifiers

1..20 /organism='Homo sapiens'
/mol_type='genomic DNA'

ORIGIN
/db_xref='taxon:9606'

Query Match 100.0%; Score 20; DB 6; Length 20;

Best Local Similarity 100.0%; Pred. No. 55;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTACTTCAGCGCGGAGCG 20
|||||
1 GGGTACTTCAGCGCGGAGCG 20

Db 1 GGGTACTTCAGCGCGGAGCG 20

RESULT 2
BD211688/c 20 bp DNA linear PAT 17-JUL-2003
LOCUS Antisense oligonucleotide sequence of neuropilin and method of
DEFINITION using the same for controlling cell proliferation.
ACCESSION BD211688
BD211688.1 GI:33021458
VERSION JP 2002512793-A/31.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 20)
Wright,V.A., Young,A.H. and Lee,Y.S.
Antisense oligonucleotide sequence of neuropilin and method of
using the same for controlling cell proliferation
Patent: JP 2002512793-A 31 08-MAY-2002;
JOURNAL GENESENSE TECHNOLOGIES INC
COMMENT OS Homo sapiens (human)
PN JP 2002512793-A/31
PD 08-MAY-2002
PP 23-APR-1999 JP 2000545999
PR 23-APR-1998 US 60/082791
PI JIM A WRIGHT, AIPING H YOUNG, YOON S LEE
PC C12N15/09; A61K31/711; A61K48/00; A61P35/00 C12N15/00 CC
Antisense oligonucleotide sequence of neuropilin and method of
using the
CC same for controlling cell proliferation
FH Location/Qualifiers
FT source 1..20
Location/Qualifiers
1..20
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTACTTCAGCGCGGAGCG 20
|||||
20 GGGTACTTCAGCGCGGAGCG 1

Db 20 GGGTACTTCAGCGCGGAGCG 1

RESULT 3
AX990338/c 100 bp DNA linear PAT 16-JAN-2004
LOCUS Sequence 1801 from Patent EPI260592.
DEFINITION AX990338
AX990338.1 GI:40996684
VERSION AX990338.1
KEYWORDS Escherichia coli
Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
1
Donner,H., Drescher,B., Huber,A. and Weber,J.
Biochip Patent: EP 1260592-A 1801 27-NOV-2002;
JOURNAL MWG -Biotech AG (DE)
Location/Qualifiers
1..100
source

ORIGIN
Query Match 76.0%; Score 15.2; DB 6; Length 100;
Best Local Similarity 85.0%; Pred. No. 1.3e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGTACTTCAGCGCGGAGCG 20
|||||
44 GGGTCTTCGCGCGGAGCG 25

Db 44 GGGTCTTCGCGCGGAGCG 25

RESULT 4
CQ000292 100 bp DNA linear PAT 16-JAN-2004
LOCUS Sequence 11754 from Patent EPI260592.
DEFINITION CQ000292
CQ000292.1 GI:41006930
VERSION CQ000292.1
KEYWORDS Escherichia coli
Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
1
Donner,H., Drescher,B., Huber,A. and Weber,J.
Biochip Patent: EP 1260592-A 11754 27-NOV-2002;
JOURNAL MWG -Biotech AG (DE)
Location/Qualifiers
1..100
/organism="Escherichia coli"
/mol_type="unassigned DNA"
/db_xref="taxon:562"
/note="yga yga yga U00096 complement(2828798_2830387)"

ORIGIN
Query Match 74.0%; Score 14.8; DB 6; Length 100;
Best Local Similarity 88.9%; Pred. No. 2e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGTAGTTCTGCGGAGCG 19
|||||
8 GGTAGTTCTGCGGAGCG 25

Db 8 GGTAGTTCTGCGGAGCG 25

RESULT 5
AX158137/c 51 bp DNA linear PAT 22-JUN-2001
LOCUS Sequence 1465 from Patent WO0140521.
DEFINITION AX158137
AX158137.1 GI:14539468
VERSION AX158137.1
KEYWORDS Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1
Shinkets,R.A. and Leach,M.
Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
Patent: WO 0140521-A 1465 07-JUN-2001;
JOURNAL Curagen Corporation (US)
Location/Qualifiers
1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="1 of 2 allelic variants (1466 is other entry)"

misc_feature

ORIGIN	Accession number CG29363109"				
Query Match	71.0%;	Score 14.2;	DB 6;	Length 51;	
Best Local Similarity	84.2%;	Pred. No. 4.2e+04;			
Matches	16;	Conservative	0;	Mismatches 3;	Indels 0;
Oy	1	GGGTAGTTCAGCGCGGAGC	19		
Db	28	GGGTGTATCAGCGCGGAGC	10		
RESULT 6					
BD080430	BD080430	57 bp	DNA	linear	PAT 27-AUG-2002
DEFINITION	Biomolecule containing rubber-elastic peptide.				
ACCESSION	BD080430				
VERSION	BD080430.1	GI:22626033			
KEYWORDS	JP 2001514263-A/1.				
SOURCE	JP 2001514263-A/1.				
ORGANISM	synthetic construct				
REFERENCE	other sequences; artificial sequences.				
AUTHORS	1 (bases 1 to 57)				
TITLE	Rejersen, H., Rees, A. and Korsnes, L.				
JOURNAL	Biomolecule containing rubber-elastic peptide				
COMMENT	Patent: JP 2001514263-A 1 11-SEP-2001;				
	DYNAL AS				
	OS Artificial Sequence				
	PN JP 2001514263-A/1				
	PD 11-SEP-2001				
	PF 28-AUG-1998 JP 2000508699				
	PR 29-AUG-1997 GB 9718463.4				
	PI HERARD RIERSEN,ANTHONY REES,LARS KORSNES				
	PC C07K41/00,A61K38/00,C07K14/78,C07K16/44,C07K19/00,C12N15/09,				
	PC G01N33/53//				
	PC A61K39/395,A61K37/02,C12N15/00				
	CC Description of Artificial Sequence:ScFv linker sequence FH				
FEATURES					
Source	FT				
	Location/Qualifiers				
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	1..57				
	Location/Qualifiers				
	1..57				
	/organism='synthetic construct'				
	/mol_type='genomic DNA'				
	/db_xref='taxon:32630'				
ORIGIN					
Query Match	71.0%;	Score 14.2;	DB 6;	Length 57;	
Best Local Similarity	84.2%;	Pred. No. 4.2e+04;			
Matches	16;	Conservative	0;	Mismatches 3;	Indels 0;
Oy	2	GGTAGTTCAGCGCGGAGC	20		
Db	16	GGCGTTTCAGCGCGGAGC	34		
RESULT 7					
COS55986/c	COS55986	65 bp	DNA	linear	PAT 30-JAN-2004
LOCUS	Sequence 25623 from Patent WO0210449.				
DEFINITION	COS55986				
ACCESSION	COS55986				
VERSION	COS55986.1	GI:41522415			
KEYWORDS					
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;				
	Sciurognathi; Muridae; Muridae; Murinae; Mus.				
REFERENCE	1				
AUTHORS	Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Paigler,S.				
TITLE	Oligonucleotide library for detecting rna transcripts and splice				
JOURNAL	variants that populate a transcriptome				
	Patent: WO 0210449-A 25623 07-FEB-2002;				

FEATURES	Compugen Inc. (US)
SOURCE	location/Qualifiers
	1..65
	/organism="Mus musculus"
	/mol_type="unassigned DNA"
	/db_xref="taxon:10090"
ORIGIN	
Query Match	71.0%; Score 14.2; DB 6; Length 65;
Best Local Similarity	84.2%; Pred. No. 4.2e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
QY	
2	GGTAGTTCAGCGGAGCG 20
65	GGTAGTTCGTGGAGCG 47
RESULT 8	
LOCUS	ECCRNAB 75 bp DNA linear BCT 11-JUN-2003
DEFINITION	E.coli gene for chimeric transfer RNA-Val.
ACCESSION	X70451
VERSION	X70451.1 GI:312130
KEYWORDS	chimeric; transfer RNA-Val.
SOURCE	Escherichia coli
ORGANISM	Escherichia coli
REFERENCE	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.
AUTHORS	1 (bases 1 to 75)
TITLE	Weinmel,T., Mechulam,Y., Lazennec,C., Blanquet,S. and Fayat,G.
JOURNAL	Critical role of the acceptor stem of tRNAs(Met) in their
PUBMED	aminoacylation by Escherichia coli methionyl-tRNA synthetase
FEATURES	J. Mol. Biol. 229 (1), 26-36 (1993)
SOURCE	8421312
	location/Qualifiers
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	/mol_type="genomic DNA"
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ORIGIN	
Query Match	71.0%; Score 14.2; DB 1; Length 75;
Best Local Similarity	80.0%; Pred. No. 4.1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	
QY	
1	GGGTAGTTCAGCGGAGCG 20
5	GGGTAGCTCAGCNGGAGAG 24
Db	
RESULT 9	
LOCUS	AX088789/c 95 bp DNA linear PAT 17-MAR-2001
DEFINITION	Sequence 115 from Patent WO0114416.
ACCESSION	AX088789
VERSION	AX088789.1 GI:13397585
KEYWORDS	
SOURCE	synthetic construct
ORGANISM	synthetic construct
REFERENCE	other sequences; artificial sequences.
AUTHORS	1
TITLE	Neper,M.P., McClements,W.L., Jansen,K.U., Schultz,L.D., Chen,L.
JOURNAL	and Wang,X.M.
FEATURES	Synthetic human papillomavirus genes
SOURCE	Patent: WO 0114416-A 115 01-MAR-2001;
	Merck & Co., Inc. (US)
	location/Qualifiers
	1..95
	/organism="synthetic construct"
	/mol_type="unassigned DNA"
	/db_xref="taxon:32630"

ORIGIN /note="Codon-Optimized HPV6 E2 fragment"

Query Match 71.0%; Score 14.2; DB 6; Length 95;
Best Local Similarity 84.2%; Pred. No. 4.1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGAGTTCAGCGCGGAGCG 20
| | | | | | | | | | | | | | | | | | | | | |
Db 92 GATCGTTCAGCGCGGTAGCG 74

RESULT 10
LOCUS AX088790 96 bp DNA linear PAT 17-MAR-2001
DEFINITION Sequence 116 from Patent WO0114416.
ACCESSION AX088790
VERSION AX088790.1 GI:13397586
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE 1
AUTHORS Neeper,M.P., McClements,W.L., Jansen,K.U., Schultz,L.D., Chen,L.
and Wang,X.M.
TITLE Synthetic human papillomavirus genes
JOURNAL Patent: WO 0114416-A 116 01-MAR-2001;
Merck & Co., Inc. (US)
Location/Qualifiers

FEATURES
source 1..96
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Codon-Optimized HPV6 E2 fragment"

ORIGIN

Query Match 71.0%; Score 14.2; DB 6; Length 96;
Best Local Similarity 84.2%; Pred. No. 4.1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGAGTTCAGCGCGGAGCG 20
| | | | | | | | | | | | | | | | | | | | | |
Db 73 GATCGTTCAGCGCGGTAGCG 91

RESULT 11
LOCUS CQ973172/c 27 bp DNA linear PAT 20-JAN-2005
DEFINITION Sequence 26 from Patent WO2004111225.
ACCESSION CQ973172
VERSION CQ973172.1 GI:57997919
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE 1
AUTHORS Wu,Q.
TITLE Novel modified corin molecules having substitute activation
JOURNAL sequences and uses thereof
Patent: WO 2004111225-A 26 23-DEC-2004;
Schering Aktiengesellschaft (DE)
Location/Qualifiers
1..27
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Forward Primer EntPCRIA"

ORIGIN

Query Match 68.0%; Score 13.6; DB 6; Length 27;
Best Local Similarity 80.0%; Pred. No. 8.7e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGAGTTCAGCGCGGAGCG 20
| | | | | | | | | | | | | | | | | | | | | |
Db 25 GGAGTTCAGCGCGTGAACG 6

RESULT 12
LOCUS CQ973152 38 bp DNA linear PAT 20-JAN-2005
DEFINITION Sequence 6 from Patent WO2004111225.
ACCESSION CQ973152
VERSION CQ973152.1 GI:57997907
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE 1
AUTHORS Wu,Q.
TITLE Novel modified corin molecules having substitute activation
JOURNAL sequences and uses thereof
Patent: WO 2004111225-A 6 23-DEC-2004;
Schering Aktiengesellschaft (DE)
Location/Qualifiers

FEATURES
source 1..38
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Reverse Primer Cor/Twb"

ORIGIN

Query Match 68.0%; Score 13.6; DB 6; Length 38;
Best Local Similarity 80.0%; Pred. No. 8.5e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGAGTTCAGCGCGGAGCG 20
| | | | | | | | | | | | | | | | | | | | | |
Db 10 GGAGTTCAGCGCTGAACG 29

RESULT 13
LOCUS E27556 63 bp DNA linear PAT 18-JUN-2001
DEFINITION Isolation and cloning of nucleic acid molecule by using hairpin
E27556
ACCESSION E27556.1 GI:13018221
VERSION JP 1999206381-A/4.
KEYWORDS unclassified
SOURCE unclassified
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 63)
AUTHORS Jun,F. and Koji,S.
TITLE Isolation and cloning of nucleic acid molecule by using hairpin
JOURNAL loop nucleic acid probe molecule
Patent: JP 1999206381-A 4 03-AUG-1999;
Aisin COSMOS R&D CO LTD
COMMENT OS Unidentified
PN JP 1999206381-A/4
PD 03-AUG-1999
PF 29-JAN-1998 JP 1998016987
PR JUN FUJIWARA,KOJI SHIGEMORI
PI C12N15/09,C12Q1/68,C12N15/00
PC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..63
FT Location/Qualifiers
1..63
/organism="unclassified".
/mol_type="genomic DNA"
/db_xref="taxon:32644"

FEATURES

source

ORIGIN

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	Best Local Similarity	80.0%;	Pred. No. 8.3e+04;			
	Matches	16;	Conservative	0;	Mismatches	4;
Oy		1 GGGTAGTTCAGCGGCGGACGC	20			
Db		30 GGGCAGGTCTCAGCGCGGCCGC	49			
RESULT 14						
ECOTRNAPHE						
LOCUS	ECOTRNAPHE	76 bp	tRNA	linear	BCT 15-APR-1994	
DEFINITION	E. coli transfer RNA-Phe.					
ACCESSION	M24882					
VERSION	M24882.1 GI:290481					
KEYWORDS	transfer RNA-Phe.					
SOURCE	Escherichia coli					
ORGANISM	Escherichia coli					
	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;					
	Enterobacteriaceae; Escherichia.					
REFERENCE	1 (bases 1 to 76)					
AUTHORS	Kitchingman,G.R. and Fournier,M.J.					
TITLE	Modification-deficient transfer ribonucleic acids from relaxed control Escherichia coli: structures of the major unmodified phenylalanine and leucine transfer RNAs produced during leucine starvation					
JOURNAL	Biochemistry	16 (10),	2213-2220 (1977)			
PUBMED	324516					
COMMENT	Original source text: Escherichia coli tRNA.					
FEATURES	location/Qualifiers					
Source	1..76					
	/organism="Escherichia coli"					
	/mol_type="tRNA"					
	/db_xref="taxon:562"					
cRNA	1..76					
	/product="tRNA-Phe"					
ORIGIN	/note="codon recognized: UUC"					
Query Match	68.0%;	Score 13.6;	DB 1;	Length 76;		
Best Local Similarity	75.0%;	Pred. No. 8.3e+04;				
Matches	15;	Conservative	2;	Mismatches	3;	Indels
Oy		1 GGGTAGTTCAGCGGCGGACGC	20			
Db		5 GGATGCTCAGDCGGADAG	24			
RESULT 15						
BD033603/c						
LOCUS	BD033603	88 bp	DNA	linear	PAT 27-AUG-2002	
DEFINITION	Sequence tag and encoded human protein.					
ACCESSION	BD033603					
VERSION	BD033603.1 GI:22575345					
KEYWORDS	JP 2001269182-A/9849.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;					
	Hominiidae; Homo.					
	1 (bases 1 to 88)					
	Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.					
	Sequence tag and encoded human protein					
	Patent: JP 2001269182-A 9849 02-OCT-2001;					
GENSET						
OS	Homo sapiens (human)					
PN	JP 2001269182-A/9849					
PD	02-OCT-2001					
PF	24-FEB-2000 JP 2000118773					
PR	26-FEB-1999 US 60/122487					
PI	JEAN BAUTIST DUMAS MILNE EDWARDS, RIMERIC DUCLAIR, JEAN YVES					
	JORDAN					

FEATURES		source	CC	FH	Key	Location/Qualifiers	Location/Qualifiers
PC	C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC						
C12N5/10							
PC	C12P21/02, C12P21/08, C12Q1/68//G06F17/30, C12N15/00, C12N5/00, PC						
G06F15/40							
CC							
FH							
Key							
Location/Qualifiers							
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/organism="Homo sapiens"							
/mol_type="genomic DNA"							
/db_xref="taxon:9606"							
ORIGIN							
Query Match	68.0%;	Score 13.6;	DB 6;	length 88;			
Best Local Similarity	80.0%;	Pred. No. 8.2e+04;					
Matches 16;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;			
OY	1	GGGTAGTTCAGGCGGAGCG	20				
DB	85	GGGAAGTTCAAGGCGGAGCG	66				

Search completed: December 24, 2005, 14:06:09
Job time : 584 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 01:41:40 ; Search time 171.4 Seconds
(without alignments)
777.677 Million cell updates/sec

Title: US-09-296-264-6

Perfect score: 20

Sequence: 1 gggtagtcagcgcgagcg 20

Scoring table: IDENTITY_NUC

Searched: 496997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 3390896

Minimum DB seq length: 20

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_21:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*
- 14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3	AAZ31436 Human neu
2	20	100.0	20	3	ADA74688 GTT3606 a
3	20	100.0	20	3	ADA74688 GTT3606 a
4	18	90.0	30	4	ADA74713 Forward p
5	18	90.0	30	4	AAAF8316 Human neu
6	15.2	76.0	100	8	ACC80171 Human neu
7	14.8	74.0	100	8	ACD70531 E. coli K
8	14.4	72.0	20	13	ACD80478 E. coli K
9	14.4	72.0	20	13	ADU78696 Antisense
10	14.2	71.0	51	4	ADU78697 Antisense
11	14.2	71.0	65	6	AA174524 Human sll
12	14.2	71.0	95	4	ABN52875 Mouse sp1
13	14.2	71.0	95	4	AAf75497 Codon-opt
14	14.2	71.0	96	4	AAf75498 Codon-opt
15	13.8	69.0	66	9	ABSS52685 Elongator
16	13.6	68.0	27	14	ADA14180 C3 nucleic
17	13.6	68.0	30	6	ADA42868 Modified
18	13.6	68.0	38	14	ABK53798 DMS:accep
19	13.6	68.0	60	14	ADA42848 Human cor
					Adv11266 Nitrous a

C	20	13.6	68.0	60	14	ADV11268	Adv11268 Nitrous a
C	21	13.6	68.0	60	14	ADV11262	Adv11262 Nitrous a
	22	13.6	68.0	63	2	AAZ09153	AAZ09153 Hairpin t
	23	13.6	68.0	74	6	ABSS2700	ABSS2700 Mutant el
	24	13.6	68.0	76	6	ABK87519	ABK87519 Human imm
	25	13.6	68.0	76	6	ABK87514	ABK87514 Human imm
	26	13.6	68.0	76	6	ABK87515	ABK87515 Human imm
	27	13.6	68.0	76	6	ABK87517	ABK87517 Human imm
	28	13.6	68.0	76	6	ABK87516	ABK87516 Human imm
	29	13.6	68.0	76	6	ABK87518	ABK87518 Human imm
C	30	13.6	68.0	88	3	AAZ09858	AAZ09858 Human sec
	31	13.4	67.0	42	12	ADI80492	ADI80492 Human mut
	32	13.4	67.0	63	2	AAV00294	AAV00294 Bacillus
	33	13.4	67.0	63	5	AAf73112	AAf73112 Oligonuc1
	34	13.2	66.0	25	13	ADW80828	ADW80828 RACE PCR
	35	13.2	66.0	28	2	AAf39026	AAf39026 Circular
	36	13.2	66.0	28	2	AAf94718	AAf94718 Target se
C	37	13.2	66.0	31	13	ADSI8022	ADSI8022 Peronospo
C	38	13.2	66.0	33	2	AAf05187	AAf05187 Mutant HS
C	39	13.2	66.0	33	2	AAf57634	AAf57634 Codons 16
C	40	13.2	66.0	33	2	AAf15363	AAf15363 Codons 16
C	41	13.2	66.0	33	8	AAf04777	AAf04777 Thymidine
C	42	13.2	66.0	37	3	AAa28282	AAa28282 Human bet
C	43	13.2	66.0	41	8	ABZ23802	ABZ23802 Glycosyl-
C	44	13.2	66.0	51	4	AAH89519	AAH89519 Human cod
C	45	13.2	66.0	51	4	AAH89518	AAH89518 Human cod

ALIGNMENTS

RESULT 1	AAZ31436	AAZ31436 standard; DNA; 20 BP.
ID	AAZ31436	
XX	AAZ31436;	
AC		
XX		
DT	07-FEB-2000	(first entry)
XX		
DE	Human neuropilin mRNA specific antisense oligo GTT3606.	
XX		
KW	Neuropilin; human; growth; metastasis; tumor; neovascularisation; cancer; papilloma; diabetic retinopathy; antisense; ss.	
XX		
OS	Synthetic.	
XX		
OS	Homo sapiens.	
XX		
PN	W09955855-A2.	
XX		
PD	04-NOV-1999.	
XX		
PF	23-APR-1999;	99WO-CA000324.
XX		
PR	23-APR-1998;	98US-0082791P.
XX		
PA	(GENE-) GENESENSE TECHNOLOGIES INC.	
XX		
PI	Wright JA, Young AH, Lee YS;	
XX		
DR	WPI; 2000-023357/02.	
XX		
PT	Antisense oligonucleotides that inhibit neuropilin expression, useful for treating cancer.	
XX		
PS	Claim 4; Page 16; 57BP; English.	
XX		
CC	Sequences AAZ31431-460 represent antisense oligonucleotides which inhibit human neuropilin expression. The antisense oligonucleotides can be used to inhibit the growth or metastasis of a mammalian tumor and inhibit neovascularisation. The oligonucleotides may be used to treat various forms of cancers or tumors, such as sarcomas, melanomas, adenomas, carcinomas of solid tissue, hypoxic tumors, squamous cell carcinomas of the mouth, throat, larynx and lung, genitourinary cancers such as	

CC cervical and bladder cancer, hematopoietic cancers, colon cancer, breast
CC cancer, pancreatic cancer, renal cancer, brain cancer, skin cancer, liver
CC cancer, head and neck cancers, and nervous system cancers, as well as
CC benign lesions such as papillomas. The methods may be used to treat
CC neovascularisation disorders such as diabetic retinopathy, and
CC retinopathy of prematurity and age related macular degeneration

XX Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTAGTTCAGCGCGAGCG 20
1 GGGTAGTTCAGCGCGAGCG 20
Db 1 GGGTAGTTCAGCGCGAGCG 20

RESULT 2

ADA74688
ID ADA74688 standard; DNA; 20 BP.

AC ADA74688;

DT 20-NOV-2003 (first entry)

DE GT13606 antisense oligonucleotide targeted to human neuropilin mRNA.

XX neuropilin; VEGF165R; vascular endothelial growth factor receptor;
KM cytosolic; growth; tumour metastasis; angiogenesis; gene therapy; ss;
XX GT13606; antisense; human; ss.

OS Homo sapiens.

PN US2003083274-A1.

PD 01-MAY-2003.

PF 22-APR-1999; 99US-00296264.

PR 23-APR-1998; 98US-0082791P.

XX (WRIG/) WRIGHT J A.
PA (YOUN/) YOUNG A H.
PA (LEEV/) LEE Y S.

PI Wright JA, Young AH, Lee YS;

DR WPI; 2003-576622/54.

PT New antisense oligonucleotide that inhibits neuropilin expression, useful
PT for inhibiting growth of mammalian tumor or inhibiting metastasis of a
PT mammalian tumor.

PS Claim 1; Page 5; 27pp; English.

CC The invention relates to a novel antisense oligonucleotide that inhibits
CC the expression of neuropilin, also known as VEGF165R (vascular
CC endothelial growth factor receptor). The oligonucleotide of the invention
CC demonstrates cytostatic activity and may be useful for inhibiting the
CC growth or metastasis of a mammalian tumour and to inhibit angiogenesis in
CC mammals. Furthermore, the oligonucleotide may be utilised during gene
CC therapy. The current sequence is that of the GT13606 antisense
CC oligonucleotide of the invention which is targeted to human neuropilin
CC mRNA.

XX Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTAGTTCAGCGCGAGCG 20

Db 1 GGGTAGTTCAGCGCGAGCG 20

RESULT 3
ADA74713/C
ID ADA74713 standard; DNA; 20 BP.

AC ADA74713;

DT 20-NOV-2003 (first entry)

DE Forward PCR primer used during development of antisense oligonucleotides.

XX neuropilin; VEGF165R; vascular endothelial growth factor receptor;
KM cytosolic; growth; tumour metastasis; angiogenesis; gene therapy; ss;
XX primer; PCR.

OS Unidentified.

PN US2003083274-A1.

PD 01-MAY-2003.

PF 22-APR-1999; 99US-00296264.

PR 23-APR-1998; 98US-0082791P.

XX (WRIG/) WRIGHT J A.
PA (YOUN/) YOUNG A H.
PA (LEEV/) LEE Y S.

PI Wright JA, Young AH, Lee YS;

DR WPI; 2003-576622/54.

PT New antisense oligonucleotide that inhibits neuropilin expression, useful
PT for inhibiting growth of mammalian tumor or inhibiting metastasis of a
PT mammalian tumor.

PS Example 2; Page 12; 27pp; English.

CC The invention relates to a novel antisense oligonucleotide that inhibits
CC the expression of neuropilin, also known as VEGF165R (vascular
CC endothelial growth factor receptor). The oligonucleotide of the invention
CC demonstrates cytostatic activity and may be useful for inhibiting the
CC growth or metastasis of a mammalian tumour and to inhibit angiogenesis in
CC mammals. Furthermore, the oligonucleotide may be utilised during gene
CC therapy. The current sequence is that of the forward PCR primer of the
CC invention which was used during development of the antisense
CC oligonucleotides.

XX Sequence 20 BP; 3 A; 11 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTAGTTCAGCGCGAGCG 20
1 GGGTAGTTCAGCGCGAGCG 1
Db 20 GGGTAGTTCAGCGCGAGCG 1

RESULT 4
AAF83316/C
ID AAF83316 standard; DNA; 30 BP.

AC AAF83316;

DT 09-JUL-2001 (first entry)

DE Human neuropilin-1 (NP-1) DNA amplifying sense primer BUL-259.

XX

KW Receptor protein; vascular endothelial growth factor receptor-2; NP-1;
 KM VEGFR-2; neuropilin-1; co-receptor; human; angiogenic; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200131346-A2.
 XX
 PD 03-MAY-2001.
 XX
 PF 26-OCT-2000; 2000WO-US029579.
 XX
 PR 28-OCT-1999; 99US-0162367P.
 XX
 PA (PROC) PROCTER & GAMBLE CO.
 XX
 PI Rosenbaum JS, Whitaker GB, Limberg BJ;
 XX
 DR WPI; 2001-308686/32.
 XX
 XX Determining compounds which bind to a complex comprising vascular
 PT endothelial growth factor receptor-2 and Neuropilin-1 to provide superior
 PT pro- and anti-angiogenic agents.
 XX
 PS Example 1; Fig 3; 82pp; English.
 XX
 CC The invention relates to determining whether a compound is capable of
 CC binding to a receptor protein complex comprising a vascular endothelial
 CC growth factor receptor-2 (VEGFR-2) receptor protein and a neuropilin-1
 CC (NP-1) receptor protein. One method comprises introducing a sample
 CC comprising the compound to the receptor protein and allowing the compound
 CC to bind to the complex. Signaling through VEGFR-2 is enhanced in the
 CC presence of the NP-1 co-receptor. The methods of the invention can be
 CC used for identifying novel pro- and anti-angiogenic compounds. Sequences
 CC AAF83314-16 represents PCR primers used for isolating human NP-1 DNA
 XX
 SQ Sequence 30 BP; 5 A; 11 C; 8 G; 6 T; 0 U; 0 Other;
 XX
 Query Match 90.0%; Score 18; DB 4; Length 30;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 GTAGTTACGCGCGGAGCG 20
 Db 30 GTAGTTACGCGCGGAGCG 13
 XX
 RESULT 5
 ACC80171/C
 ID ACC80171 standard; DNA; 30 BP.
 XX
 AC ACC80171;
 XX
 DT 04-AUG-2003 (first entry)
 XX
 DE Human neuropilin-1 gene PCR primer #4.
 XX
 KM Cytostatic; Neuropilin-1 receptor; NP-1 receptor; angiogenesis; cancer;
 KM Vascular Endothelial Growth Factor Receptor-2; VEGFR-2; PlGF; VEGF;
 KM Placental Growth Factor; Vascular Endothelial Growth Factor;
 KM anti-angiogenic; human; PCR; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2003029275-A2.
 XX
 PD 10-APR-2003.
 XX
 PF 02-OCT-2002; 2002WO-US031386.
 XX
 PR 03-OCT-2001; 2001US-0326712P.
 XX
 PA (REGG-) REGENERON PHARM INC.
 PA (PROC) PROCTER & GAMBLE CO.

XX
 PI Rosenbaum JS, Jones DR, Whitaker GB;
 XX
 DR WPI; 2003-371982/35.
 XX
 PT New anti-angiogenic peptides that are capable of binding to NP-1 or
 PT vascular endothelial growth factor receptor (VEGFR)-2/NP-1 complex,
 PT useful for treating diseases characterized by abnormal angiogenesis, such
 PT as cancer.
 XX
 PS Disclosure; Page 21; 115pp; English.
 XX
 CC The present invention relates to peptides that are capable of binding to
 CC Neuropilin-1 (NP-1) receptor or the Vascular Endothelial Growth Factor
 CC Receptor (VEGFR)-2/NP-1 complex. The peptides are derived from a
 CC combination of peptides from Exon 6 of Placental Growth Factor (PlGF),
 CC coupled at the carboxyl terminus to either Exon 8 of Vascular Endothelial
 CC Growth Factor (VEGF) isoform 165 (VEGF165, also referred to as p68) or
 CC Exon 7 of PlGF (referred to as p67). The peptides and compositions are
 CC useful for treating diseases characterized by abnormal angiogenesis, such
 CC as cancer. The present peptide is a PCR primer, which was used to
 CC illustrate the invention
 XX
 SQ Sequence 30 BP; 5 A; 11 C; 8 G; 6 T; 0 U; 0 Other;
 XX
 Query Match 90.0%; Score 18; DB 8; Length 30;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 GTAGTTACGCGCGGAGCG 20
 Db 30 GTAGTTACGCGCGGAGCG 13
 XX
 RESULT 6
 ACD70531/C
 ID ACD70531 standard; DNA; 100 BP.
 XX
 AC ACD70531;
 XX
 DT 18-SEP-2003 (first entry)
 XX
 DE E. coli K12 MG1655 biochip probe SEQ ID 1801.
 XX
 KM Biochip; gene expression; gut; diagnostic; detection; probe; ss.
 XX
 OS Escherichia coli.
 XX
 PN EP1260592-A1.
 XX
 PD 27-NOV-2002.
 XX
 PF 17-MAY-2001; 2001EP-00112179.
 XX
 PR 17-MAY-2001; 2001EP-00112179.
 XX
 PA (MMGB-) MMGB-BIOTECH AG.
 XX
 PI Donner H, Drescher B, Huber A, Weber J;
 XX
 DR WPI; 2003-241155/24.
 XX
 PT Biochip containing probes complementary with open reading frames in
 PT Escherichia coli K12, useful for detecting gene expression and expression
 PT patterns.
 XX
 PS Claim 3; Page 290; 2004pp; German.
 XX
 CC This invention describes a novel biochip comprising probe spots, each
 CC containing many identical probes. The probes are nucleotide sequences of
 CC 30-80 bases, are prepared ex situ from synthetic oligonucleotides and at
 CC least one includes a segment of at least 20 bases identical with, or
 CC complementary to, a segment of an open reading frame (orf) of Escherichia

CC coli K12. The biochip is used for specific detection of gene expression
CC in K12 and for determining the gene expression pattern. e.g. for
CC diagnostic determination of which E. coli strains are present in the gut,
CC and to determine the effects of e.g. growth media on gene expression. The
CC biochip provides as comprehensive as possible detection of the K12
CC genome, with simultaneous analysis of many different genes with a single
CC device, and comparison of gene expression between K12 and its mutants or
CC other E. coli strains in a single experiment. Apart from qualitative and
CC quantitative information about gene expression, it also allows
CC measurements of population densities for the various strains. The use of
CC synthetic oligonucleotides for preparation of probes allows free
CC variation in probe length and ensures high purity (and thus selectivity,
CC reactivity and reproducibility); also synthetic probes are generally
CC shorter than probes prepared by polymerase chain reaction. ACD68731 to
CC ACD81540 represent oligonucleotide probes used with the biochip described
CC in the invention

SQ Sequence 100 BP; 17 A; 28 C; 26 G; 29 T; 0 U; 0 Other;

Query Match 76.0%; Score 15.2; DB 8; Length 100;
Best Local Similarity 85.0%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGTACTCAGCGCGGAGCG 20
|||||
DB 44 GGGTCGTTCCGCGGAGACG 25

RESULT 7
ACD80478
ID ACD80478 standard; DNA; 100 BP.
XX
XX ACD80478;
XX
XX 19-SEP-2003 (first entry)
XX
XX
DE E. coli K12 MG1655 biochip probe SEQ ID 11754.
XX
XX
KM Biochip; gene expression; gut; diagnostic; detection; probe; ss.
XX
XX Escherichia coli.
XX
XX PN EP1260592-A1.
XX
XX PD 27-NOV-2002.
XX
XX PF 17-MAY-2001; 2001EP-00112179.
XX
XX PR 17-MAY-2001; 2001EP-00112179.
XX
XX PA (MMGB-) MMGB-BIOTECH AG.
XX
XX PI Donner H, Drescher B, Huber A, Weber J;
XX
XX DR MPI; 2003-241155/24.
XX
XX PT Biochip containing probes complementary with open reading frames in
XX PT Escherichia coli K12, useful for detecting gene expression and expression
XX PT patterns.
XX
XX PS Claim 3; Page 1831; 2004PP; German.
XX
XX
CC This invention describes a novel biochip comprising probe spots, each
CC containing many identical probes. The probes are nucleotide sequences of
CC 30-80 bases, are prepared ex situ from synthetic oligonucleotides and at
CC least one includes a segment of at least 20 bases identical with, or
CC complementary to, a segment of an open reading frame (orf) of Escherichia
CC coli K12. The biochip is used for specific detection of gene expression
CC in K12 and for determining the gene expression pattern, e.g. for
CC diagnostic determination of which E. coli strains are present in the gut,
CC and to determine the effects of e.g. growth media on gene expression. The
CC biochip provides as comprehensive as possible detection of the K12
CC genome, with simultaneous analysis of many different genes with a single

CC device, and comparison of gene expression between K12 and its mutants or
CC other E. coli strains in a single experiment. Apart from qualitative and
CC quantitative information about gene expression, it also allows
CC measurements of population densities for the various strains. The use of
CC synthetic oligonucleotides for preparation of probes allows free
CC variation in probe length and ensures high purity (and thus selectivity,
CC reactivity and reproducibility); also synthetic probes are generally
CC shorter than probes prepared by polymerase chain reaction. ACD68731 to
CC ACD81540 represent oligonucleotide probes used with the biochip described
CC in the invention

SQ Sequence 100 BP; 19 A; 25 C; 33 G; 23 T; 0 U; 0 Other;

Query Match 74.0%; Score 14.8; DB 8; Length 100;
Best Local Similarity 88.9%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGTAGTTCAGCGCGGAGC 19
|||||
DB 8 GGTAGTTCAGCGGAGACG 25

RESULT 8
ADU78696/c
ID ADU78696 standard; DNA; 20 BP.
XX
XX
XX ADU78696;
XX
XX
XX 27-JUN-2005 (first entry)
XX
XX
DE Antisense oligonucleotide, SEQ ID 69.
XX
XX
XX Antisense oligonucleotide; Neuroleptic; Tranquillizer;
XX
XX Antiparkinsonian; Nootropic; Antidiabetic; Anorectic;
XX
XX Cardiovascular-Gen.; Antiartherosclerotic; Antilipemic;
XX
XX Alzheimer's disease; neurological disorder; phosphatase; enzyme;
XX
XX antisense; ss.
XX
XX OS Homo sapiens.
XX
XX
XX PN US2004226056-A1.
XX
XX PD 11-NOV-2004.
XX
XX PF 09-FEB-2004; 2004US-00776013.
XX
XX PR 22-DEC-1998; 98US-0113534P.
XX
XX PR 12-MAR-1999; 99US-0124120P.
XX
XX PR 30-JUN-1999; 99US-0141243P.
XX
XX PR 21-DEC-1999; 99US-00466139.
XX
XX PR 17-OCT-2000; 2000US-0240790P.
XX
XX PR 13-JUL-2001; 2001US-0304775P.
XX
XX PR 10-SEP-2001; 2001US-00948904.
XX
XX PR 12-OCT-2001; 2001US-00975072.
XX
XX PR 15-JUL-2002; 2002US-00194967.
XX
XX
XX PA (MYRI-) MYRIAD GENETICS INC.
XX
XX PI Roch J, Bartel P, Heichman K;
XX
XX DR MPI; 2004-794772/78.
XX
XX
XX PT Selecting agents useful for treating Alzheimer's disease comprises
XX PT selecting agents useful for treating Alzheimer's disease, comprising a
XX PT biological activity related to focal adhesion kinase 2 function with or
XX PT without the test agent.
XX
XX
XX PS Disclosure; SEQ ID NO 69; 247pp; English.
XX
XX
XX CC The present invention relates to a method for selecting agents that are
XX CC potentially useful for the treatment of Alzheimer's disease. The method
XX CC comprises selecting Focal Adhesion Kinase 2 (FAK2) with a test agent and
XX CC measuring a biological activity related to FAK2 function in the presence

and absence of the test agent. The method is useful for screening compounds or agents that can be used to treat neurological disorders, ailments and diseases including mild cognitive impairment, depression, schizophrenia, obsessive-compulsive disorder, bipolar disorder, and neurodegenerative diseases and disorders and motor neuron diseases and disorders such as Alzheimer's disease, Parkinson's disease, dementia with Lewy bodies, amyotrophic lateral sclerosis or Lou Gehrig's disease, Alpers' disease, Leigh's disease, Pelizaeus-Werthefer disease, Olivopontocerebellar atrophy, Friedrich's ataxia, leukodystrophies, Rett syndrome, Ramey Hunt syndrome type II, and Down's syndrome, as well as for treating or preventing other diseases such as dislipidemia, diabetes, obesity, cardiovascular diseases such as atherosclerosis and coronary heart disease. Also disclosed is the coding sequence for a novel human phosphatase called PN7740 (ADU18628 and ADU78629). PN7740 contains a protein phosphatase 2C domain, which likely acts to dephosphorylate specific phospho-serine or phospho-threonine residues on particular protein substrates. Although the precise role played by protein phosphatase 2C6 in Alzheimer's disease pathogenesis has yet to be defined, the inventors have discovered that fragments of PN7740 interact with the first phosphorytyrosine binding domain (PTB) domain of Fe65 (also known as APM81 (710) or amyloid beta (A4) precursor protein-binding, family B, member 1, isoform B9 (710)), suggesting that PN7740 may well be involved somehow. Fe65 is known to interact with the cytosolic C-terminal region of Amyloid beta (A4) precursor protein (APP) and APP metabolism is critical to the pathogenesis of Alzheimer's disease, because it leads to the release of either toxic Abeta or tropic secreted APP (sAPP) metabolites. The present sequence is an antisense oligonucleotide which can be used in antisense therapy for Alzheimer's disease.

SQ Sequence 20 BP; 6 A; 7 C; 3 G; 4 T; 0 U; 0 Other;

Query Match	72.0%	Score 14.4	DB 13	Length 20
Best Local Similarity	93.8%	Pred. No. 2.4e+03		
Matches 15; Conservative	0	Mismatches 1	Indels 0	Gaps 0

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QY      3 GTAGTCAGCGCGAG 18
          |||||
Db      18 GTAGTCATGCGGAG 3

```

RESULT 9
ADU78697/c
ID ADU78697 standard; DNA; 20 BP.

AC ADU78697;

DT 27-JAN-2005 (first entry)

AA Antisense oligonucleotide, SEQ ID 70.

KM Neuroprotective; Antidepressant; Neuroleptic; Tranquillizer;
 KM Antiparkinsonian; Nootropic; Antidiabetic; Anorectic;
 KM Cardiovascular-gen.; Antilatteriosclerotic; Antilipemic;
 KM Alzheimer's disease; neurological disorder; phosphatase; enzyme
 KM antisenese; ss.

Homo sapiens.

PN US2004226056-A1.

AA PD 11-NOV-2004

AA 09-FEB-2004; 2004US-00776013.
PF

22-DEC-1998; 98US-0113534P.

PR	12-MAR-1999;	99US-0124120P.
PR	30-JUN-1999;	99US-0141243P.

PR 17-OCT-2000; 2000US-0240790P.
FK 21-DEC-1999; 99US-00466139.

PR 13-JUL-2001; 2001US-03047/5P.
PR 10-SEP-2001; 2001US-00948904.

PR 12-OCT-2001: 2001US-009150/2.
PR 15-JUL-2002: 2002US-00194967.

XX
PA (MYRI-) MYRIAD GENETICS INC

PI Roch J, Barcel P, Heichman K;

DR WPI; 2004-794772/78.

PR Selecting agents useful for treating Alzheimer's disease comprises
PR contacting focal adhesion kinase 2 with a test agent and measuring a
PR biological activity related to focal adhesion kinase 2 function with or
PR without the test agent.

PS Disclosure; SEQ ID NO 70; 247pp; English.

The present invention relates to method for selecting agents that are potentially useful for the treatment of Alzheimer's disease. The method comprises contacting Focal Adhesion Kinase 2 (FAK) with a test agent and measuring a biological activity related to FAK function in the presence and absence of the test agent. The method is useful for screening compounds or agents that can be used to treat neurological disorders, ailments and diseases including mild cognitive impairment, depression, schizophrenia, obsessive-compulsive disorder, bipolar disorder, and neurodegenerative diseases and disorders and motor neuron diseases and disorders such as Alzheimer's disease, Parkinson's disease, dementia with Lewy bodies, amyotrophic lateral sclerosis or Lou Gehrig's disease, Alpers' disease, Leigh's disease, Pelizaeus-Wertheimer disease, Reticular dysmaturation, Friedreich's ataxia, leukodystrophies, Rett syndrome, Ramsay Hunt syndrome type II, and Down's syndrome, as well as for treating or preventing other diseases such as dilipidemia, diabetes, obesity, cardiovascular diseases such as atherosclerosis and coronary heart disease. Also disclosed is the coding sequence for a novel human phosphatase called PN7740 (ADU78628 and ADU78629). PN7740 contains a protein phosphatase 2C domain, which likely acts to dephosphorylate specific phospho-serine or phospho-threonine residues on particular protein substrates. Although the precise role played by protein phosphatase 2Cs in Alzheimer's disease pathogenesis has yet to be defined, the inventors have discovered that fragments of PN7740 interact with the first phosphorytyrosine binding domain (PTB) domain of Fe65 (also known as APPB1 710) or amyloid beta (A4) precursor protein-binding, family B, member 1, isoform B9 (710)), suggesting that PN7740 may well be involved somehow. Fe65 is known to interact with the cytosolic C-terminal region of amyloid beta (A4) precursor protein (APP) and APP metabolism is critical to the pathogenesis of Alzheimer's disease, because it leads to the release of either toxic A-beta or nontoxic secreted APP (sAPP) metabolites. The present sequence is an antisense oligonucleotide which can be used in antisense therapy for Alzheimer's disease.

Sequence 20 BP; 5 A; 7 C; 4 G; 4 T; 0 U; 0 Other;

Query Match	72.0%	Score 14.4	DB 13	Length 20
Best Local Similarity	93.8%	Pred. No. 2.4e+03		
Matches 15; Conservative	0	Mismatches 1	Indels 0	Gaps 0

QY	3	GTAGTCAGCGGGAG	18
Db	16	GTAGTCATGCGGGAG	1

RESULT 10
AA174524/c
ID AA174524 standard; DNA; 51 BP.

XX
AC AAI74524;

DT	09-NOV-2001	(first entry)
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XX	Human silent SNP containing nucleic acid SEQ:1465
DE	

Human; single nucleotide polymorphism; SNP; genome; gene therapy;

quantitation; restorative therapy; polymorphic; ds

xx Homo sapiens

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XX XX MO200140521-A2.
XX PN
XX PD 07-JUN-2001.
XX PF 30-NOV-2000; 2000WO-US032758.
XX PR 30-NOV-1999; 99US-0168138P.
XX PR 29-NOV-2000; 2000US-00726173.
XX PA (CURA-) CURAGEN CORP.
XX PI Shinketsu RA, Leach M;
XX DR WPI; 2001-356160/37.
XX PT Polymorphic nucleic acid sequences, useful in genetic testing and
XX PT therapy.
XX PS Claim 1; Page 502; 2653pp; English.
XX CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide
XX CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
XX CC AA53114 to AA53329 represent peptides related to human polymorphic
XX CC polynucleotide sequences. The sequences can be used in gene and protein
XX CC therapy, and in vaccine production. (I) and the polypeptides encoded by
XX CC them may be used in the prevention, diagnosis and treatment of diseases
XX CC associated with inappropriate expression of polymorphic polypeptides. For
XX CC example, (I) may be used to treat disorders by rectifying mutations or
XX CC deletions in a patient's genome that affect the activity of polypeptides
XX CC by expressing inactive proteins or to supplement the patients own
XX CC production of polypeptide. Additionally, (I) and its complementary
XX CC sequences may also be used as DNA probes in diagnostic assays to detect
XX CC and quantitate the presence of similar nucleic acids in samples, and
XX CC therefore which patients may be in need of restorative therapy. The
XX CC polypeptides encoded by (I) may be used as antigens in the production of
XX CC antibodies specific for polymorphic polypeptides. The antibodies may also
XX CC be used to down regulate expression and activity. The antibodies may also
XX CC be used as diagnostic agents for detecting the presence of polymorphic
XX CC polypeptides in samples
XX SQ Sequence 51 BP; 10 A; 19 C; 10 G; 12 T; 0 U; 0 Other;
XX
Query Match 71.0%; Score 14.2; DB 4; Length 51;
Best Local Similarity 84.2%; Pred. No. 3.2e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GGGTAGTTTCAGCGCGAGC 19
Db 28 GGGTGGTACAGCGCGAGC 10
RESULT 11
ABN52875/c
ID ABN52875 standard; DNA; 65 BP.
XX AC ABN52875;
XX DT 15-JUL-2002 (first entry)
XX DE Mouse spliced transcript detection oligonucleotide SEQ ID NO:25623.
XX KM Human; mouse; rat; splice transcript; detection; RNA transcript;
XX KM splice variant; transcriptome; oligonucleotide library; ss.
XX OS Mus musculus.
XX PN WO200210449-A2.
XX PD 07-FEB-2002.
XX PF 20-JUL-2001; 2001WO-IB001903.
XX XX
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PR 28-JUL-2000; 2000US-0221607P.
PR 02-MAY-2001; 2001US-0287724P.
XX XX
XX PA (COMP-) COMPUGEN INC.
XX PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX DR WPI; 2002-257383/30.
XX PT New oligonucleotide libraries comprising oligonucleotides which
XX PT selectively hybridize to mRNAs transcribed from a transcription unit of a
XX PT genome, useful for detecting tissue-, pathology-, and developmental-
XX PT specific genes.
XX PS Example 1; SEQ ID NO 25623; 47pp; English.
XX CC The present invention describes oligonucleotide libraries for detecting
XX CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-)
XX CC transcriptome comprises messenger RNAs transcribed from multiple
XX CC transcription units that populate a genome. The library comprises several
XX CC oligonucleotides, each capable of hybridising selectively to a set of
XX CC messenger RNAs transcribed from a given transcription unit of the genome,
XX CC which encodes one or more messenger RNA splice variants. The
XX CC oligonucleotide libraries are useful for detecting mRNAs from a
XX CC biological sample, in expression profiling studies, in qualitatively or
XX CC quantitatively characterising the corresponding transcriptome, and in
XX CC detecting RNA transcripts and splice variants of human or animal
XX CC transcriptomes. The libraries may also be used as specialised mini
XX CC libraries to detect transcripts of a sub-transcriptome under a particular
XX CC biological or pathological state, and so allowing the detection of tissue
XX CC - and pathology-specific genes such as those genes only expressed in
XX CC specific tissue under a specific pathological condition; to detect
XX CC developmental specific genes; and to detect RNA transcripts and splice
XX CC variants of a transcriptome of a patient suffering from a particular
XX CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
XX CC rats, humans and mice, which are used in the exemplification of the
XX CC present invention. N.B. The sequence data for this patent did not form
XX CC part of the printed specification, but was obtained in electronic format
XX CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 65 BP; 19 A; 19 C; 13 G; 14 T; 0 U; 0 Other;
XX
Query Match 71.0%; Score 14.2; DB 6; Length 65;
Best Local Similarity 84.2%; Pred. No. 3.3e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 GGTAGTTTCAGCGCGAGCG 20
Db 65 GGTAGTTCTCTGTGGAGCG 47
RESULT 12
AAF75497/c
ID AAF75497 standard; DNA; 95 BP.
XX AC AAF75497;
XX DT 14-MAY-2001 (first entry)
XX DE Codon-optimised HPV6 E2 fragment 6M.
XX KM Human papillomavirus; HPV; HPV6a; HPV18; L1; E2; E7; E1;
XX KM antiviral; immunostimulant; vaccine; immunogen; infection; ss.
XX OS Human papillomavirus.
XX OS Synthetic.
XX PN WO200114416-A2.
XX PD 01-MAR-2001.
XX PF 21-AUG-2000; 2000WO-US022932.
XX XX
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PR 25-AUG-1999; 99US-0150728P.
PR 07-JUN-2000; 2000US-0210143P.
XX
XX (MERI ) MERCK & CO INC.
XX
XX Neoper MP, McClements WL, Jansen KU, Schultz LD, Chen L, Wang X;
XX WPI; 2001-218428/22.
XX
XX Novel synthetic polynucleotide encoding human papillomavirus (HPV)
PT protein or mutated HPV protein useful as anti-HPV vaccines, comprises
PT optimized-codons for expression of the viral proteins in human host
PT cells.
XX
XX Example 6; Fig 23; 119pp; English.
XX
XX The present sequence is an oligomer which was used in the assembly of one
CC of a number of synthetic polynucleotides that encode a human
CC papillomavirus (HPV) protein, or a mutated form of a HPV protein. The
CC mutated HPV proteins have reduced protein function as compared to wild
CC type proteins but maintain immunogenicity. The proteins comprise codons
CC for optimized expression in humans. The polynucleotides are useful as a
CC vaccine which provides effective immunoprophylaxis against papillomavirus
CC infection through stimulation of neutralising antibody and cell-mediated
CC immunity
XX
XX Sequence 95 BP; 23 A; 36 C; 23 G; 13 T; 0 U; 0 Other;
SQ
Query Match 71.0%; Score 14.2; DB 4; Length 95;
Best Local Similarity 84.2%; Pred. No. 3.4e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 GGTAGTTCAGCGCGGAGCG 20
DB 92 GATCGTTCAAGCGCGTAGCG 74

RESULT 13
AAF75498
ID AAF75498 standard; DNA; 96 BP.
XX
XX AAF75498;
XX
XX 14-MAY-2001 (first entry)
XX
XX Codon-optimised HPV6 E2 fragment 6N.
XX
XX Human papillomavirus; HPV; HPV16; HPV6a; HPV18; L1; E2; E7; E1;
KW antiviral; immunostimulant; vaccine; immunogen; infection; ss.
XX
XX Human papillomavirus.
OS Synthetic.
OS
OS WO200114416-A2.
PN
XX
XX 01-MAR-2001.
PD
XX
XX 21-AUG-2000; 2000WO-US022932.
PF
XX
XX 25-AUG-1999; 99US-0150728P.
PR 07-JUN-2000; 2000US-0210143P.
XX
XX (MERI ) MERCK & CO INC.
PA
XX
XX Neoper MP, McClements WL, Jansen KU, Schultz LD, Chen L, Wang X;
PI WPI; 2001-218428/22.
XX
XX Novel synthetic polynucleotide encoding human papillomavirus (HPV)
PT protein or mutated HPV protein useful as anti-HPV vaccines, comprises
PT optimized-codons for expression of the viral proteins in human host
PT cells.
XX

```

```

PS Example 6; Fig 23; 119pp; English.
XX
XX The present sequence is an oligomer which was used in the assembly of one
CC of a number of synthetic polynucleotides that encode a human
CC papillomavirus (HPV) protein, or a mutated form of a HPV protein. The
CC mutated HPV proteins have reduced protein function as compared to wild
CC type proteins but maintain immunogenicity. The proteins comprise codons
CC for optimized expression in humans. The polynucleotides are useful as a
CC vaccine which provides effective immunoprophylaxis against papillomavirus
CC infection through stimulation of neutralising antibody and cell-mediated
CC immunity
XX
XX Sequence 96 BP; 13 A; 23 C; 40 G; 20 T; 0 U; 0 Other;
SQ
Query Match 71.0%; Score 14.2; DB 4; Length 96;
Best Local Similarity 84.2%; Pred. No. 3.4e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 GGTAGTTCAGCGCGGAGCG 20
DB 73 GATCGTTCAAGCGCGTAGCG 91

RESULT 14
ABS52695
ID ABS52695 standard; RNA; 74 BP.
XX
XX ABS52695;
XX
XX 15-NOV-2002 (first entry)
XX
XX Elongator tRNA Aaa-CA.
XX
XX Translation; ss; cell-free translation system; insulin; tRNA;
KW growth hormone; erythropoietin; ribosome display; mRNA display.
XX
XX Unidentified.
XX
XX
XX Key Location/Qualifiers
XX PH 1..7
XX FT /*tag= a
XX FT /bound_moiety= "Nucleotides 71-65 of the present
XX FT sequence"
XX
XX modified_base 8
XX FT /*tag= b
XX FT /note= "Shown as S4U in the specification"
XX
XX stem_loop 10..25
XX FT /*tag= c
XX FT /label= OTHER
XX
XX misc_difference 16
XX FT /*tag= d
XX FT /label= OTHER
XX
XX misc_difference 20
XX FT /*tag= d
XX FT /label= OTHER
XX
XX stem_loop 27..43
XX FT /*tag= e
XX
XX misc_difference 34
XX FT /*tag= f
XX FT /label= OTHER
XX
XX modified_base 37
XX FT /*tag= g
XX FT /note= "OTHER= Q"
XX
XX misc_difference 39
XX FT /*tag= h
XX FT /label= OTHER
XX
XX modified_base 46
XX FT /*tag= i
XX FT /label= SmG
XX
XX stem_loop 49..64
XX

```

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FT      misc_difference 55      /*tag= k
FT      /*tag= j
FT      /label= OTHER
FT      /note= "OTHER= Psi"
FT      misc_binding
FT      65. .71
FT      /*tag= 1
FT      /bound_molecy= "Nucleotides 7-1 of the present sequence"
XX
XX      WO200259293-A2.
XX
XX      01-AUG-2002.
XX
XX      25-JAN-2002; 2002WO-US002344.
XX
XX      25-JUN-2001; 2001US-0264147P.
XX
XX      (FORS/) FORSTER A C.
XX      (BLAC/) BLACKLOW S C.
XX
XX      Forster AC, Blacklow SC;
XX
XX      MPI; 2002-608454/65.
XX
XX      A new reconstituted cell-free translation system comprising translation
XX      factors and tRNA species capable of translating exogenously added mRNAs,
XX      useful for the synthesis of peptides or protein ligands or catalysts,
XX      e.g. insulin.
XX
XX      Disclosure; Fig 14; 83pp; English.
XX
XX      This invention relates to a novel reconstituted cell-free translation
XX      system comprising translation factors and transfer ribonucleic acid
XX      (tRNA) species which translate exogenously added messenger RNA (mRNA)
XX      with highly selective incorporation at each codon to form a peptide or a
XX      peptidomimetic product when the system includes one or more tRNA species
XX      charged with a synthetic amino acid or amino acid analogue. The
XX      translation system of the invention is useful for the synthesis of
XX      peptide or protein ligands or catalysts, such as insulin, growth hormone
XX      or erythropoietin, and for pure ribosome display and pure mRNA display
XX      selection experiments. The translation process provides a simplified,
XX      highly purified system that offers potentially improved routes to all
XX      peptides and proteins currently synthesised by alternative routes. This
XX      overcomes the limitations of the prior art, e.g. difficulty in
XX      maintaining purified components and trace contaminants or inefficient
XX      processivity. There are several advantages associated with performing
XX      peptide and protein display in a pure system, such as an expected lack of
XX      post-translational modification of peptides, lack of proteases which
XX      often cause protein degradation problem and a lack of competition from
XX      contaminants in the selection steps. The present sequence represents the
XX      Cys tRNA molecule used in an example of the cell free translation method
XX      of the invention
XX
XX      Sequence 74 BP; 15 A; 17 C; 21 G; 1 T; 15 U; 5 Other;
XX
XX      Query Match          70.0%; Score 14; DB 6; Length 74;
XX      Best Local Similarity 68.8%; Pred. No. 4.2e+03;
XX      Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      3 GTAGTTCAGCGCGGAG 18
       |:|:|:|:|:|:|:|
DB      7 GUAGUUCAGNCGGNAG 22
```

```
RESULT 15
ADA14190
ID      ADA14190 standard; DNA; 66 BP.
XX
XX      ADA14190;
AC
XX      20-NOV-2003 (first entry)
DT
XX
XX      C3 nucleic acid ligand sequence SEQ ID NO:139.
DE
```

```
XX      detection; photoreactive nucleic acid ligand; photocrosslink;
XX      solid support; HIV; gp120; photocrosslinking nucleic acid ligand; ss.
XX
XX      Synthetic.
XX
XX      Key      Location/Qualifiers
XX      modified_base 1..66
XX      /*tag= b
XX      /mod_base= OTHER
XX      /note= "t is 5-Brdu"
XX
XX      modified_base 1
XX      /*tag= a
XX      /mod_base= OTHER
XX      /note= "5'-amino-c6-g"
XX
XX      WO2003070984-A1.
XX
XX      28-AUG-2003.
XX
XX      10-FEB-2003; 2003WO-US004142.
XX
XX      15-FEB-2002; 2002US-0357297P.
XX      01-APR-2002; 2002US-00114187.
XX      26-JUL-2002; 2002US-0398666P.
XX      02-AUG-2002; 2002US-0400759P.
XX
XX      (SOMA-) SOMALOGIC INC.
XX
XX      Gold L, Zichi DA, Smith JD, Schneider DJ, Greef C;
XX
XX      MPI; 2003-697627/66.
XX
XX      Detecting the presence of a target molecule suspected of being contained
XX      in a test mixture, where the target molecule is a protein contacting the
XX      solid support with a Universal Protein Stain and detecting the presence
XX      of target molecule.
XX
XX      Example 4; Fig 3; 136pp; English.
XX
XX      The present invention describes a method for detecting the presence of a
XX      target molecule suspected of being contained in a test mixture, where the
XX      target molecule is a protein. The method comprises: (a) providing a solid
XX      support, comprising a photoreactive nucleic acid ligand having specific
XX      affinity for the target protein and that binds specifically to the target
XX      molecule through non-Watson-Crick interactions; (b) contacting the solid
XX      support with the test mixture suspected of containing the target
XX      molecule, where a nucleic acid ligand-target molecule complex is formed
XX      if the target molecule is present; (c) irradiating the solid support,
XX      where the nucleic acid ligand-target molecule complex photocrosslinks;
XX      (d) removing non-specifically bound material from the solid support; (e)
XX      contacting the solid support with a universal protein stain (UPS),
XX      comprising one or more reagents that label proteins with a detectable
XX      molecy; and (f) detecting the presence of the target molecule by
XX      detecting the presence of the detectable molecy on the solid support.
XX      Also described: (1) a biochip comprising an array of nucleic acid ligands
XX      attached to a solid support; (2) attaching a nucleic acid ligand to a
XX      solid support; (3) simultaneously measuring the dose-response
XX      characteristics of species of photocrosslinking nucleic acid ligands,
XX      each of which having specific affinity for a cognate target protein; and
XX      (4) a purified and isolated non-naturally occurring nucleic acid ligand
XX      to HIV gp120. The method is useful for detecting the presence of a target
XX      molecule suspected of being contained in a test mixture, where the target
XX      molecule is a protein. The present sequence represents a
XX      photocrosslinking nucleic acid ligand oligonucleotide, which is used in
XX      an example from the present invention.
XX
XX      Sequence 66 BP; 15 A; 17 C; 22 G; 12 T; 0 U; 0 Other;
XX
XX      Query Match          69.0%; Score 13.8; DB 9; Length 66;
XX      Best Local Similarity 88.2%; Pred. No. 5.2e+03;
XX      Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Qy 1 GGCTAGTTCAGCGCGGA 17
|||
Db 36 GGCTAGTTCAGCGCGGA 52
|||

Search completed: December 24, 2005, 12:28:57
Job time : 172.4 secs

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RESULT 2	97 bp	mrna	linear	EST 17-MAY-1997
AA046204/c				
LOCUS				
DEFINITION	AA046204.1 Soares testis NHT Homo sapiens cDNA clone IMAGE:742855			
ACCESSION	20 KD SUBUNIT PRECURSOR ;			
VERSION	AA046204			
KEYWORDS	EST.			
SOURCE	AA046204.1 GI:2064185			
ORGANISM	Homo sapiens (human)			
REFERENCE	Homo sapiens			
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.			
TITLE	1 (bases 1 to 97)			
JOURNAL	Hillier L., Allen M., Bowles L., Dubuque T., Giesel G., Joat S., Kucaba T., Lacey M., Le N., Lennon G., Marr M., Martin J., Moore B., Schellenberg K., Steptoe M., Tan F., Theising B., White Y., Wyllie T., Waterston R. and Wilson R.			
COMMENT	WashU-Merck EST Project 1997 Unpublished (1997) Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LML ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: similarity on wrong strand Seq primer: -41m3 fwd. ET from Amerham High quality sequence ecop:1.1 Location/Qualifiers 1..97 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="GDB:5929850" /db_xref="taxon:9606" /clone="IMAGE:742855" /sex="male" /lab_host="DH10B" /clone_lib="Soares testis NHT" /note="Vector: pRT3D-Pac polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT) primer 15', TGTTTCACATCTGAAGTGGAGGCGCGCCCAATTTTCTTTTCTTTT 3'. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT3D vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo."			
ORIGIN				
Query Match	71.0%;	Score 14.2;	DB 1;	Length 97;
Best Local Similarity	84.2%;	Pred. No. 4.2e+04;		
Matches	16;	Conservative 0;	Mismatches 3;	Indels 0;
Gaps	0;			
Db	2 GGTAGTTCAGCGCGAGCG 20			
	42 GGAAGATCAAGCGGAGCG 24			
RESULT 3				
LOCUS	CNS02VXN	97 bp	DNA	linear
DEFINITION	Tetradon nigroviridis genome survey sequence T7 end of clone 175809 of library G from Tetradon nigroviridis, genomic survey sequence.			
ACCESSION	AL216356			

VERSION	AL216356.1	GI:7875175
KEYWORDS	GSS; genome survey sequence.	
SOURCE	Tetradodon nigroviridis	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetradodon.	
REFERENCE	1 Roest Crolius,H., Jalllon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizesmes,C., Wincker,P., Brottier,P., Quetier,F., Saurit,W. and Weissenbach,J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetradodon nigroviridis Genome Res. 10 (7), 939-949 (2000)	
JOURNAL	2 Roest Crolius,H., Jalllon,O., Dasilva,C., Ozouf-Coataz,C., Fizesmes,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F., Saurit,W., Bernot,A. and Weissenbach,J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetradodon nigroviridis Genome Res. 10 (7), 939-949 (2000)	
PUBMED	10835645	
REFERENCE	3 (bases 1 to 97) Genoscope. Direct Submission Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr) This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetradodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon. Location/Qualifiers	
FEATURES	1..97 /organism="Tetradodon nigroviridis" /mol_type="genomic DNA" /db_xref="taxon:99883" /clone="175B09" /clone_1id="G" /note="Genoscope sequence ID : C0AG175CA051P1 end : T7"	
source		
COMMENT		
ORIGIN		
Query Match	71.0%; Score 14.2; DB 10; Length 97;	
Beet Local Similarity	84.2%; Pred. No. 4.2e+04;	
Matches	16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
CY	2 GGAGTTTCAGCGCGGACGC 20	
DB	55 GGTCGTTCAGCGCAGGAGG 73	
RESULT 4		
CD959631/c		
LOCUS	CD959631	100 bp mRNA linear EST 15-JUL-2003
DEFINITION	SCW 46 Genetag2 Zea mays cDNA, mRNA sequence.	
ACCESSION	CD959631	
VERSION	CD959631.1	GI:32807397
KEYWORDS	EST.	
SOURCE	Zea mays	
ORGANISM	Zea mays	
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.	
AUTHORS	1 (bases 1 to 100)	
TITLE	Genoplane.	
JOURNAL	Genoplane, a major partnership french program in plant genomes unpublished (2003)	
COMMENT	Contact: Genoplane Genoplane 93, rue Henri Rochefort 91025 EVRY CEDEX France	

Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genome programme 'Genoplante' (<http://www.genoplante.com>
and <http://genoplante-info.infobiogen.fr>).
Location/Qualifiers

FEATURES

source

1..100
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="mixtured"
/db_xref="taxon:4577"
/clone_1ib="Genetag2"

ORIGIN

Query Match 70.0%; Score 14; DB 6; Length 100;
Best Local Similarity 100.0%; Pred. No. 5.2e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 TAGTTCAGGCGGGA 17
|||||
Db 33 TAGTTCAGGCGGGA 20

RESULT 5
CG918269/c
LOCUS CH240_142F20.TV CHORI-240 Bos taurus genomic clone CH240_142F20,
DEFINITION genomic survey sequence.
ACCESSION CG918269
VERSION CG918269.1 GI:39777952
KEYWORDS GSS.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 70)
Costa, J.N., Mota, M. and Caetano A.R.
Brazil's Contribution to End-Sequencing the Bovine BAC Library
CHORI-240
Unpublished (2003)
Other GSSes: CH240_142F20.TV
Contact: Caetano AR
Department of Biotechnology
Embrapa Recursos Geneticos e Biotecnologia
Parque Estacao Biologica, Final AV. W/5 Norte, Brasilia-DF C.P.
02372, 70770-900 Brasilia
Tel: 55 61 448 4778
Fax: 55 61 340 3658
Email: acetanoc@cenargen.embrapa.br
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/ordering_information.htm).
Bases shown have phred quality value equal to or higher than 20.
For BAC library availability, please contact Pieter de Jong
(pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering_information.htm).
This work was undertaken as part of the International Bovine BAC
Mapping Consortium (IBBMC) by Embrapa Recursos Geneticos e
Biotecnologia with financing from Conselho Nacional de
Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil
Plate: 142 Row: F Column: 20
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 70.
Location/Qualifiers

FEATURES

source

1..70
/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="bred: Hereford"
/db_xref="taxon:9913"
/clone="CH240_142F20"

/sex="Male"
/cell_type="Blood"
/clone_1ib="CHORI-240"
/note="Vector: pTARBA01.3; Site 1: MboI; Site 2: MboI;
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC
library produced by Pieter de Jong"

ORIGIN

Query Match 69.0%; Score 13.8; DB 10; Length 70;
Best Local Similarity 88.2%; Pred. No. 6.5e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 GGGTAGTTCAGGCGGGA 17
|||||
Db 30 GGAGAGTTCAGGCGGGA 14

RESULT 6
CD533699/c
LOCUS 33E1 Arabidopsis leaf Senescence Library Arabidopsis thaliana cDNA
DEFINITION 3', mRNA sequence.
ACCESSION CD533699
VERSION CD533699.1 GI:40453711
KEYWORDS EST.
SOURCE Arabidopsis thaliana (chale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 85)
Guo, Y., Cai, Z. and Gan, S.
Transcriptome of Arabidopsis leaf senescence
Plant Cell Environ. 27 (5), 521-549 (2004)
Contact: Susheng Gan
Department of Horticulture
Cornell University
119 Plant Science, Cornell University, Ithaca, NY 14853-5904, USA
Tel: 607 254 5418
Fax: 607 255 0599
Email: sg288@cornell.edu
Insert Length: 85 Std Error: 0.00
Seq primer: 17
POLYA-No.

FEATURES

source

Location/Qualifiers
1..85
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/ecotype="landsberg erecta"
/db_xref="taxon:3702"
/tissue_type="leaf"
/dev_stage="Yellow leaf with Greenish Base Area"
/lab_host="E. coli"
/clone_1ib="Arabidopsis leaf Senescence Library"
/note="Organ: Rosette leaf; Vector: pBluscript SKII+;
Site 1: EcoRI; Site 2: EcoRI; Senescent rosette leaves #5
and #6 (counted from the bottom) were harvested and
immediately frozen in liquid N2. The leaves were visibly
yellow excepted for the leaf base areas that were still
greenish."

ORIGIN

Query Match 69.0%; Score 13.8; DB 6; Length 85;
Best Local Similarity 78.9%; Pred. No. 6.5e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 2 GGGTAGTTCAGGCGGAGCG 20
|||||
Db 75 GGAGAGTTCAGGCGGAGCG 57

RESULT 7
T72387/c

LOCUS	T72387	99 bp	mRNA	linear	EST 01-MAR-1995
DEFINITION	yc1d12.i1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:86135' similar to gb:X06985_1nal HEME OXYGENASE 1 (HUMAN); mRNA sequence.				
ACCESSION	T72387				
KEYWORDS	EST.	G1:686908			
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 99) Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiappelli,B., Chisoe,S., Dietrich,N., Dubuque,T., Favello,A., Glen,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mandis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevaekis,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M. Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)				
AUTHORS	Contact: Wilson RK Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel.: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu				
TITLE	Inser Size: 43				
JOURNAL	High quality sequence strates: 1 High quality sequence stops: 1				
PUBMED	Source: IMAGE Consortium, LNL This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Trace considered overall poor quality Seq primer: M13Rp1				
COMMENT	High quality sequence stop: 1. Location/Qualifiers 1..99 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="GDB:503192" /db_xref="taxon:9606" /clone="IMAGE:86135" /sex="male" /dev_stage="49 years old" /lab_host="SOLR cells (kanamycin resistant)" /clone_lib="Stratagene liver (#937224)" /note="Organ: liver; Vector: pluscript SK; Site: 1; ECOR1; Site:2: XhoI; Cloned unidirectionally. Primer: Oligo dt. Hepatectomy from normal male caucasian. Average insert size: 1.1 kb; Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACAG 3' ~3' adaptor sequence: 5' CTCGAGTTT TTTTTTTT 3'"				
FEATURES					
SOURCE					
Query Match	69.0%;	Score 13.8;	DB 8;	Length 99;	
Best Local Similarity	78.9%;	Pred. NO. 6.5e+04;			
Matches	15;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;
OY	2 GGTAATTGAGCGGAGCGC 20				
Db	49 GGGAGTTCATGCGGNNCGC 31				
RESULT 8	AZ377853/c	32 bp	DNA	linear	GSS 02-OCT-2000
LOCUS	DEFINITION	IM0132821F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0132821 F, genomic survey sequence.			
ACCESSION	AZ377853				
VERSION	AZ377853.1	GI:10491553			
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				

ORGANISM	Mus musculus Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 32)
REFERENCE	Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Rellay, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R., Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts Unpublished (2000)
TITLE	University of Utah University of Utah Genome Center Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
JOURNAL	Genome Research
COMMENT	84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0132 row: E column: 21 Seq primer: CGTGTAAACGACGCGCAGT Class: plasmid High quality sequence stop: 32.
FEATURES	Location/Qualifiers 1..32 /organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UUCGM0132E21" /sex="Male" /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /clone_id="Mouse 10kb plasmid UUCGM library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g1473114[gb AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
ORIGIN	1 68.0%; Score 13.6; DB 9; Length 32; Best Local Similarity 80.0%; Pred. No. 8.1e+04; Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
CY	1 GCGTAGTTCAGCGCGGAGCG 20
DB	20 GGATTAAGCCAGCGCGGAGCG 1
RESULT 9	
AZ920486/c	AZ920486 61 bp DNA linear GSS 17-DEC-2001
LOCUS	1006020A02.x1 1006 - Rescuedu Grid G Zea may genomic, genomic survey sequence.
DEFINITION	
ACCESSION	AZ920486
VERSION	AZ920486.1 GI:13391189
KEYWORDS	GSS.

SOURCE Zea mays
ORGANISM Zea mays
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 61)
AUTHORS Walbot, V.
TITLE Maize genomic sequences found using engineered Rescemu transposon
JOURNAL Unpublished (2001)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2221
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 1006020 row: 38
Classes: transposon-tagged,
Location/Qualifiers
1..61
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/issue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1006 - Rescemu Grid G"
/note="Organ: leaf; Vector: Rescemu (engineered from
bluescript backbone); Site 1: BamHI; Site 2: BglII;
Rescemu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on Rescemu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'Rescemu.' Grid G was grown at Stanford in 2000. DNA was
extracted from leaf punches, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."

ORIGIN
Query Match 68.0%; Score 13.6; DB 9; Length 61;
Best Local Similarity 80.0%; Pred. No. 8.1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 GGGTAGTTCAGCGGAGCG 20
DB 61 GGGTAGTTCAGCGGAGCG 42

RESULT 10
AJ744102/c 69 bp mRNA linear EST 17-FEB-2005
LOCUS AJ744102 riken1 gallus gallus cdna clone 22K1382, mRNA sequence.
DEFINITION AJ744102
ACCESSION AJ744102.1 GI:53909461
VERSION
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianidae; Gallus.
1 (bases 1 to 69)
REFERENCE Caldwell, R.B., Kleerek, A.M., Arakawa, H., Bezzubov, Y., Zaim, J.,
Fiedler, P., Kutter, S., Blagoderetski, A., Kostovska, D., Koter, M.,
Plachy, J., Carninci, P., Hayashizaki, Y. and Buerstedde, J.M.,
Full-length cDNAs from chicken bursal lymphocytes to facilitate
gene function analysis
JOURNAL Genome Biol. 6 (1), R6 (2005)
PUBMED 15642098
COMMENT Contact: Caldwell RB
GSF - Forschungszentrum, Institut fuer Molekulare Strahlenbiologie

FEATURES Ingolstaedter landstr. 1, D-85764 Neuberg, GERMANY.
source Location/Qualifiers
1..69
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="22K1382"
/cell_type="bursal lymphocyte"
/dev_stage="2-3 weeks old"
/clone_lib="riken1"
/note="CB inbred strain"

ORIGIN
Query Match 68.0%; Score 13.6; DB 1; Length 69;
Best Local Similarity 80.0%; Pred. No. 8.1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 GGGTAGTTCAGCGGAGCG 20
DB 35 GAGGGGCTCAGCGGAGCG 16

RESULT 11
BH412029/c 92 bp DNA linear GSS 12-DEC-2001
LOCUS BH412029 1007024H03.y1 1007 - Rescemu Grid H Zea mays genomic, genomic
DEFINITION survey sequence.
ACCESSION BH412029
VERSION BH412029.1 GI:17584839
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 92)
REFERENCE Walbot, V.
TITLE Maize genomic sequences found using engineered Rescemu transposon
AUTHORS Unpublished (2001)
JOURNAL Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2221
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 1007024 column: 14
Classes: transposon-tagged,
Location/Qualifiers
1..92
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/issue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1007 - Rescemu Grid H"
/note="Organ: leaf; Vector: Rescemu (engineered from
pbluescript backbone); Site 1: BamHI; Site 2: BglII;
Rescemu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on Rescemu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'Rescemu.' Grid H was grown at Berkeley in 2001. DNA
was extracted from leaf punches, double digested using
BamHI and BglII, and ligated to form circular plasmids.
DH10B cells were transformed and then screened on LB
plates with ampicillin."

ORIGIN
Query Match 68.0%; Score 13.6; DB 9; Length 92;

/strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGGCTM0231A18"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGGCIM library"
 /note="Vector: PWD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 66.0%; Score 13.2; DB 9; Length 38;
 Best Local Similarity 83.3%; Pred. No. 1.3e+05;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGATGTCAGCGGAGC 19
 |||||
 Db 30 GGTAATTAGCGAGAC 13

RESULT 15
 AI033458 51 bp mRNA linear EST 28-AUG-1998
 LOCUS
 DEFINITION
 ow94h01.91 Soares fetal_liver_spleen_INFLS_S1 Homo sapiens CDNA
 clone IMAGE:1654513 3' similar to gb:M81181
 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-2 (HUMAN);, mRNA
 sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strauberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Trace considered overall poor quality
 Insert length: 400 Std Error: 0.00
 Seq primer: -40m13 fwd. ET from Amerham
 High quality sequence stop: 1.

FEATURES

source
 1..51
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1654513"
 /sex="male"
 /dev_stage="20 week-post conception fetus"
 /lab_host="DH10B (ampicillin resistant)"

/clone_lib="Soares fetal liver spleen INFLS_S1"
 /note="Organ: Liver and Spleen; Vector: pT73D (Pharmacia)
 with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;
 This is a subtracted version of the original Soares fetal
 liver spleen INFLS library. 1st strand cDNA was primed
 with a Pac I - oligo(dT) primer [5',
 AACCTGAGAAATTAATTAAGATCTTTTCTTTTCTTTT 3'],
 double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Pac I and cloned into the Pac I
 and Eco RI sites of the modified pT73 vector. Library
 went through one round of normalization. Library
 constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 66.0%; Score 13.2; DB 1; Length 51;
 Best Local Similarity 83.3%; Pred. No. 1.3e+05;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GTAGTTCAGCGGAGCG 20
 |||||
 Db 33 GTAGCTCAGCTGAGCTG 50

Search completed: December 24, 2005, 18:28:32
 Job time : 1575 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 11:34:25 / Search time 48.1 Seconds
(without alignments)
739.111 Million cell updates/sec

Title: US-09-296-264-6
Perfect score: 20
Sequence: 1 gggatgctcagcgagcgagcg 20

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1134872

Minimum DB seq length: 20
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/pdata/1/ina/5 COMB. seq.*
3: /cgn2_6/pdata/1/ina/6A COMB. seq.*
4: /cgn2_6/pdata/1/ina/6B COMB. seq.*
5: /cgn2_6/pdata/1/ina/H COMB. seq.*
6: /cgn2_6/pdata/1/ina/PCTUS COMB. seq.*
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8: /cgn2_6/pdata/1/ina/RE COMB. seq.*
9: /cgn2_6/pdata/1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13.6	68.0	88	3	US-09-513-999C-13933
2	13.4	67.0	42	2	US-08-879-565-9
3	13.4	67.0	63	2	US-08-530-492-6
4	13.4	67.0	73	3	US-08-906-517-6
5	13.4	67.0	73	2	US-07-982-712-12
6	13.2	66.0	28	2	US-08-408-656-7
7	13.2	66.0	28	6	PCT-US95-03602-7
8	13.2	66.0	33	2	US-08-432-871C-14
9	13.2	66.0	33	3	US-09-270-956-14
10	13.2	66.0	75	3	US-09-513-999C-34512
11	13.2	66.0	97	3	US-09-513-999C-17808
12	12.8	64.0	21	3	US-09-262-773-105
13	12.8	64.0	40	3	US-09-830-337-6
14	12.8	64.0	48	2	US-08-391-000-11
15	12.8	64.0	48	2	US-08-741-931-11
16	12.8	64.0	50	3	US-10-131-827-2780
17	12.8	64.0	60	3	US-09-144-428-62
18	12.8	64.0	88	3	US-09-513-999C-36170
19	12.6	63.0	25	3	US-09-396-196G-55656
20	12.6	63.0	38	3	US-09-771-035A-42
21	12.6	63.0	100	3	US-09-621-976-8298
22	12.4	62.0	24	2	US-08-508-088-5
23	12.4	62.0	24	2	US-09-009-925-5
24	12.4	62.0	27	3	US-09-314-847A-13

25	12.4	62.0	27	3	US-10-037-677A-15	Sequence 15, Appl
26	12.4	62.0	62	2	US-09-935-338-71	Sequence 71, Appl
27	12.4	62.0	65	2	US-08-453-104-11	Sequence 11, Appl
28	12.4	62.0	65	2	US-08-694-824-11	Sequence 11, Appl
29	12.4	62.0	73	2	US-08-453-104-20	Sequence 20, Appl
30	12.4	62.0	73	2	US-08-694-824-20	Sequence 20, Appl
31	12.4	62.0	99	3	US-09-407-605-86	Sequence 86, Appl
32	12.2	61.0	20	3	US-09-344-529-15	Sequence 15, Appl
33	12.2	61.0	20	3	US-09-907-884-30	Sequence 30, Appl
34	12.2	61.0	25	2	US-08-412-376-3	Sequence 3, Appl
35	12.2	61.0	25	2	US-08-859-998-1021	Sequence 1021, Ap
36	12.2	61.0	25	3	US-08-646-273-32	Sequence 32, Appl
37	12.2	61.0	25	3	US-09-225-928-1021	Sequence 1021, Ap
38	12.2	61.0	25	3	US-09-225-201B-1021	Sequence 1021, Ap
39	12.2	61.0	25	3	US-09-396-196G-53377	Sequence 53377, A
40	12.2	61.0	29	3	US-10-083-246A-128	Sequence 128, App
41	12.2	61.0	31	6	PCT-US92-10792-29	Sequence 29, Appl
42	12.2	61.0	70	3	US-09-871-579-2	Sequence 2, Appl
43	12.2	61.0	70	3	US-09-871-579-14	Sequence 14, Appl
44	12.2	61.0	72	3	US-09-871-579-7	Sequence 7, Appl
45	12.2	61.0	74	3	US-09-621-976-12304	Sequence 12304, A

ALIGNMENTS

RESULT 1
US-09-513-999C-13933/c
Sequence 13933, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Ductert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59, US2, REG
CURRENT APPLICATION NUMBER: US/09/513, 999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 13933
LENGTH: 88
TYPE: DNA
ORGANISM: Homo sapiens
US-09-513-999C-13933
Query Match
Best Local Similarity 68.0%; Score 13.6; DB 3; Length 88;
Matches 16; Conservative 0; Pred. No. 2.1e+03; Indels 0; Gaps 0;
Oy 1 GGGATGCTCAGCGAGCGAGCG 20
Db 85 GGGAAGTTCAGAGCGAGCG 66
RESULT 2
US-08-879-565-9
Sequence 9, Application US/08879565A
Patent No. 6093573
GENERAL INFORMATION:
APPLICANT: Beamert, Lesa J.
APPLICANT: Carroll, Stephen F.
APPLICANT: Eisenberg, David
TITLE OF INVENTION: THREE-DIMENSIONAL STRUCTURE OF
TITLE OF INVENTION: BACTERICIDAL/PERMEABILITY-INCREASING PROTEIN
FILE REFERENCE: 1103/11034US01
CURRENT APPLICATION NUMBER: US/08/879, 565A
CURRENT FILING DATE: 1997-06-20
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 9
LENGTH: 42
TYPE: DNA
ORGANISM: Human
FEATURE:
OTHER INFORMATION: Oligonucleotide complementary to SEQ ID NO:8
US-08-879-565-9

Query Match 67.0%; Score 13.4; DB 3; Length 42;
Best Local Similarity 93.3%; Pred. No. 2.4e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GTTCAGCGCGGAGCC 20
DB 3 GTTCAGCGCGGAGCC 17

RESULT 3

US-08-530-492-6
Sequence 6, Application US/0850492
Patent No. 5689052
GENERAL INFORMATION:
APPLICANT: Brown, Sherri M.
APPLICANT: Dean, Duff A.
APPLICANT: Fromm, Michael E.
APPLICANT: Sanders, Patricia R.
TITLE OF INVENTION: Synthetic DNA Sequences Having Enhanced
TITLE OF INVENTION: Expression in Monocotyledonous Plants and Method For
NUMBER OF SEQUENCES: 164
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BBAF
STREET: 700 Chesterfield Parkway No. 5689052ch
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/530,492
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/172,333
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10605)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (synthetic)
US-08-530-492-6

Query Match 67.0%; Score 13.4; DB 2; Length 63;
Best Local Similarity 93.3%; Pred. No. 2.5e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AGTTCAGCGCGGAGC 19
DB 26 AGTTCAGCGCGGAGC 40

RESULT 4
US-08-906-517-6
Sequence 6, Application US/08906517
Patent No. 6180774

GENERAL INFORMATION:
APPLICANT: Brown, Sherri M.
APPLICANT: Dean, Duff A.
APPLICANT: Fromm, Michael E.
APPLICANT: Sanders, Patricia R.
TITLE OF INVENTION: Synthetic DNA Sequences Having Enhanced
TITLE OF INVENTION: Expression in Monocotyledonous Plants and Method For
NUMBER OF SEQUENCES: 164
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/906,517
FILING DATE: Concurrently Herewith
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: NOBT:170
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-474-7577
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-906-517-6

Query Match 67.0%; Score 13.4; DB 3; Length 63;
Best Local Similarity 93.3%; Pred. No. 2.5e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AGTTCAGCGCGGAGC 19
DB 26 AGTTCAGCGCGGAGC 40

RESULT 5
US-07-982-712-12
Sequence 12, Application US/07982712
Patent No. 5436391

GENERAL INFORMATION:
APPLICANT: Hideya FUJIMOTO, Kimiko ITOH
APPLICANT: Mikihito YAMAMOTO, and Ko SHIMAMOTO
TITLE OF INVENTION: Insecticidal Protein-encoding Gene, Gramineous
TITLE OF INVENTION: Plants Transformed with the Gene, and Production Thereof
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 144 mb

COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/992,712
FILING DATE: 19921127
CLASSIFICATION: 800
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 73 bases
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
US-07-982-712-12

Query Match 67.0%; Score 13.4; DB 2; Length 73;
Best Local Similarity 93.3%; Pred. No. 2.5e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AGTCAGCGCGGAGC 19
DB 29 AGTCAGAGGAGC 43

RESULT 6
US-08-408-656-7
Sequence 7, Application US/08408656
Patent No. 5674683
GENERAL INFORMATION:
APPLICANT: KOOL, Eric T.
TITLE OF INVENTION: STEM-LOOP AND CIRCULAR OLIGONUCLEOTIDES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
ZIP: 11530-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/408,656
FILING DATE: 21-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9373
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: circular
US-08-408-656-7

Query Match 66.0%; Score 13.2; DB 2; Length 28;
Best Local Similarity 83.3%; Pred. No. 2.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGTAGTTCAGCGGAG 18
DB 6 GGGTGTCAGAGGAG 23

RESULT 7
PCT-US95-03602-7
Sequence 7, Application PC/TUS9503602
GENERAL INFORMATION:
APPLICANT: Research Corporation Technologies, Inc.
TITLE OF INVENTION: STEM-LOOP AND CIRCULAR OLIGONUCLEOTIDES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
ZIP: 11530-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03602
FILING DATE: 21-MAR-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9373
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
PCT-US95-03602-7

Query Match 66.0%; Score 13.2; DB 6; Length 28;
Best Local Similarity 83.3%; Pred. No. 2.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGTAGTTCAGCGGAG 18
DB 6 GGGTGTCAGAGGAG 23

RESULT 8
US-08-432-871C-14/C
Sequence 14, Application US/08432871C
Patent No. 5877010
GENERAL INFORMATION:
APPLICANT: Loeb, Lawrence A.
ADDRESSEE: Black, Margaret E.
TITLE OF INVENTION: THYMIDINE KINASE MUTANTS
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle

```
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/432,871C
FILING DATE: 02-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 240052.409C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
TELEX: 3723836
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..33
US-08-432-871C-14

Query Match      66.0%; Score 13.2; DB 2; Length 33;
Best Local Similarity 83.3%; Pred. No. 3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GGGTAGTTCAGCGCGGAG 18
Db      26 GGGTAGCACAGGAGGAG 9

RESULT 9
US-09-270-956-14/C
Sequence 14, Application US/09270956
Patent No. 6451571
GENERAL INFORMATION:
APPLICANT: Loeb, Lawrence A.
APPLICANT: Black, Margaret E.
TITLE OF INVENTION: THYMIDINE KINASE MUTANTS
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/270,956
FILING DATE: 17-MAR-1999
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 240052.409C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
TELEX: 3723836
```

```
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: join(1..33)
US-09-270-956-14

Query Match      66.0%; Score 13.2; DB 3; Length 33;
Best Local Similarity 83.3%; Pred. No. 3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GGGTAGTTCAGCGCGGAG 18
Db      26 GGGTAGCACAGGAGGAG 9

RESULT 10
US-09-513-999C-34512/C
Sequence 34512, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Ductert, A.
APPLICANT: Dumas Milne Edwards, J.B.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59. US2. REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 34512.
LENGTH: 75
TYPE: DNA
ORGANISM: Homo sapiens
US-09-513-999C-34512

Query Match      66.0%; Score 13.2; DB 3; Length 75;
Best Local Similarity 83.3%; Pred. No. 3.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GGGTAGTTCAGCGCGGAG 18
Db      68 GGGTAGTGAGGAGGAGGAG 51

RESULT 11
US-09-513-999C-17808
Sequence 17808, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Ductert, A.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59. US2. REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 17808
LENGTH: 97
TYPE: DNA
ORGANISM: Homo sapiens
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/741,931
FILING DATE: 31-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/391,000
FILING DATE: 21-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Neuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 028750-123
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-741-931-11

Query Match 64.0%; Score 12.8; DB 2; Length 48;
Best Local Similarity 87.5%; Pred. No. 4.8e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TAGTTCAGGCGGGAGC 19
|||||
Db 17 TAGTTCAGGCGGTAGC 2

Search completed: December 24, 2005, 18:36:28
Job time : 48.1 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 14:06:30 ; Search time 337.6 seconds
(without alignments)
489.892 Million cell updates/sec

Title: US-09-296-264-6
Perfect score: 20
Sequence: 1 gggtagtcagcgagcgagcg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 9887334

Minimum DB seq length: 20
Maximum DB seq length: 100.

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA Main:

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3	US-09-296-264-6
2	20	100.0	20	3	US-09-296-264-31
3	18	90.0	30	6	US-10-263-162-59
4	14.4	72.0	20	8	US-10-776-013-69
5	14.4	72.0	20	8	US-10-776-013-70
6	14.2	71.0	25	10	US-11-036-317-78024
7	14.2	71.0	25	10	US-11-036-317-531280
8	14.2	71.0	65	3	US-09-908-975-25623
9	14.2	71.0	95	9	US-10-728-131-115
10	14.2	71.0	96	9	US-10-728-131-116
11	13.8	69.0	25	7	US-10-719-956-405220
12	13.8	69.0	25	7	US-10-719-956-224531
13	13.8	69.0	25	9	US-10-956-157-167244
14	13.8	69.0	25	10	US-11-060-756-179496
15	13.8	69.0	57	9	US-10-790-273-6
16	13.6	68.0	25	10	US-11-036-317-953755
17	13.6	68.0	27	8	US-10-865-978-26
18	13.6	68.0	38	8	US-10-865-978-5
19	13.4	67.0	25	8	US-10-719-900-395307
20	13.4	67.0	42	7	US-10-162-743-9
21	13.4	67.0	42	7	US-10-960-853-13
22	13.2	66.0	25	7	US-10-719-956-117106
23	13.2	66.0	25	7	US-10-719-956-421274

24	13.2	66.0	25	8	US-10-719-900-215966	Sequence 215966,
25	13.2	66.0	25	8	US-10-719-900-378428	Sequence 378428,
26	13.2	66.0	25	9	US-10-843-527-5709	Sequence 5709, Ap
27	13.2	66.0	25	9	US-10-843-527-6198	Sequence 6198, Ap
28	13.2	66.0	25	9	US-10-843-527-231979	Sequence 231979,
29	13.2	66.0	25	9	US-10-843-527-232468	Sequence 232468,
30	13.2	66.0	25	10	US-11-036-317-78914	Sequence 78914, A
31	13.2	66.0	25	10	US-11-036-317-812158	Sequence 812158,
32	13.2	66.0	25	10	US-11-036-317-812158	Sequence 812158,
33	13.2	66.0	31	8	US-10-638-464-12	Sequence 12, Appl
34	13.2	66.0	60	3	US-09-908-975-9754	Sequence 9754, Ap
35	13.2	66.0	60	3	US-09-908-975-22705	Sequence 22705, A
36	13.2	66.0	65	3	US-09-908-975-2370	Sequence 2370, Ap
37	13.2	66.0	65	3	US-09-908-975-28457	Sequence 28457, A
38	13.2	66.0	70	6	US-10-403-232-34	Sequence 34, Appl
39	13.2	66.0	94	3	US-09-783-530-6963	Sequence 6963, Ap
40	13	65.0	25	7	US-10-719-956-40713	Sequence 40713, A
41	13	65.0	25	9	US-10-843-527-119022	Sequence 119022,
42	13	65.0	25	9	US-10-843-527-119155	Sequence 119155,
43	12.8	64.0	25	5	US-10-211-059-236	Sequence 236, App
44	12.8	64.0	25	5	US-10-211-059-237	Sequence 237, App
45	12.8	64.0	25	5	US-10-211-059-238	Sequence 238, App

ALIGNMENTS

```

RESULT 1
US-09-296-264-6
Sequence 6, Application US/09296264
Publication No. US20030083274A1
GENERAL INFORMATION:
APPLICANT: WRIGHT, Jim A.
APPLICANT: YOUNG, Aiping H.
TITLE OF INVENTION: NEUROFILIN ANTISENSE OLIGONUCLEOTIDE SEQUENCES AND
TITLE OF INVENTION: METHODS OF USING SAME TO MODULATE CELL GROWTH
FILE REFERENCE: 032396-043
CURRENT APPLICATION NUMBER: US/09/296,264
CURRENT FILING DATE: 1999-04-22
EARLIER APPLICATION NUMBER: US 60/082,791
EARLIER FILING DATE: 1998-04-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 20
TYPE: DNA
ORGANISM: Human
US-09-296-264-6

Query Match      100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 GGGTAGTCAGCGGAGCG 20
Db 1 GGGTAGTCAGCGGAGCG 20

RESULT 2
US-09-296-264-31/C
Sequence 31, Application US/09296264
Publication No. US20030083274A1
GENERAL INFORMATION:
APPLICANT: WRIGHT, Jim A.
APPLICANT: YOUNG, Aiping H.
APPLICANT: YOUNG, Yoon S.
TITLE OF INVENTION: NEUROFILIN ANTISENSE OLIGONUCLEOTIDE SEQUENCES AND
TITLE OF INVENTION: METHODS OF USING SAME TO MODULATE CELL GROWTH
FILE REFERENCE: 032396-043
CURRENT APPLICATION NUMBER: US/09/296,264
CURRENT FILING DATE: 1999-04-22
EARLIER APPLICATION NUMBER: US 60/082,791

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EARLIER FILING DATE: 1998-04-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 31
LENGTH: 20
TYPE: DNA
ORGANISM: Human
US-09-296-264-31

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTAGTTCAGCGCGGAGCG 20
Db 20 GGGTAGTTCAGCGCGGAGCG 1

RESULT 3
US-10-263-162-59/c

Sequence 59, Application US/10263162
Publication No. US20030186868A1
GENERAL INFORMATION:
APPLICANT: Rosenbaum, et al.
TITLE OF INVENTION: Anti-Angiogenic Peptides
FILE REFERENCE: REG 810
CURRENT APPLICATION NUMBER: US/10/263,162
PRIOR FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: 60/326,712
PRIOR FILING DATE: 2001-10-03
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patent In version 3.0
SEQ ID NO 59
LENGTH: 30
TYPE: DNA
ORGANISM: homo sapiens
US-10-263-162-59

Query Match 90.0%; Score 18; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GTAGTTCAGCGCGGAGCG 20
Db 30 GTAGTTCAGCGCGGAGCG 13

RESULT 4
US-10-776-013-69/c

Sequence 69, Application US/10776013
Publication No. US20040226056A1
GENERAL INFORMATION:
APPLICANT: MYRIAD GENETICS, INC.
APPLICANT: Koch, Jean-Marc
APPLICANT: Bartel, Paul
APPLICANT: Heichman, Karen
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING NEUROLOGICAL DISORDERS AND
FILE REFERENCE: 1600.24
CURRENT APPLICATION NUMBER: US/10/776,013
PRIOR FILING DATE: 2004-02-09
PRIOR APPLICATION NUMBER: 09/948904
PRIOR FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 09/466139
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 60/113534
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/124120
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/141243
PRIOR FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: 09/975072
PRIOR FILING DATE: 2001-10-12

PRIOR APPLICATION NUMBER: 60/240790
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 10/194967
PRIOR FILING DATE: 2002-07-15
PRIOR APPLICATION NUMBER: 60/304775
PRIOR FILING DATE: 2001-07-13
NUMBER OF SEQ ID NOS: 695
SOFTWARE: Patent In version 3.2
SEQ ID NO 69
LENGTH: 20
TYPE: DNA
ORGANISM: Homo sapiens
US-10-776-013-69

Query Match 72.0%; Score 14.4; DB 8; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.9e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GTAGTTCAGCGCGGAG 18
Db 18 GTAGTTCATGCGGAG 3

RESULT 5
US-10-776-013-70/c

Sequence 70, Application US/10776013
Publication No. US20040226056A1
GENERAL INFORMATION:
APPLICANT: MYRIAD GENETICS, INC.
APPLICANT: Koch, Jean-Marc
APPLICANT: Bartel, Paul
APPLICANT: Heichman, Karen
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING NEUROLOGICAL DISORDERS AND
FILE REFERENCE: 1600.24
CURRENT APPLICATION NUMBER: US/10/776,013
PRIOR FILING DATE: 2004-02-09
PRIOR APPLICATION NUMBER: 09/948904
PRIOR FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 09/466139
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 60/113534
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/124120
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/141243
PRIOR FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: 09/975072
PRIOR FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240790
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 10/194967
PRIOR FILING DATE: 2002-07-15
PRIOR APPLICATION NUMBER: 60/304775
PRIOR FILING DATE: 2001-07-13
NUMBER OF SEQ ID NOS: 695
SOFTWARE: Patent In version 3.2
SEQ ID NO 70
LENGTH: 20
TYPE: DNA
ORGANISM: Homo sapiens
US-10-776-013-70

Query Match 72.0%; Score 14.4; DB 8; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.9e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GTAGTTCAGCGCGGAG 18
Db 16 GTAGTTCATGCGGAG 1

RESULT 6


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US-11-036-317-78024/c
: Sequence 78024, Application US/11036317
: Publication No. US20050214823A1
: GENERAL INFORMATION:
: APPLICANT: Williams, Alan
: TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
: FILE REFERENCE: 3654.1
: CURRENT APPLICATION NUMBER: US/11/036,317
: CURRENT FILING DATE: 2005-01-13
: PRIOR APPLICATION NUMBER: US 60/536,639
: PRIOR FILING DATE: 2004-01-13
: NUMBER OF SEQ ID NOS: 991174
: SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
: SEQ ID NO 78024
: LENGTH: 25
: TYPE: DNA
: ORGANISM: Mus musculus
US-11-036-317-78024

```

Query Match	71.0%;	Score 14.2;	DB 10;	Length 25;
Best Local Similarity	84.2%;	Pred. No. 3.6e+03;		
Matches 16; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

```

QY      1 GGGTAGTTCAGCGCGGAGC 1
          | | | | | | | | | |
Db      20 GAGCAGCTCAGGCGGGAGC 2

```

```

RESULT 7
US-11-036-317-531280/c
: Sequence 531280, Application US/11036317
: Publication No. US20050214822A1
: GENERAL INFORMATION:
: APPLICANT: Williams, Alan
: APPLICANT: Blume, John
: TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
: FILE REFERENCE: 3654.1
: CURRENT APPLICATION NUMBER: US/11/036,317
: CURRENT FILING DATE: 2005-01-13
: PRIOR APPLICATION NUMBER: US 60/536,639
: PRIOR FILING DATE: 2004-01-13
: NUMBER OF SEQ ID NOS: 991174
: SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
: SEQ ID NO 531280
: LENGTH: 25
: TYPE: DNA
: ORGANISM: Mus musculus
: US-11-036-317-531280

```

Query Match	71.0%;	Score 14.2;	DB 10;	Length 25;
Best Local Similarity	84.2%;	Pred. No. 3.6e+03;		
Matches	16;	Conservative	0;	Mismatches 3;
			Indels	0;
			Gaps	0;

```

Qy      1 GGGTAGTTCAGGCGGGAGC 15
          | | | | | | | | | |
Db      20 GAGCAGCTCAGGCGGGAGC 2

```

```

RESULT 8
US-09-908-975-25623/c
; Sequence 25623, Application US/09908975
; Publication No. US20030165843A1
;
; GENERAL INFORMATION:
;
; APPLICANT: SHOSHAN, AVI
; APPLICANT: WASSERMAN, ALON
; APPLICANT: MINTZ, ELI
; APPLICANT: MINTZ, LIAT
; APPLICANT: FAIGLER, SIMCHON
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICING
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975

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:
: CURRENT FILING DATE: 2001-07-20
:
: PRIOR APPLICATION NUMBER: US 60/287,722
:
: PRIOR FILING DATE: 2001-05-02
:
: PRIOR APPLICATION NUMBER: US 60/221,607
:
: PRIOR FILING DATE: 2000-07-28
:
: NUMBER OF SEQ ID NOS: 32337
:
: SOFTWARE: PatentIn version 3.0
:
: SEQ ID NO 25623
:
: LENGTH: 65
:
: TYPE: DNA
:
: ORGANISM: Mus musculus
:
: US-09-908-975-25623

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Query Match	71.0%	Score 14.2;	DB 3;	Length 65;
Best Local Similarity	84.2%	Pred. No. 3.3e+03;		
Matches 16; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

QY 2 GGTAAGTTCAGCGGGAGCG 20
|||
Db 65 GGTAAGTTCCTGTGGAGCG 47

```

RESULT 9
US-10-728-131-115/c
Sequence 115, Application US/10728131
Publication No. US20050075303A1
GENERAL INFORMATION:
APPLICANT: Neepert, Michael P.
APPLICANT: McClements, William L.
APPLICANT: Jansen, Kathrin U.
APPLICANT: Schultz, Loren D.
APPLICANT: Chen, Ling
APPLICANT: Wang, Xin-Min
TITLE OF INVENTION: SYNTHETIC HUMAN PAPILLOMAVIRUS GENES
FILE REFERENCE: 20413YCA
CURRENT APPLICATION NUMBER: US/10/728,131
CURRENT FILING DATE: 2003-12-04
PRIORITY FILING DATE: 09/642,405
PRIORITY FILING DATE: 2000-08-21
PRIORITY APPLICATION NUMBER: PCT/US00/22932
PRIORITY FILING DATE: 2000-08-21
PRIORITY APPLICATION NUMBER: 60/210,143
PRIORITY FILING DATE: 2000-06-07
PRIORITY APPLICATION NUMBER: 60/150,728
PRIORITY FILING DATE: 1999-08-25
NUMBER OF SEQ ID NOS: 150
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 115
LENGTH: 95
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Codon-Optimized HPV6 E2 fragment
US-10-728-131-115

```

Query Match	71.0%	Score 14.2;	DB 9;	Length 95;
Best Local Similarity	84.2%	Pred. No. 3.2e+03;		
Matches 16;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;

Qy 2 GGTA⁺GTCAGCGCGGAGCG 20
Db 92 GATCGTTCAGCGCGGTAGCG 74

RESULT 10
US-10-728-131-116
Sequence 116, Application US/10728133A1
Publication No. US20050075303A1
GENERAL INFORMATOR:
APPLICANT: Neepser, Michael P.
APPLICANT: McClements, William L.
APPLICANT: Jansen, Kathrin U.
APPLICANT: Schultz, Loren D.

```

; APPLICANT: Chen, Ling
; TITLE OF INVENTION: SYNTHETIC HUMAN PAPILLOMAVIRUS GENES
; FILE REFERENCE: 20413YCA
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: 09/542,405
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: PCT/US00/22932
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 60/210,143
; PRIOR FILING DATE: 2000-06-07
; PRIOR APPLICATION NUMBER: 60/150,728
; PRIOR FILING DATE: 1999-08-25
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 116
; LENGTH: 96
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Codon-Optimized HPV6 E2 fragment
US-10-728-131-116

Query Match          71.0%; Score 14.2; DB 9; Length 96;
Best Local Similarity 84.2%; Pred. No. 3.2e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 GGTAGTTCAGCGCGGAGCG 20
DB      73 GATCGTTTCAGCGCGGAGCG 91

RESULT 11
US-10-719-956-405220/c
; Sequence 405220, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 659466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 405220
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-405220

Query Match          69.0%; Score 13.8; DB 7; Length 25;
Best Local Similarity 88.2%; Pred. No. 5.7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 GTAGTTCAGCGCGGAGC 19
DB      17 GTAGTTCAGCGCGGAGC 1

RESULT 12
US-10-719-900-224531
; Sequence 224531, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
```

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; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 224531
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-224531

Query Match          69.0%; Score 13.8; DB 8; Length 25;
Best Local Similarity 88.2%; Pred. No. 5.7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 GTAGTTCAGCGCGGAGC 19
DB      6 GTCGTTCAGGAGGAGC 22

RESULT 13
US-10-956-157-187244/c
; Sequence 187244, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: Patent version 3.2
; SEQ ID NO 187244
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-187244

Query Match          69.0%; Score 13.8; DB 9; Length 25;
Best Local Similarity 88.2%; Pred. No. 5.7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GGTAGTTCAGCGCGGAG 18
DB      17 GGTAGTTCAGGAGGAGC 1

RESULT 14
US-11-060-756-179496/c
; Sequence 179496, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: Patent version 3.2
; SEQ ID NO 179496
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-179496

Query Match          69.0%; Score 13.8; DB 10; Length 25;
Best Local Similarity 88.2%; Pred. No. 5.7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GGTAGTTCAGCGCGGAG 18
DB      17 GGTAGTTCAGCGCGGAG 18
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Db 17 GGTAGTTCAGAGCGAGC 1

RESULT 15

US-10-790-273-6
; Sequence 6, Application US/10790273
; Publication No. US20050191710A1
; GENERAL INFORMATION:
; APPLICANT: Hanrahan, John W.
; APPLICANT: Luo, Yishan
; TITLE OF INVENTION: METHOD FOR LABELING A MEMBRANE-LOCALIZED PROTEIN
; FILE REFERENCE: MGU-0027
; CURRENT APPLICATION NUMBER: US/10/790,273
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 57
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide primer
US-10-790-273-6

Query Match 69.0%; Score 13.8; DB 9; Length 57;
Best Local Similarity 88.2%; Pred. No. 5.3e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GTAGTTCAGAGCGAGC 19
|||
Db 22 GTCGTTTCAGAGCGAGC 38

Search completed: December 25, 2005, 04:14:22
Job time : 338.6 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 18:29:07 ; Search time 135.3 Seconds
(without alignments)
76.712 Million cell updates/sec

Title: US-09-296-264-6

Perfect score: 20

Sequence: 1 GGGTAGTCAGCGCGAGCG 20

Scoring table: IDENTITY_NTC

Gapop 10.0 , Gapext 1.0

Searched: 4168288 seqs, 259477437 residues 1608458

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 20

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications NA New:*

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- 2: /cgn2_6/prodata/2/pubpna/US06_NEW_PUB.seq:*
- 3: /cgn2_6/prodata/2/pubpna/US07_NEW_PUB.seq:*
- 4: /cgn2_6/prodata/2/pubpna/US09_NEW_PUB.seq:*
- 5: /cgn2_6/prodata/2/pubpna/US10_NEW_PUB.seq:*
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- 8: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq:*
- 9: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq:*
- 10: /cgn2_6/prodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	13.8	69.0	25	US-11-121-849-39004	Sequence 39004, A
C 2	13.4	67.0	25	US-11-121-849-11305	Sequence 11305, A
C 3	13.2	66.0	21	US-10-770-726-5453	Sequence 5453, Ap
C 4	13.2	66.0	21	US-10-770-726-5454	Sequence 5454, Ap
C 5	13.2	66.0	25	US-11-121-849-247302	Sequence 247302, A
C 6	13.2	66.0	25	US-11-121-849-490840	Sequence 490840, A
C 7	13.2	66.0	25	US-11-121-849-514561	Sequence 514561, A
C 8	13.2	66.0	25	US-11-121-849-191523	Sequence 191523, A
C 9	12.8	64.0	25	US-11-121-849-11984	Sequence 11984, A
C 10	12.8	64.0	25	US-11-121-849-242741	Sequence 242741, A
C 11	12.8	64.0	25	US-11-121-849-332708	Sequence 332708, A
C 12	12.8	64.0	25	US-11-121-849-332709	Sequence 332709, A
C 13	12.8	64.0	25	US-11-121-849-332710	Sequence 332710, A
C 14	12.8	64.0	25	US-11-121-849-488425	Sequence 488425, A
C 15	12.8	64.0	25	US-11-121-849-488425	Sequence 488425, A
C 16	12.6	63.0	25	US-11-121-849-58824	Sequence 58824, A
C 17	12.6	63.0	25	US-11-121-849-58825	Sequence 58825, A
C 18	12.6	63.0	25	US-11-121-849-59759	Sequence 59759, A
C 19	12.6	63.0	25	US-11-121-849-59760	Sequence 59760, A
C 20	12.6	63.0	25	US-11-121-849-360118	Sequence 360118, A
C 21	12.6	63.0	25	US-11-121-849-466071	Sequence 466071, A
C 22	12.6	63.0	25	US-11-121-849-615229	Sequence 615229, A
C 23	12.6	63.0	25	US-11-121-849-629144	Sequence 629144, A

C 24	12.6	63.0	25	US-11-121-849-660189	Sequence 660189, A
C 25	12.4	62.0	25	US-11-121-849-13534	Sequence 13534, A
C 26	12.4	62.0	25	US-11-121-849-358636	Sequence 358636, A
C 27	12.4	62.0	25	US-11-121-849-467927	Sequence 467927, A
C 28	12.2	61.0	25	US-11-121-849-56129	Sequence 56129, A
C 29	12.2	61.0	25	US-11-121-849-176620	Sequence 176620, A
C 30	12.2	61.0	25	US-11-121-849-176621	Sequence 176621, A
C 31	12.2	61.0	25	US-11-121-849-176622	Sequence 176622, A
C 32	12.2	61.0	25	US-11-121-849-176623	Sequence 176623, A
C 33	12.2	61.0	25	US-11-121-849-176624	Sequence 176624, A
C 34	12.2	61.0	25	US-11-121-849-176898	Sequence 176898, A
C 35	12.2	61.0	25	US-11-121-849-176899	Sequence 176899, A
C 36	12.2	61.0	25	US-11-121-849-176900	Sequence 176900, A
C 37	12.2	61.0	25	US-11-121-849-176901	Sequence 176901, A
C 38	12.2	61.0	25	US-11-121-849-268934	Sequence 268934, A
C 39	12.2	61.0	25	US-11-121-849-325562	Sequence 325562, A
C 40	12.2	61.0	25	US-11-121-849-350301	Sequence 350301, A
C 41	12.2	61.0	25	US-11-121-849-653557	Sequence 653557, A
C 42	12.2	61.0	41	US-11-032-236-2	Sequence 2, Appl1
C 43	12	60.0	25	US-11-121-849-731374	Sequence 731374, A
C 44	12	60.0	25	US-11-121-849-241316	Sequence 241316, A
C 45	12	60.0	25	US-11-121-849-529576	Sequence 529576, A

ALIGNMENTS

RESULT 1
US-11-121-849-39004/c
; Sequence 39004, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-39004

Query Match
Best Local Similarity 69.0%; Score 13.8; DB 7; Length 25;
Matches 15; Conservative 0; Pred. No. 5.2e+02;
Mismatch 2; Indels 0; Gaps 0;

Qy 3 GTAGTTCAGCGCGAGC 19
Db 17 GTAGTTCAGCGCGAGC 1

RESULT 2
US-11-121-849-113305/c
; Sequence 113305, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 113305

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; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-849-113305

Query Match
Best Local Similarity 93.3%; Pred. No. 8.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AGTTGCGGCGGAGC 19
DB 16 AGTTGCGCTGGAGC 2

RESULT 3
US-10-770-726-5454/C
; Sequence 5453, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5453
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-770-726-5453

Query Match
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GTAGTTCAGCGCGAGCG 20
DB 21 GTAGATCATCGCGAGCG 4

RESULT 4
US-10-770-726-5454/C
; Sequence 5454, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5454
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi
US-10-770-726-5454

Query Match
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GTAGTTCAGCGCGGAGCG 20
DB 19 GTAGATCATCGCGGAGCG 2

; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-849-247302/C
; Sequence 247302, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 247302
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-849-247302

Query Match
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGSTAGTTCAGCGCGGAG 18
DB 20 GTGTATTTCAGCGCGCAG 3

RESULT 6
US-11-121-849-490840/C
; Sequence 490840, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 490840
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-849-490840

Query Match
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GTAGTTCAGCGCGGAGCG 20
DB 18 GTAGTTCAGCGCGGAGCG 1

RESULT 7
US-11-121-849-514561/C
; Sequence 514561, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
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PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 514561
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-514561

Query Match 66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGTAGTTCAGCGCGGAGC 19
Db 19 GGAGTTCAGCGCGGAGC 2

RESULT 8

US-11-121-849-191523/c
Sequence 191523, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:

APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 191523
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-191523

Query Match 65.0%; Score 13; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GTTCAGCGCGGAGC 18
Db 18 GTTCAGCGCGGAGC 6

RESULT 9

US-11-121-849-11984/c
Sequence 11984, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:

APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 11984
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-11984

Query Match 64.0%; Score 12.8; DB 7; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 AGTTCAGCGCGGAGCG 20
Db 16 ACTTCAGGTGGAGCG 1

RESULT 10

US-11-121-849-242741
Sequence 242741, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:

APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 242741
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-242741

Query Match 64.0%; Score 12.8; DB 7; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TAGTTCAGCGCGGAGC 19
Db 6 TAGTTCAGCGCGGAGC 21

RESULT 11

US-11-121-849-332708/c
Sequence 332708, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:

APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 332708
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-332708

Query Match 64.0%; Score 12.8; DB 7; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TAGTTCAGCGCGGAGC 19
Db 20 TGGTTCAGCGCTGGAGC 5

RESULT 12

US-11-121-849-332709/c
Sequence 332709, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:

APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 332709
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-332709

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FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 332709
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-332709

Query Match      64.0%; Score 12.8; DB 7; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4 TAGTTCAGCGCGGAGC 19
Db      16 TGGTTCAGGCTGAGC 3

RESULT 13
US-11-121-849-332710/c
; Sequence 332710, Application US/11/121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 332710
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-332710

Query Match      64.0%; Score 12.8; DB 7; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4 TAGTTCAGCGCGGAGC 19
Db      16 TGGTTCAGGCTGAGC 1

RESULT 14
US-11-121-849-488425/c
; Sequence 488425, Application US/11/121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 488425
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-488425
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Query Match      64.0%; Score 12.8; DB 7; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4 TAGTTCAGCGCGGAGC 19
Db      16 TAGTTAGAGCGCGGAGC 1

RESULT 15
US-11-121-849-498584
; Sequence 498584, Application US/11/121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 498584
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-498584

Query Match      64.0%; Score 12.8; DB 7; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GGTAGTTCAGCGCGGA 17
Db      4 GGTATTTCAGGCTGGA 19
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Search completed: December 25, 2005, 04:37:03
Job time : 136.3 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 10:28:41 : Search time 582 Seconds
(without alignments)
1953.383 Million cell updates/sec

Title: US-09-296-264-8

Perfect score: 20
Sequence: 1 gtgccagccagcagcagcactg 20

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 1858228

Minimum DB seq length: 20

Maximum DB seq length: 100

Post-processing: Minimum Match 10%

Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ba: *
2: gb_in: *
3: gb_env: *
4: gb_dm: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pr: *
9: gb_ro: *
10: gb_bcs: *
11: gb_ey: *
12: gb_un: *
13: gb_vl: *
14: gb_hlg: *
15: gb_pl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6	BD211665
2	15.4	77.0	50	6	AX430850
3	14.8	74.0	50	6	CQ002433
4	14.2	71.0	42	6	AX231094
5	14.2	71.0	42	6	AX231098
6	14.2	71.0	42	6	AX231555
7	14.2	71.0	42	6	AX232206
8	14.2	71.0	42	6	AX233340
9	14.2	71.0	91	8	HSTINOSX01
10	13.8	69.0	26	6	BD084096
11	13.8	69.0	100	6	CQ000039
12	13.8	69.0	100	6	CQ001129
13	13.6	68.0	30	6	CQ082140
14	13.6	68.0	50	6	CQ008899
15	13.6	68.0	51	6	AR444776
16	13.4	67.0	51	6	AX157921
17	13.4	67.0	51	6	AX157922
18	13.4	67.0	99	10	G34988

c 19	13.4	67.0	100	6	CQ055901
c 20	13.4	67.0	100	6	CQ075146
c 21	13.4	67.0	100	6	CQ106093
c 22	13.4	67.0	100	6	CQ144785
c 23	13.4	67.0	100	6	CQ180232
c 24	13.4	67.0	100	6	CQ204623
c 25	13.4	67.0	100	6	CQ227975
c 26	13.4	67.0	100	6	CQ266129
c 27	13.4	67.0	100	6	CQ303173
c 28	13.4	67.0	100	6	CQ340406
c 29	13.2	66.0	27	6	AX306740
c 30	13.2	66.0	28	6	AX306741
c 31	13.2	66.0	28	6	AR130372
c 32	13.2	66.0	28	6	AR455456
c 33	13.2	66.0	39	6	AX663324
c 34	13.2	66.0	51	6	AX115349
c 35	13.2	66.0	76	6	AR121636
c 36	13.2	66.0	76	6	E55383
c 37	13.2	66.0	90	6	AX306734
c 38	13.2	66.0	100	10	HSA308722
c 39	13	65.0	92	15	ATH525570
c 40	13	65.0	92	15	ATH525987
c 41	13	65.0	92	15	ATH528787
c 42	12.8	64.0	27	6	133657
c 43	12.8	64.0	30	6	158430
c 44	12.8	64.0	31	6	158435
c 45	12.8	64.0	35	6	113710

ALIGNMENTS

RESULT 1
BD211665
LOCUS
DEFINITION Antisense oligonucleotide sequence of neuropilin and method of using the same for controlling cell proliferation.
ACCESSION BD211665.1 GI:33021435
VERSION BD211665
KEYWORDS JP 2002512793-A/8.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS Wright,J.A., Young,A.H. and Lee,Y.S.
TITLE Antisense oligonucleotide sequence of neuropilin and method of using the same for controlling cell proliferation
JOURNAL Patent:JP 2002512793-A 8 08-MAY-2002;
GENSENSE TECHNOLOGIES INC
OS Homo sapiens (human)
PN JP 2002512793-A/8
PD 08-MAY-2002
PF 23-APR-1999 JP 2000545999
PR 23-APR-1998 US 60/082791
PI JIM A WRIGHT,ALPING H YOUNG,YOON S LEE
PC C12N15/09,A61K31/711,A61K48/00,A61P35/00,C12N15/00 CC
Antisense oligonucleotide sequence of neuropilin and method of using the same for controlling cell proliferation
FH key
FT source
CC same for controlling cell proliferation
FH key
FT source

FEATURES

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Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 83;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCAGCCAGAGCGACTG 20
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Db 1 GTGCCAGCCAGAGCGACTG 20

RESULT 2
AX430850/c
LOCUS AX430850 50 bp RNA linear PAT 28-JUN-2002
DEFINITION Sequence 4 from Patent WO0240994.
ACCESSION AX430850
VERSION AX430850.1 GI:21655915
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
AUTHORS Meshorer, E., Shoham, S., Soreq, H. and Sklan, E.
TITLE System and method for assaying drugs
JOURNAL Patent: WO 0240994-A 4 23-MAY-2002;
YISSUM RES DEV CO (IL)
FEATURES
source 1..50
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

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Query Match 77.0%; Score 15.4; DB 6; Length 50;
Best Local Similarity 94.1%; Pred. No. 1.4e+04;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGCCCGAGCCAGAGCGAC 18
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Db 50 TGCCCGAGCCAGAGCGAC 34

RESULT 3
CQ002433/c
LOCUS CQ002433 50 bp DNA linear PAT 16-JAN-2004
DEFINITION Sequence 1073 from Patent WO0147944.
ACCESSION CQ002433
VERSION CQ002433.1 GI:41009065
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
AUTHORS Shinkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
JOURNAL methods of use thereof
PATENT: WO 0147944-A 1073 05-JUL-2001;
Curagen Corporation (US)
FEATURES
source 1..50
/organism="Homo sapiens"
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/note="Nucleotide deleted between bases 25 and 26
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Query Match 74.0%; Score 14.8; DB 6; Length 50;
Best Local Similarity 88.9%; Pred. No. 2.6e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGCCCGAGCCAGAGCGACT 19

Db 49 GTGCCAGCCAGCGCCCT 32
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RESULT 4
AX231094 42 bp DNA linear PAT 11-SEP-2001
LOCUS AX231094
DEFINITION Sequence 490 from Patent WO0162787.
ACCESSION AX231094
VERSION AX231094.1 GI:15592450
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
AUTHORS Herath, H.M., Parekh, R.B., Rohlf, C.O., Terrett, J.A. and Tyson, K.L.
TITLE Diagnosis and treatment of bipolar affective disorder
JOURNAL Patent: WO 0162787-A 490 30-AUG-2001;
Oxford Glycosciences (UK) Limited (GB)
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source 1..42
/organism="Homo sapiens"
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/db_xref="GI:15592451"
/translation="EWVAIESDSVQPPV"

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Best Local Similarity 84.2%; Pred. No. 5.2e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGCCAGCCAGAGCGACT 19
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Db 7 GTGCCAGCCAGAGCGACT 25

RESULT 5
AX231098 42 bp DNA linear PAT 11-SEP-2001
LOCUS AX231098
DEFINITION Sequence 494 from Patent WO0162787.
ACCESSION AX231098
VERSION AX231098.1 GI:15592454
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
AUTHORS Herath, H.M., Parekh, R.B., Rohlf, C.O., Terrett, J.A. and Tyson, K.L.
TITLE Diagnosis and treatment of bipolar affective disorder
JOURNAL Patent: WO 0162787-A 494 30-AUG-2001;
Oxford Glycosciences (UK) Limited (GB)
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/organism="Homo sapiens"
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Best Local Similarity 84.2%; Pred. No. 5.2e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGCCAGCCAGAGCGACT 19
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Db 7 GTGCCATCGAGAGCGACT 25

RESULT 6
AX231555 42 bp DNA linear PAT 11-SEP-2001
LOCUS Sequence 453 from Patent WO0163294.
ACCESSION AX231555
VERSION AX231555.1 GI:15592461
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE
1 Herath,H.M., Parekh,R.B. and Rohlf,C.
AUTHORS Diagnosis of bipolar affective disorder (bad) and unipolar
TITLE depression
JOURNAL Patent: WO 0163294-A 453 30-AUG-2001;
Oxford Glycosciences (UK) Limited (GB)
FEATURES
source location/Qualifiers
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/organism="Homo sapiens"
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/note="unnamed protein product"
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/translation="EMVAIESDSVQVPV"

ORIGIN
Query Match 71.0%; Score 14.2; DB 6; Length 42;
Best Local Similarity 84.2%; Pred. No. 5.2e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GTGCCAGCCAGAGCGACT 19
Db 7 GTGCCATCGAGAGCGACT 25

RESULT 7
AX232206 42 bp DNA linear PAT 11-SEP-2001
LOCUS Sequence 484 from Patent WO0163293.
ACCESSION AX232206
VERSION AX232206.1 GI:15592539
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE
1 Herath,M.A., Parekh,R.B. and Rohlf,C.O.
AUTHORS Diagnosis and treatment of schizophrenia
TITLE Patent: WO 0163293-A 484 30-AUG-2001;
JOURNAL Oxford Glycosciences (UK) Limited (GB)
FEATURES
source location/Qualifiers
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/translation="EMVAIESDSVQVPV"

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Query Match 71.0%; Score 14.2; DB 6; Length 42;
Best Local Similarity 84.2%; Pred. No. 5.2e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GTGCCAGCCAGAGCGACT 19
Db 7 GTGCCATCGAGAGCGACT 25

RESULT 8
AX233340 42 bp DNA linear PAT 11-SEP-2001
LOCUS Sequence 664 from Patent WO0162785.
ACCESSION AX233340
VERSION AX233340.1 GI:15592679
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE
1 Herath,H.M., Parekh,R.B., Rohlf,C.C., Terrett,J.A. and Tyson,K.L.
AUTHORS Protein and gene and their use for diagnosis and treatment of
TITLE schizophrenia
JOURNAL Patent: WO 0162785-A 664 30-AUG-2001;
Oxford Glycosciences (UK) Limited (GB)
FEATURES
source location/Qualifiers
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/translation="EMVAIESDSVQVPV"

ORIGIN
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Best Local Similarity 84.2%; Pred. No. 5.2e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GTGCCAGCCAGAGCGACT 19
Db 7 GTGCCATCGAGAGCGACT 25

RESULT 9
HSINOSX01 91 bp DNA linear PRI 27-JAN-1998
LOCUS Human inducible nitric oxide synthase (iNOS) pseudogene, exon 1.
DEFINITION U65689
ACCESSION U65689
VERSION U65689.1 GI:1621317
KEYWORDS
SOURCE 1 of 11
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE
1 (bases 1 to 91)
AUTHORS Park,C.S., Park,R., Lee,H.S., Lee,H.Y. and Krishna,G.
TITLE Direct Submision
JOURNAL Submitted (31-JUL-1996) Section of Chemical Pharmacology, National
Institutes of Health, Bethesda, MD 20892, USA
2 (bases 1 to 91)
AUTHORS Park,C.S., Lee,H.S., Lee,H.Y. and Krishna,G.
TITLE An unprocessed pseudogene of inducible nitric oxide synthase gene
JOURNAL in human
PUBMED Nitric Oxide 1 (4), 294-300 (1997)
9441901

FEATURES
source
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Query Match
Best Local Similarity 84.2%; Pred. No. 5e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGCCAGCCAGCGACT 19
DB 34 GTGCCAGCCAGCGTCT 52

RESULT 10
LOCUS BD084096 26 bp DNA linear PAT 27-AUG-2002
DEFINITION Human pancreatic cancer antigen.
ACCESSION BD084096.1 GI:22629706
VERSION JP 2001340081-A/3.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 26)
AUTHORS Kawakami,H., Akada,M. and Fujita,T.
TITLE Human pancreatic cancer antigen
JOURNAL Patent: JP 2001340081-A 3 11-DEC-2001;
KEIO UNIVERSITY
COMMENT OS Artificial Sequence
PN JP 2001340081-A/3
PD 11-DEC-2001
PF 31-MAY-2000 JP 2000161930
PI HIROSHI KAWAKAMI, MASANORI AKADA, TOMONOBU FUJITA PC
C12N15/00,A01K67/027,A61K38/00,A61K39/395,A61K45/00,A61P35/00, PC
C07K14/00,
PC C07K14/47,C07K16/18,C07K19/00,C12N1/15,C12N1/19,C12N1/21 PC
,C12N5/10,C12Q1/02,
PC C12Q1/68,G01N33/15,G01N33/50,G01N33/53,G01N33/577//C12P21/02,
PC C12P21/08,
PC (C12N15/09,C12R1:91),(C12N5/10,C12R1:91),(C12P21/02,C12R1:91),
PC C12N15/00,
PC A61K37/02,C12N5/00,(C12N15/00,C12R1:91),(C12N5/00,C12R1:91) CC
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Location/Qualifiers
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location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32630"

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QY 2 TGCCAGCCAGCGAC 18
DB 1 TGCCAGCCAGAGATAC 17

RESULT 11
LOCUS CQ000039/c 100 bp DNA linear PAT 16-JUN-2004
DEFINITION Sequence 11501 from Patent EP1260592.
ACCESSION CQ000039
VERSION CQ000039.1 GI:41006413
KEYWORDS
SOURCE Escherichia coli
ORGANISM Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
REFERENCE 1
AUTHORS Donner,H., Drescher,B., Huber,A. and Weber,J.
TITLE Biochip
JOURNAL Patent: EP 1260592-A 11501 27-NOV-2002;
MWG - Biotech AG (DE)
FEATURES
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/organism="Escherichia coli"
/mol_type="unassigned DNA"
/db_xref="taxon:562"
/note="ctcd b0625 U00096 complement(656778_657161)"

ORIGIN
Query Match
Best Local Similarity 69.0%; Score 13.8; DB 6; Length 100;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGCCAGCCAGCGAC 18
DB 70 TGCCAGCCAGCGC 54

RESULT 12
LOCUS CQ001129/c 100 bp DNA linear PAT 16-JUN-2004
DEFINITION Sequence 12591 from Patent EP1260592.
ACCESSION CQ001129
VERSION CQ001129.1 GI:41007767
KEYWORDS
SOURCE Escherichia coli
ORGANISM Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
REFERENCE 1
AUTHORS Donner,H., Drescher,B., Huber,A. and Weber,J.
TITLE Biochip
JOURNAL Patent: EP 1260592-A 12591 27-NOV-2002;
MWG - Biotech AG (DE)
FEATURES
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/organism="Escherichia coli"
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/db_xref="taxon:562"
/note="mtr b4352 U00096 4584519_4585433"

ORIGIN
Query Match
Best Local Similarity 69.0%; Score 13.8; DB 6; Length 100;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGCCAGCCAGCGAC 18
DB 36 TGCCAGCCAGTCCGC 20

RESULT 13
LOCUS CQ821440/c 30 bp DNA linear PAT 21-JUN-2004
DEFINITION Sequence 11 from Patent EP1428875.
ACCESSION CQ821440
VERSION CQ821440.1 GI:49019139
KEYWORDS

SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE
AUTHORS 1 Boutin, P., Dubois, S., Dina, C. and Froguet, P.
TITLE Method of diagnosis of obesity
JOURNAL Patent: EP 1428875-A 11 16-JUN-2004;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)

FEATURES
source 1.30
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: Primer to amplify SNP 1.6 kb"

ORIGIN

Query Match 68.0%; Score 13.6; DB 6; Length 30;
Best Local Similarity 80.0%; Pred. No. 1e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GTGCCAGCCAGAGCGACTG 20
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Db 29 GCGCCTGGCCAGAGCGCCTG 10

RESULT 14
CQ008899/c 50 bp DNA linear PAT 16-JAN-2004
LOCUS CQ008899
DEFINITION Sequence 7539 from Patent WO0147944.
ACCESSION CQ008899
VERSION CQ008899.1 GI:41015621
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE
AUTHORS 1 Shinkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0147944-A 7539 05-JUL-2001;
Curagen Corporation (US)

FEATURES
source 1.50
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/note="Nucleotide deleted between bases 25 and 26
Accession number c944034179"

ORIGIN

Query Match 68.0%; Score 13.6; DB 6; Length 50;
Best Local Similarity 80.0%; Pred. No. 1e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GTGCCAGCCAGAGCGACTG 20
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Db 27 GTGCCAGCCAGCGCTAGT 8

RESULT 15
AR444776 51 bp DNA linear PAT 20-FEB-2004
LOCUS AR444776/c
DEFINITION Sequence 1187 from patent US 6670464.
ACCESSION AR444776
VERSION AR444776.1 GI:42672555
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 51)
AUTHORS Shinkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: US 6670464-A 1187 30-DEC-2003;
Curagen Corporation; New Haven, CT

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/organism="unknown"
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ORIGIN

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Best Local Similarity 80.0%; Pred. No. 1e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GTGCCAGCCAGAGCGACTG 20
| | | | | | | | | | | | | | | | | | | | | |
Db 33 GTGCCAGCCAGAGCGACTG 14

Search completed: December 24, 2005, 14:06:12
Job time : 585 secs

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OM nucleic - nucleic search, using bw model

Run on: December 24, 2005, 01:41:40 : Search time 171.4 Seconds
(without alignments)
777.677 Million cell updates/sec

Title: US-09-296-264-8

Perfect score: 20

Sequence: 1 gtgccagccagagcagctg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 3390896

Minimum DB seq length: 20

Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

N_Geneseq_21:*

- 1: geneeqn19808:*
- 2: geneeqn19908:*
- 3: geneeqn20008:*
- 4: geneeqn20018:*
- 5: geneeqn20028:*
- 6: geneeqn20038:*
- 7: geneeqn20048:*
- 8: geneeqn20058:*
- 9: geneeqn20068:*
- 10: geneeqn20078:*
- 11: geneeqn20088:*
- 12: geneeqn20098:*
- 13: geneeqn20108:*
- 14: geneeqn20118:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3	AA231438 Human neu
2	20	100.0	20	9	ADA74690 GTI3608 a
3	15.4	77.0	50	6	ABK90054 Human ace
4	14.8	74.0	50	4	AA127865 Human SNP
5	14.2	71.0	42	4	AA12579 DNA encod
6	14.2	71.0	42	4	AA542471 Schizophr
7	14.2	71.0	42	4	AA543073 BSR AA526
8	14.2	71.0	42	12	ADO79046 Schizophr
9	14	70.0	41	12	ADH05972 Gene poly
10	14	70.0	41	12	ADH91759 1-beta-me
11	14	70.0	80	2	AAQ11150 Probe GTR
12	13.8	69.0	26	6	ABA97968 Human pan
13	13.8	69.0	36	8	AA155205 Pshl-Ffl
14	13.8	69.0	71	14	ADV87091 Non-speci
15	13.8	69.0	100	8	ACD80225 E. coli K
16	13.8	69.0	100	8	ACD81315 E. coli K
17	13.6	68.0	21	13	ADU43644 Knock-dow
18	13.6	68.0	29	3	AAA47678 Primer (S
19	13.6	68.0	30	12	ADP27364 Human 5'

C	20	13.6	68.0	31	2	AA38710 Human gen
C	21	13.6	68.0	50	4	AA134331 Human SNP
C	22	13.6	68.0	51	3	AA177504 Human typ
C	23	13.4	67.0	51	4	AA174309 Human b11
C	24	13.4	67.0	51	4	AA174308 Human b11
C	25	13.4	67.0	100	4	AA121013 Probe #10
C	26	13.4	67.0	100	4	ABA66085 Human foe
C	27	13.4	67.0	100	4	AA146266 Probe #14
C	28	13.4	67.0	100	4	ABA48205 Human bre
C	29	13.4	67.0	100	4	ABA33162 Probe #11
C	30	13.4	67.0	100	4	AAK40250 Human bon
C	31	13.4	67.0	100	4	AAK4509 Human bra
C	32	13.4	67.0	100	4	AB339824 Human 11v
C	33	13.4	67.0	100	5	AA106730 Probe #67
C	34	13.4	67.0	100	6	AB314287 Human gen
C	35	13.2	66.0	25	9	AC135993 Human m1c
C	36	13.2	66.0	27	6	ABK16832 Human pro
C	37	13.2	66.0	27	6	ABK16831 Human pro
C	38	13.2	66.0	27	12	ADG82567 Human end
C	39	13.2	66.0	28	2	AA748247 HSV thym1
C	40	13.2	66.0	28	4	AA502243 Cytosolic
C	41	13.2	66.0	28	4	AA502251 Reverse P
C	42	13.2	66.0	32	14	ADX69401 Bifidobac
C	43	13.2	66.0	33	6	ABA9259 Human end
C	44	13.2	66.0	34	3	AAA64022 PCR prime
C	45	13.2	66.0	34	3	AAA64024 PCR prime

ALIGNMENTS

RESULT 1	AA231438	AA231438 standard; DNA; 20 BP.
ID	AA231438;	
XX	AA231438;	
DT	07-FEB-2000	(first entry)
XX		
DE	Human neuropilin mRNA specific antisense oligo GTI3608.	
XX		
KW	Neuropilin; human; growth; metastasis; tumor; neovascularisation; cancer;	
KW	papilloma; diabetic retinopathy; antisense; ss.	
OS	Synthetic.	
XX		
OS	Homo sapiens.	
XX		
PN	W09955855-A2.	
XX		
PD	04-NOV-1999.	
XX		
PF	23-APR-1999;	99WO-CA000324.
XX		
PR	23-APR-1998;	98US-0082791P.
XX		
PA	(GENB-) GENESENSE TECHNOLOGIES INC.	
XX		
PI	Wright JA, Young AH, Lee YS;	
XX		
DR	WPI; 2000-023357/02.	
XX		
PT	Antisense oligonucleotides that inhibit neuropilin expression, useful for	
PT	treating cancer.	
XX		
PS	Claim 4; Page 16; 57pp; English.	
XX		
CC	Sequences AA231431-460 represent antisense oligonucleotides which inhibit	
CC	human neuropilin expression. The antisense oligonucleotides can be used	
CC	to inhibit the growth or metastasis of a mammalian tumor and inhibit	
CC	neovascularisation. The oligonucleotides may be used to treat various	
CC	forms of cancers or tumors, such as sarcomas, melanomas, adenomas,	
CC	carcinomas of solid tissue, hypoxic tumors, squamous cell carcinomas of	
CC	the mouth, throat, larynx and lung, genitourinary cancers such as	

```
CC cervical and bladder cancer, hematopoietic cancers, colon cancer, breast
CC cancer, pancreatic cancer, renal cancer, brain cancer, skin cancer, liver
CC cancer, head and neck cancers, and nervous system cancers, as well as
CC benign lesions such as papillomas. The methods may be used to treat
CC neurovascularisation disorders such as diabetic retinopathy, and
CC retinopathy of prematurity and age related macular degeneration
XX
SQ Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGCCAGCCAGAGCACTG 20
Db 1 GTGCCAGCCAGAGCACTG 20
RESULT 2
ADA74690
ID ADA74690 standard; DNA; 20 BP.
XX
AC ADA74690;
XX
DT 20-NOV-2003 (first entry)
XX
DE GT13608 antisense oligonucleotide targeted to human neuropilin mRNA.
XX
KW neuropilin; VEGFR15R; vascular endothelial growth factor receptor;
KW cytoskeletal; growth; tumour metastasis; angiogenesis; gene therapy;
KW GT13608; antisense; human; ss.
XX
OS Homo sapiens.
XX
PN US2003083274-A1.
XX
PD 01-MAY-2003.
XX
PF 22-APR-1999; 99US-00296264.
XX
PR 23-APR-1998; 98US-0082791P.
XX
PA (WRIGHT) WRIGHT J A.
XX PA (YOUNG) YOUNG A H.
XX PA (LEEY/) LEE Y S.
XX
PI Wright JA, Young AH, Lee YS;
XX
DR WPI; 2003-576622/54.
XX
PT New antisense oligonucleotide that inhibits neuropilin expression, useful
PT for inhibiting growth of mammalian tumor or inhibiting metastasis of a
PT mammalian tumor.
XX
PS Claim 1; Page 5; 27pp; English.
XX
CC The invention relates to a novel antisense oligonucleotide that inhibits
CC the expression of neuropilin, also known as VEGFR15R (vascular
CC endothelial growth factor receptor). The oligonucleotide of the invention
CC demonstrates cytostatic activity and may be useful for inhibiting the
CC growth or metastasis of a mammalian tumour and to inhibit angiogenesis in
CC mammals. Furthermore, the oligonucleotide may be utilised during gene
CC therapy. The current sequence is that of the GT13608 antisense
CC oligonucleotide of the invention which is targeted to human neuropilin
CC mRNA.
XX
SQ Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGCCAGCCAGAGCACTG 20
```

```
Db 1 GTGCCAGCCAGAGCACTG 20
RESULT 3
ABK90054/c
ID ABK90054 standard; RNA; 50 BP.
XX
AC ABK90054;
XX
DT 05-NOV-2002 (first entry)
XX
DE Human acetylcholinesterase (ACHE) mRNA probe.
XX
KW Nervous system; drug assay; acetylcholinesterase; AChE; brain;
KW isoform variance; AChE blocker; muscarinic receptor; M1; M2;
KW pyridostigmine; muscarinic receptor blocker; scopolamine;
KW M1 receptor blocker; pirenzepine; anxiety; post-traumatic stress;
KW Alzheimer's disease; muscle malfunctioning; neurodegenerative disorder;
KW xenobiotic damage; panic; neuromuscular disorder; Parkinson's disease;
KW Huntington's chorea; muscle fatigue; multiple chemical sensitivity;
KW autism; multiple sclerosis; Sjogren's disease; human; probe; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..50
FT /tag= b
FT /mod_base= OTHER
FT /note= "OTHER= 2-O-methylated"
FT modified_base 1
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= labelled with 5'-biotin"
XX
PN WO200240994-A2.
XX
PD 23-MAY-2002.
XX
PF 14-NOV-2001; 2001WO-11001051.
XX
PR 14-NOV-2000; 2000US-0247970P.
XX
PA (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
XX
PI Soreq H, Meshorer E, Sklan E, Shoham S;
XX
DR WPI; 2002-490152/52.
XX
PT Evaluating effect of drugs on nervous system by comparing effect of drug
PT on acetylcholinesterase, AChE activity in brain of test animal following
PT challenge by AChE blocker and comparing it with control group.
XX
PS Example; Page 55; 114pp; English.
XX
CC The present invention relates to a method and system for evaluating an
CC effect on the nervous system of a test drug. The method comprises
CC comparing the effect of the drug on acetylcholinesterase (AChE) catalytic
CC activity or isoform variance in a brain of a test animal following a
CC challenge by an AChE blocker or a blocker of AChE and muscarinic
CC receptors M1 and M2 (e.g. pyridostigmine) and comparing this effect with
CC that of a known agent, preferably a non-selective muscarinic receptor
CC blocker (e.g. scopolamine) or a specific M1 receptor blocker (e.g.
CC pirenzepine). The method is useful for evaluating an effect on the
CC nervous system of a test drug, including drugs for the treatment of
CC anxiety conditions, post-traumatic stress, Alzheimer's disease, muscle
CC malfunctioning, neurodegenerative disorders, damage resulting from
CC exposure to xenobiotics, panic, neuromuscular disorders, Parkinson's
CC disease, Huntington's chorea, muscle fatigue, multiple chemical
CC sensitivity, autism, multiple sclerosis and Sjogren's disease. The
CC present sequence represents a probe for human AChE mRNA
XX
SQ Sequence 50 BP; 5 A; 17 C; 16 G; 0 T; 12 U; 0 Other;
```


Query Match 77.0%; Score 15.4; DB 6; Length 50;
Best Local Similarity 94.1%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGCCGAGCCGAGCGAC 18
Db 50 TCCCGAGCCGAGCGAC 34

RESULT 4
AAL27865/c
ID AAL27865 standard; DNA; 50 BP.

XX AAL27865;
AC
XX
XX 24-JAN-2002 (first entry)
DE Human SNP oligonucleotide #1073.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
XX neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
XX amyloid protein; angiotensin; apoptosis related protein; cadherin;
XX cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
XX complement related protein; cytochrome; kinase; cytokine; interferon;
XX interleukin; G-protein coupled receptor; thioesterase; inflammation;
XX multifactorial disease; autoimmune disease; infection;
XX nervous system disease; ss.

XX Homo sapiens.
PN WO200147944-A2.

XX 05-JUL-2001.
XX
XX 28-DEC-2000; 2000WO-US035498.
XX
XX 28-DEC-1999; 99US-0173419P.
XX 27-DEC-2000; 2000US-0017341S.

XX (CURA-) CURAGEN CORP.

XX Shinkets RA, Leach M;

XX WPI; 2001-465210/50.

XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
XX oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
XX autoimmune diseases and infections.

XX Claim 1; Page 1687; 4143pp; English.

XX The present invention relates to oligonucleotides encoding polymorphic
XX variants of proteins related to amylases, amyloid protein, angiotensin,
XX apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
XX histones, kinases, colony stimulating factors, complement related
XX proteins, cytochromes, kinases, cytokines, interferons, interleukins, G-
XX protein coupled receptors and thioesterases. The present sequence is one
XX such oligonucleotide. The oligonucleotides and the peptides encoded by
XX them may be used in the prevention, diagnosis and treatment of diseases
XX associated with inappropriate expression of the proteins listed above.
XX Disorders that may be prevented, diagnosed and/or treated include
XX multifactorial diseases with a genetic component, such as autoimmune
XX diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
XX systemic lupus erythematosus and Grave's disease), inflammation, cancer
XX (e.g. cancers of the bladder, brain, breast, colon and kidney,
XX leukaemia), diseases of the nervous system and an infection of pathogenic
XX organisms

XX Sequence 50 BP; 3 A; 14 C; 24 G; 9 T; 0 U; 0 Other;

Query Match 74.0%; Score 14.8; DB 4; Length 50;
Best Local Similarity 88.9%; Pred. No. 4.8e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGCCGAGCCGAGCGACT 19
Db 49 TGCCGAGCCGAGCGCCT 32

RESULT 5
AAS12579
ID AAS12579 standard; DNA; 42 BP.

XX AAS12579;
AC
XX

XX 03-JAN-2002 (first entry)
DT

XX DNA encoding peptide sequence #1 identified from DPI-45 and DPI-213.

XX Human; depression associated protein isoform; tryptic digest peptide;
XX DPI; cerebrospinal fluid; CSF; BAD; bipolar affective disorder;
XX neuropsychiatric disorder; bipolar mood disorder; neuroleptic; DPI-213;
XX manic-depressive illness; schizoaffective disorder; DPI-45; ds.

XX Homo sapiens.

XX Key Location/Qualifiers
XX CDS 1..42
XX FT /*tag= a
XX FT /product= "Peptide sequence #1 from DPI-45 and DPI-213"
XX FT /note= "This sequence lacks both start and stop codons"

XX WO200162787-A1.

XX 30-AUG-2001.

XX 23-FEB-2001; 2001WO-GB000786.

XX 24-FEB-2000; 2000GB-00004412.

XX 08-DEC-2000; 2000GB-00030050.

XX 12-DEC-2000; 2000US-0254830P.

XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX Herath HMC, Parekh RB, Rohlf C, Terrett JA, Tyson KL;

XX WPI; 2001-570626/64.

XX P-PSDB; AAU28402.

XX Novel nucleic acid encoding a protein associated with bipolar affective
XX disorder, which is used for diagnosis, prophylaxis and therapy of
XX neuropsychiatric disorders, such as bipolar affective disorder.

XX Claim 1; Page 145; 153pp; English.

XX The present invention relates to the identification of depression
XX associated protein isoforms (DPIs), particularly the tryptic digest
XX peptides of these proteins. Some of the DPIs (AAU28404-AAU28625)
XX described are decreased in the cerebrospinal fluid (CSF) of BAD (bipolar
XX affective disorder) subjects, whilst other DPIs (AAU28626-AAU28887) are
XX increased in BAD subjects. Also described are peptide sequences
XX identified from DPI-45 and DPI-213 and the nucleic acid sequences they are
XX encoded by. The sequences of the invention are useful for clinical
XX screening, diagnosis, prognosis, therapy and prophylaxis of
XX neuropsychiatric disorders e.g. BAD (also known as bipolar mood disorder,
XX BP), manic-depressive illnesses, attention deficit disorders,
XX schizoaffective disorders, and unipolar affective disorders. The present
XX DNA sequence encodes for peptide sequence #1 identified from DPI-45 and
XX DPI-213

XX Sequence 42 BP; 6 A; 12 C; 15 G; 9 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 4; Length 42;
Best Local Similarity 84.2%; Pred. No. 8.8e+03;

Qy	Matches	16;	Conservative	0;	Mismatches	3;	Indels	0;	Gaps	0;
1	GTGCCACCGCAGAGCACT	19								
Db	7	GTGGCCATCGACGAGCACT	25							
RESULT 6										
AA542471										
ID	AA542471	standard;	DNA;	42	BP.					
XX	AA542471;									
AC	18-DEC-2001	(first entry)								
DT										
XX										
XX	Schizophrenia-Associated Protein Isoform (SPI) 238/240 peptide DNA #1.									
DE										
XX	Schizophrenia-associated protein isoform; SPI; SPI-206; SPI-238; SPI-240;									
KM	neuroleptic; gene therapy; cerebrospinal fluid; serum; plasma; ds.									
XX										
OS	Homo sapiens.									
XX	WO200162785-A2.									
PN	30-AUG-2001.									
PD										
XX	23-FEB-2001; 2001WO-GB000792.									
PF										
XX	24-FEB-2000; 2000GB-00004415.									
PR	28-DEC-2000; 2000US-00750395.									
XX	(OXFO-) OXFORD GLYCOSCIENCES UK LTD.									
PA										
XX	Herath HMC, Parekh RB, Rohlf C, Terrett JA, Tyson KL;									
PI										
XX	WPI; 2001-570624/64.									
DR	P-PSDB; AAU25420.									
XX										
PT	New schizophrenia associated protein isoforms and encoding nucleic acid									
PT	molecules, useful for treatment, diagnosis and prognosis of schizophrenia									
PT	and screening for potential drugs for treatment and new drug targets.									
XX										
PS	Disclosure; Page 80; 148BP; English.									
XX										
XX	The sequence represents DNA encoding a schizophrenia-associated protein									
CC	isoform (SPI). These protein isoforms, e.g. SPI-206, SPI-238 and SPI-240									
CC	are detectable in cerebrospinal fluid, serum or plasma and are useful									
CC	markers of schizophrenia. The sequences can be used for treatment and									
CC	diagnosis of schizophrenia, screening, prognosis, monitoring the results									
CC	of therapy, identifying patients most likely to respond to a particular									
CC	therapy and identification of new targets for drug treatment. SPI DNA is									
CC	useful as a nucleic acid probe to detect the presence of nucleic acids or									
CC	SPI									
XX										
XX	Sequence 42 BP; 6 A; 12 C; 15 G; 9 T; 0 U; 0 Other;									
Qy										
Query Match		71.0%;	Score 14.2;	DB 4;	Length 42;					
Best Local Similarity		84.2%;	Pred. No. 8	8e+03;						
Matches	16;	Conservative	0;	Mismatches	3;	Indels	0;	Gaps	0;	
1	GTGCCACCGCAGAGCACT	19								
7	GTGGCCATCGACGAGCACT	25								
RESULT 7										
AA543073										
ID	AA543073	standard;	DNA;	42	BP.					
XX	AA543073;									
AC										
XX										
DT	18-DEC-2001	(first entry)								

DE	EST AAS26679/AI589129 encoding Peptide #1.
XX	
XX	Human; Bipolar Affective Disorder; BAD; Depression-Associated feature;
KW	DP; Depression-associated protein isoform; DPl; Cerebro-spinal fluid;
KM	CSF; antidepressant; antimanic; nootropic; tranquiliser; neuroleptic;
KW	attention deficient disorder; schizoaffective disorder; AAS26679; ss;
KX	unipolar affective disorder; EST; expressed sequence tag; AI589129.
OS	Homo sapiens.
XX	
PN	WO200163294-A2.
XX	
PD	30-AUG-2001.
XX	
PF	23-FEB-2001; 2001WO-GB000791.
XX	
PR	24-FEB-2000; 2000GB-00004412.
XX	
PR	08-DEC-2000; 2000GB-00030050.
PR	12-DEC-2000; 2000US-0254830P.
XX	
PA	(OXFO-) OXFORD GLYSCSCIENCES UK LTD.
XX	
PI	Herath HMAc, Parekh RB, Rohlf C;
DR	WPI; 2001-582081/65.
XX	P-PBDB; AAU26555.
PT	Preparation for diagnosing or treating bipolar affected disorder (BAD) or
PT	unipolar depression, or for screening for modulators, comprises a BAD-
PT	associated protein isoform.
XX	
PS	Disclosure; Page 74; 163pp; English.
XX	
CC	The invention relates to a preparation comprising an isolated Bipolar
CC	Affected Disorder (BAD)-Associated Protein Isoform (DPIs). The DPI's are
CC	used to screen, diagnose or prognose of BAD or unipolar depression,
CC	determine the stage or severity of BAD or unipolar depression, identify a
CC	subject at risk of developing BAD or unipolar depression, or monitor the
CC	effect of therapy in a subject. They are also used to screen for or
CC	identify agents that interact with a DPI. These agents, antibodies
CC	against the DPIs, and nucleic acids encoding the DPIs are used to treat
CC	or prevent BAD or unipolar depression. Diseases that can be treated are
CC	attention deficit disorder, a schizoaffective disorder, a bipolar or a
CC	unipolar affective disorder. The DPIs are used in proteomics. The
CC	proteomic approach of using DPIs for screening, diagnosis or prognosis of
CC	BAD or unipolar depression overcomes the problems of using gene
CC	expression analysis, such as not being able to obtain central nervous
CC	system (CNS) tissue from a living patient under normal circumstances. The
CC	present sequence is part of a PCR fragment generated from two EST
CC	(expressed sequence tags) sequences AAS26679 and AI589129, which express
DIPs	
XX	
SQ	Sequence 42 BP; 6 A; 12 C; 15 G; 9 T; 0 U; 0 Other;
XX	
Query Match	71.0%; Score 14.2; DB 4; Length 42;
Best Local Similarity	84.2%; Pred. No. 8.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0.	
QY	1 GTGCCAGCGGAGCGACT 19
Db	7 GTGCCATCGAGGCGACT 25
RESULT 8	
ID ADO79046	ADO79046 standard; DNA; 42 BP.
AC ADO79046;	
DT 26-AUG-2004	(first entry)
XX Schizophrenia-Associated Protein Isoform (SPI) DNA seqid 664.	
XX	

KW neuroleptic; Schizophrenia; immunospecific binding;
 KW Schizophrenia-Associated Protein Isoform; SPI; schizophrenia screening;
 KW Schizophrenia diagnosis; schizophrenia prognosis;
 KW Schizophrenia treatment; drug development; cerebrospinal fluid; human;
 ds.
 XX
 OS Homo sapiens.
 XX
 PN US2004110938-A1.
 XX
 PD 10-JUN-2004.
 XX
 PF 23-FEB-2001; 2001US-00791377.
 XX
 PR 24-FEB-2000; 2000GB-00044156.
 XX
 PR 28-DEC-2000; 2000US-00750395.
 XX
 PA (PARE/) PAREKH R B.
 PA (HERA/) CHANDRASIRI HERATH H M A.
 PA (ROHL/) ROHLFF C.
 PA (TERR/) TERRETT J A.
 PA (TYSON/) TYSON K L.
 XX
 PI Parekh RB, Chandrasiri Herath HMA, Rohlf C, Terrett JA, Tyson KL;
 XX
 DR WPI: 2004-440403/41.
 XX
 DR P-PSDB; ADO79047.
 XX
 PT New isolated nucleic acid molecule, useful for diagnosing Schizophrenia,
 PT for monitoring the effectiveness of Schizophrenia treatment or for
 PT screening agents for treating Schizophrenia.
 XX
 PS Disclosure; SEQ ID NO 664; 170bp; English.
 XX
 CC The invention describes an isolated nucleic acid molecule (I) that
 CC hybridizes to two short nucleic acid sequences and the 1515 amino acid
 CC sequence fully defined in the specification. Also described are: a
 CC preparation comprising an isolated peptide coded for by the nucleic acid
 CC molecule above, or comprising an isolated human protein comprising one or
 CC more of the following sequences: Glu-Leu-Asp-Val-Leu-Gln-Gly-Arg; and Gly
 CC -Ile-Leu-Ile-Leu-Gln-Gln-Asp-Thr-Leu-Gly-Arg; methods for
 CC diagnosing Schizophrenia; antibodies capable of immunospecific binding to
 CC a Schizophrenia-Associated Protein Isoform (SPI); methods of treating
 CC Schizophrenia; and methods of screening for agents that modulate a
 CC characteristic (e.g., expression or binding activity) of an SPI, an SPI
 CC analogue, or an SPI-related polypeptide. The nucleic acid molecule and
 CC encoded proteins, as well as the methods and compositions are useful for
 CC screening, diagnosing, and prognosing Schizophrenia, for monitoring the
 CC effectiveness of Schizophrenia treatment, for identifying patients most
 CC likely to respond to a particular therapeutic treatment and for
 CC developing drug. They are also useful for screening modulators of
 CC Schizophrenia-Associated Protein Isoform useful for treating
 CC Schizophrenia. This sequence encodes a schizophrenia-associated protein
 CC isoform.
 CC
 XX
 SQ Sequence 42 BP; 6 A; 12 C; 15 G; 9 T; 0 U; 0 Other;
 XX
 Query Match 71.0%; Score 14.2; DB 12; Length 42;
 Best Local Similarity 84.2%; Pred. No. 8.8e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 XX
 QY 1 GTGCCAGCCAGAGCACT 19
 |||||
 DB 7 GTGCCAGCCAGAGCACT 25
 |||||
 RESULT 9
 ADH05972/C
 ID ADH05972 standard; DNA; 41 BP.
 XX
 AC ADH05972;
 XX
 DT 11-MAR-2004 (first entry)

XX
 DE Gene polymorphism detection method-related primer/probe #938.
 XX
 KW gene polymorphism detection; primer; probe; SNP analysis;
 KW single nucleotide polymorphism analysis; drug selection; ss.
 XX
 OS Unidentified.
 XX
 PN WO2003097877-A1.
 XX
 PD 27-NOV-2003.
 XX
 PF 16-MAY-2003; 2003WO-JP006141.
 XX
 PR 17-MAY-2002; 2002JP-00143185.
 XX
 PR 17-OCT-2002; 2002JP-00303528.
 XX
 PA (RIKE) RIKEN KK.
 PA (NAKA/) NAKAMURA Y.
 PA (SEKI/) SEKINE A.
 PA (IIDA/) IIDA A.
 PA (SAIT/) SAITO S.
 XX
 PI Nakamura Y, Sekine A, Iida A, Saito S;
 XX
 DR WPI: 2004-012542/01.
 XX
 PT Detecting gene polymorphism for single nucleotide polymorphism analysis
 PT and drug selection.
 XX
 PS Claim 2; SEQ ID NO 938; 166bp; Japanese.
 XX
 CC The invention comprises a method for detecting gene polymorphisms, the
 CC method involves constructing an oligonucleotide primer and/or probe
 CC containing the polymorphism site in a receptor gene or its complementary
 CC sequence, amplifying that part and detecting it with the probe and/or
 CC primer. The method of the invention is useful for the analysis of SNPs
 CC and in drug selection. The present DNA sequence represents a primer/probe
 CC of the invention.
 CC
 XX
 SQ Sequence 41 BP; 10 A; 9 C; 12 G; 9 T; 0 U; 1 Other;
 XX
 Query Match 70.0%; Score 14; DB 12; Length 41;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 GTGCCAGCCAGAG 14
 |||||
 DB 37 GTGCCAGCCAGAG 24
 |||||
 RESULT 10
 ADH91759/C
 ID ADH91759 standard; DNA; 41 BP.
 XX
 AC ADH91759;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE 1-beta-methylcarbapenem compound-related human DNA sequence #938.
 XX
 KW 1-beta-methylcarbapenem compound; antimicrobial; bacterial infection;
 KW respiratory infection; human; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO2003095454-A1.
 XX
 PD 20-NOV-2003.
 XX
 PF 14-MAY-2003; 2003WO-JP006028.
 XX
 PR 14-MAY-2002; 2002JP-00138448.
 XX

```

XX (SANY ) SANKYO CO LTD.
PA Kobayashi Y, Ashida Y, Uchida T, Kojima K;
XX WPI; 2004-081882/08.
XX New carapenem compounds resistant to beta-lactamase (except metallo-beta
XX -lactamase), useful for treating microbial infections especially
XX respiratory infections.
XX Disclosure; SEQ ID NO 938; 726bp; Japanese.
XX The invention comprises 1-beta-methylcarapenem compounds which are
XX useful as antimicrobials to treat bacterial infections, especially
XX respiratory infections in warm-blooded animals (e.g. humans). The present
XX human DNA sequence is included in the sequence listing of this patent.
XX
SQ Sequence 41 BP; 10 A; 9 C; 12 G; 9 T; 0 U; 1 Other;

Query Match          70.0%; Score 14; DB 12; Length 41;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCAGCCAGCAG 14
DB 37 GTGCCAGCCAGCAG 24

RESULT 11
ID AAQ11150 standard; DNA; 80 BP.
XX AAQ11150;
XX 04-JUN-1991 (first entry)
XX
DE Probe GTR-2 based on the 3' end of human and rat GTP sequences.
XX
XX Glucose transporter protein; serum-independence; Chinese Hamster;
XX Insulin-independence; ss.
XX
XX Cricetus sp.
XX
XX MO9103554-A.
XX
XX 21-MAR-1991.
XX
XX 01-SEP-1989; 89US-00402204.
XX
XX 01-SEP-1989; 89US-00402204.
XX
XX 20-JUN-1990; 90US-00541426.
XX
XX (GETH ) GENENTECH INC.
XX
XX Thomas JN, Williams SR;
XX
XX WPI; 1991-102073/14.
XX
XX Transfecting eukaryotic cells with a replicable vector - comprising
XX nucleic acid sequence encoding a GTP operably linked to control sequences
XX recognised by transfected cells.
XX
XX Example 1; Page 20; 58pp; English.
XX
XX A cDNA library was prepared in lambda gt10 from total cellular RNA from
XX CHO-PR4 cells. The library was screened with 3 probes (GTR1- GTR-3) based
XX on highly conserved regions of the known rat and human facilitative GTP
XX sequences (Birbaum et al., Proc. Natl. Acad. Sci. USA, 83:5784-
XX 5788, (1986); Mueckler et al., Science, 229:941-945, (1985)). One positive
XX plaque was identified (out of 150000), replated and screened with probes
XX GTR-1 and GTR-3. Phage DNA was prepared from one of the positive plaques
XX and its 2.5kb cDNA insert excised using EcoRI. The insert was ligated

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CC into pRK5 and transformed into E.coli strain SR101. Recombinant clones
CC were picked for sequencing and the complete CHO GTP-encoding sequence
CC determined. See also AAQ11148-9 and AAQ11151
XX
SQ Sequence 80 BP; 18 A; 23 C; 28 G; 11 T; 0 U; 0 Other;

Query Match          70.0%; Score 14; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCAGCCAGAGCGCAG 18
DB 50 CCAGCCAGAGCGCAG 63

RESULT 12
ID ABA97968 standard; DNA; 26 BP.
XX ABA97968;
XX
XX 25-APR-2002 (first entry)
XX
XX Human pancreatic cancer antigen related PCR primer SEQ ID NO 3.
XX
XX Human; pancreatic cancer; antigen; oesophageal cancer; colon cancer;
XX breast cancer; PCR primer; ss.
XX
XX Synthetic.
XX
XX JP2001340081-A.
XX
XX 11-DEC-2001.
XX
XX 31-MAY-2000; 2000JP-00161930.
XX
XX 31-MAY-2000; 2000JP-00161930.
XX
XX PA (KEIO-) GH KEIO GIJUKU.
XX
XX WPI; 2002-144963/19.
XX
XX New DNA encoding a human pancreatic cancer antigen protein for treating
XX PT and diagnosing cancer, especially pancreatic, esophagus, colon and breast
XX cancer.
XX
XX Example; Page 10; 20pp; Japanese.
XX
XX The invention relates to a DNA (ABA97973) encoding a human pancreatic
XX cancer antigen protein (AB808656) or a protein consisting of the amino
XX acid sequence of human pancreatic antigen protein in which at least one
XX amino acid is deleted, replaced or added and having immunity-inducing
XX activity. The antigen and the DNA are useful for treating and diagnosing
XX pancreatic cancer, oesophagus cancer, colon cancer and breast cancer. The
XX present sequence is that of a PCR primer, useful to the invention
XX
SQ Sequence 26 BP; 10 A; 9 C; 5 G; 2 T; 0 U; 0 Other;

Query Match          69.0%; Score 13.8; DB 6; Length 26;
Best Local Similarity 88.2%; Pred. No. 1.3e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGCCAGCCAGAGCGAC 18
DB 1 TGCCAGCCAGAGATAC 17

RESULT 13
ID AAL55205/c standard; RNA; 36 BP.
XX AAL55205;
XX
XX AAL55205;
XX

```

```

DT 01-MAY-2003 (first entry)
XX
XX pshn1-Ff1 RNA oligomer, SEQ ID NO 10.
XX
XX Cytostatic; RNA interference; RNAi agent; non-embryonic mammal;
XX gene therapy; vaccination; vaccine; animal model; cancer; enzyme; ss.
XX
XX Unidentified.
XX
XX MO2003010180-A1.
XX
XX 06-FEB-2003.
XX
XX 19-JUL-2002; 2002WO-US022869.
XX
XX 23-JUL-2001; 2001US-0307411P.
XX 27-FEB-2002; 2002US-0360664P.
XX
XX (STRD ) UNIV LELAND STANFORD JUNIOR.
XX
XX Kay M, Mc Caffrey A;
XX
XX WPI; 2003-229634/22.
XX
XX Reducing coding sequence expression in a target cell of a non-embryonic
XX mammal, useful for producing animal models of RNA virus infection or in
XX therapeutic applications, comprises administering to the mammal an RNA
XX interference agent.
XX
XX Disclosure; Page 63; 65pp; English.
XX
XX The invention relates to a novel method for reducing expression of a
XX coding sequence in a target cell of a non-embryonic mammal. The method
XX comprises administering to the mammal an RNA interference (RNAi) agent
XX specific for the coding sequence to reduce expression of the coding
XX sequence. The RNAi agent is useful for modulating, i.e., reducing, the
XX coding sequence expression in a target cell of a non-embryonic mammal
XX used in academic, research or therapeutic applications, e.g. gene therapy
XX or vaccination applications. Academic or research applications include
XX producing animal models of RNA virus infection, determining potential
XX targets for pharmaceuticals, understanding normal and pathological events
XX associated with development, determining signaling pathways responsible
XX for post-natal development or ageing, or identifying gene function in non
XX -embryonic mammals. The method is useful for treating different
XX conditions in which the modulation of target gene expression in a
XX mammalian host is desired, e.g. cancer. This polynucleotide sequence
XX represents a pshn1-Ff1 RNA oligomer relating to the RNAi agents of the
XX invention
XX
XX Sequence 36 BP; 6 A; 8 C; 11 G; 0 T; 11 U; 0 Other;
XX
XX Query Match 69.0%; Score 13.8; DB 8; Length 36;
XX Best Local Similarity 88.2%; Pred. No. 1.3e+04;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 3 GCCCAGCCGAGCGACT 19
XX ||||| ||||| |||||
XX Db 30 GCCCAGCCGAGCGACT 14
XX
XX RESULT 14
XX ADV87091
XX ID ADV87091 standard; DNA; 71 BP.
XX
XX ADV87091;
XX
XX 10-MAR-2005 (first entry)
XX
XX Non-specific shRNA expression construct DNA insert.
XX
XX RNA interference; RNAi; probe; gene silencing; short hairpin RNA; shRNA;
XX myosin D; ss.
XX

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OS Synthetic.
XX
XX WO200411190-A2.
XX
XX 23-DEC-2004.
XX
XX 26-MAY-2004; 2004WO-US016844.
XX
XX 27-MAY-2003; 2003US-0473809P.
XX
XX (COLD-) COLD SPRING HARBOR LAB.
XX
XX Mittal V, Kumar R;
XX
XX WPI; 2005-040085/04.
XX
XX Determining whether an RNAi probe can inhibit expression of a target gene
XX by detecting expression of a target-reporter fusion construct, useful for
XX high-throughput screens to identify effective RNAi probes.
XX
XX Example 1; SEQ ID NO 50; 59pp; English.
XX
XX The invention provides a reliable and quantitative approach for the rapid
XX and efficient identification of an effective RNAi probe (e.g. a short
XX interfering RNA (siRNA) or short hairpin RNA (shRNA)) against any gene,
XX and for selecting the best RNAi probe from among a group of RNAi
XX candidates. This method may be used for high-throughput screens, e.g.
XX based on microarray cell transfections, of RNAi probes. The method is
XX based upon introduction into a target cell of both an RNAi probe and a
XX cognate target-reporter fusion expression construct, where expression of
XX the target-reporter fusion may be easily quantitated based upon the
XX reporter. The ability of an RNAi probe to suppress target-reporter fusion
XX expression, as quantified by reporter expression, specifically correlates
XX with the ability of the identified RNAi probe to effectively suppress
XX expression of the cognate endogenous gene. The present sequence is that
XX of the 3'-5' strand of a double-stranded DNA insert of a non-specific
XX shRNA expression construct. This shRNA was compared with mouse myod-
XX specific shRNA expression constructs in examples from the invention.
XX
XX Sequence 71 BP; 23 A; 19 C; 16 G; 13 T; 0 U; 0 Other;
XX
XX Query Match 69.0%; Score 13.8; DB 14; Length 71;
XX Best Local Similarity 88.2%; Pred. No. 1.4e+04;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 3 GCCCAGCCGAGCGACT 19
XX ||||| ||||| |||||
XX Db 36 GCCCAGCCGAGCGACT 52
XX
XX RESULT 15
XX ACD80225/C
XX ID ACD80225 standard; DNA; 100 BP.
XX
XX ACD80225;
XX
XX 19-SEP-2003 (first entry)
XX
XX E. coli K12 MG1655 biochip probe SEQ ID 11501.
XX
XX Biochip; gene expression; gut; diagnostic; detection; probe; ss.
XX
XX Escherichia coli.
XX
XX EP1260592-A1.
XX
XX 27-NOV-2002.
XX
XX 17-MAY-2001; 2001EP-00112179.
XX
XX 17-MAY-2001; 2001EP-00112179.
XX
XX (MWGB-) MWG-BIOTECH AG.
XX

```

XX
PI Donner H, Drescher B, Huber A, Weber J;
XX
DR WPI, 2003-241155/24.

XX Biochip containing probes complementary with open reading frames in
PT Escherichia coli K12, useful for detecting gene expression and expression
PT patterns.

XX
PS Claim 3; Page 1791; 2004pp; German.

XX
CC This invention describes a novel biochip comprising probe spots, each
CC containing many identical probes. The probes are nucleotide sequences of
CC 30-80 bases, are prepared ex situ from synthetic oligonucleotides and at
CC least one includes a segment of at least 20 bases identical with, or
CC complementary to, a segment of an open reading frame (orf) of Escherichia
CC coli K12. The biochip is used for specific detection of gene expression
CC in K12 and for determining the gene expression pattern, e.g. for
CC diagnostic determination of which E. coli strains are present in the gut,
CC and to determine the effects of e.g. growth media on gene expression. The
CC biochip provides as comprehensive as possible detection of the K12
CC genome, with simultaneous analysis of many different genes with a single
CC device, and comparison of gene expression between K12 and its mutants or
CC other E. coli strains in a single experiment. Apart from qualitative and
CC quantitative information about gene expression, it also allows
CC measurements of population densities for the various strains. The use of
CC synthetic oligonucleotides for preparation of probes allows free
CC variation in probe length and ensures high purity (and thus selectivity,
CC reactivity and reproducibility); also synthetic probes are generally
CC shorter than probes prepared by polymerase chain reaction. ACD68731 to
CC ACD81540 represent oligonucleotide probes used with the biochip described
CC in the invention

XX
SQ Sequence 100 BP; 20 A; 22 C; 25 G; 33 T; 0 U; 0 Other;

Query Match 69.0%; Score 13.8; DB 8; Length 100;

Best Local Similarity 88.2%; Pred. No. 1.4e+04;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGCCGAGCCGAGCGAC 18

DB 70 TGCCGAGCCGAGCGGC 54

Search completed: December 24, 2005, 12:29:00
Job time : 174.4 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd

OM nucleic - nucleic search, using sw model

```
Run on:      December 24, 2005, 10:37:31 ; Search time 1572 Seconds
```

595.256 Million cell updates/sec

Title: US-09-296-264-8

Sequence: 1 gtcgccagccagcgactg 20

Scoring table: IDENTITY_NUC

Searched: 41078325 beqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 768474

Minimum DB seq length:	20
Maximum DB seq length:	100

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

```

1:  gb_est1: *
2:  gb_est2: *
3:  gb_est3: *
4:  gb_hic: *
5:  gb_est4: *
6:  gb_est5: *
7:  gb_est6: *
8:  gb_est7: *
9:  gb_gsa1: *
10: gb_gsa2: *
11: gb_gsa3: *

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	15.8	79.0	64	9	A2783365	A2783365 2M0025F03
2	15.2	76.0	85	1	AA797827	AA797827 9Y04D03..x
3	15	75.0	70	10	CG552451	CG552451 OST16165
4	14.2	71.0	94	10	CG476111	CG476111 OST5407
5	13.8	69.0	51	11	DQ045724	DQ045724 Pan tLoc
6	13.8	69.0	4	1	A1037190	A1037190 otd60a09..y
7	13.8	69.0	98	10	CG637147	CG637147 OST36277Y
8	13.6	68.0	55	9	A2487430	A2487430 IM0317A10
9	13.6	68.0	60	9	B2586445	B2586445 3590.1.16
10	13.6	68.0	76	4	AK197036	AK197036 Mus mtrac
11	13.4	67.0	20	9	A2946089	A2946089 ZM0207A13
12	13.4	67.0	73	8	DN460399	DN460399 EST956198
13	13.4	67.0	86	9	A2475290	A2475290 IM0293H07
14	13.4	67.0	89	10	CL271491	CL271491 Ggal 7361
15	13.4	67.0	94	6	CB884871	CB884871 M615038 H
16	13.4	67.0	95	8	T80645	T80645 yd92f03..81
17	13.2	66.0	42	10	AJ832995	AJ832995 Drosoph
18	13.2	66.0	50	1	AU104251	AU104251 AUI04251
19	13.2	66.0	50	8	H74150	H74150 yB16C04..x1
20	13.2	66.0	54	10	CL42297	CL42297 AUI0289 S
21	13.2	66.0	57	6	CA795292	CA795292 CgC_EU_223
22	13.2	66.0	58	9	BH635408	BH635408 1008004F0

C 23	13.2	66.0	73	1	AJ158821	u438e10.r
C 24	13.2	66.0	74	1	AJ721334	AJ721334
C 25	13.2	66.0	77	10	AJ832938	Droscopio
C 26	13.2	66.0	83	10	CL422932	CL422932
C 27	13.2	66.0	84	6	CF021696	CF021696
C 28	13.2	66.0	87	9	BZ690230	QB4401.x
C 29	13.2	66.0	91	10	CL518055	M018C07 G
C 30	13	65.0	9	9	BH903823	SAD7608 F
C 31	13	65.0	76	1	AA118149	SALK_1035
C 32	13	65.0	82	3	BJ902359	mm11a12.r
C 33	12.8	64.0	39	10	AG195605	ib66d03.x
C 34	12.8	64.0	42	9	AZ811797	pan trogl1
C 35	12.8	64.0	50	1	AJ102538	AG195605 Pan trogl1
C 36	12.8	64.0	51	1	AJ833237	AZ811797 2M0078P06
C 37	12.8	64.0	51	10	BX96100	AJ102538
C 38	12.8	64.0	52	1	AW059751	AJ833237
C 39	12.8	64.0	70	11	CR118936	Reverbe b
C 40	12.8	64.0	76	1	AA451089	LE3C07.yg
C 41	12.8	64.0	79	1	AJ019859	Reverbe b
C 42	12.8	64.0	83	1	AA587260	vf67d06.r
C 43	12.8	64.0	83	10	BX136297	AJ019859 u462h04.r
C 44	12.8	64.0	83	10	CG488672	AA587260 m70f0f5.g
C 45	12.8	64.0	83	10	CG568842	BX136297 Danilo re
						CG488672 OST24685
						CG568842 OST196266

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION
AZ783365	AZ783365	64 bp DNA linear GSS 16-FEB-2000
	2M0025F03F	Mouse 10kb plasmid U06C1M library Mus musculus genomic
	clone U06C2M0025F03 F,	genomic survey sequence.

KEYWORDS GSS.

ORGANISM

AUTHORS

TITLE

JOURNAL

COMMENT

11

sour

		64 bp	DNA	linear	GSS 16-FEB-2001
0					
0	73	1	A1158821	u638610.r	
0	74	1	AJ721334	AJ721334	
0	77	10	AJ832938	Drosophila	
0	83	6	CF021696	QBP4A01.x	
0	84	10	B2690230	M018C07 F	
0	87	9	B2690230	M018C07 G	
0	91	10	CL518055	SAD7G08 F	
0	61	9	BH903823	SAIK 1035	
0	76	1	AA118149	mm11612.r	
0	82	3	BI902359	ib86d03.x	
0	39	10	AG195605	AG195605 Pan t10G1	
0	42	9	AZ811797	2M0078P06	
0	50	1	AI102538	AI102538	
0	51	1	AI833237	BT76805.x	
0	51	10	BX936100	Reverse b	
0	52	1	AW059751	LE3C07.Y9	
0	70	11	CR118936	Reverse b	
0	76	1	AA451089	V887406.x	
0	79	1	AI019859	u892H04.x	
0	83	1	AA587260	nm70F05.b	
0	83	10	BX196297	Danilo ter	
0	83	10	CG488672	OST24685	
0	83	10	CG568842	OST196266	

ALIGNMENTS

33F Mouse 10kb plasmid UUGCIM library Mus musculus genomic

UUGC2M0025F03 F, genomic survey sequence.

1.1 GI:12918022

ulus (house mouse)

ulus

a; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
a; Eutheria; Eucarchontoglires; Glires; Rodentia;
achi; Muridae; Muridae; Murinae; Mus.

8.1 to 64)

oyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Longacre,S., Mammoud,M., Meenen,E., Pedersen,T.,
Rose,M., Rose,R., Stokes,R., Tingey,A., von
useern,A. and Wright,D.,Weiss,R.

ole genome scaffolding with paired end reads from 10kb
inserts

inserts

hed (2000)

Robert B. Weiss

ty of Utah Genome Center

ty of Utah

Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT

SA

585 5606

585 7177

du@genetics.utah.edu

length: 10000 Std Error: 0.00

025 row: F column: 03

er: CATTGTAAACGACGGCAGCT

lasmid ends

ility sequence stop: 64.

Location/Qualifere

1..64

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="CS7B1/60"

/db_xref="taxon:10090"

/clone="UUGC2M0025F03"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGCIM library"

(note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 79.0%; Score 15.8; DB 9; Length 64;
Best Local Similarity 89.5%; Pred. No. 1.2e+04;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGCCGACGACGACTG 20
|||||
Db 31 TGCCGACGACGACTG 49

RESULT 2 85 bp mRNA linear EST 10-FEB-1998
AA797827
LOCUS vy04003.r1 Stratagene mouse macrophage (#937306) Mus musculus cDNA
DEFINITION clone IMAGE:1294445 similar to SW:YKNO.YEAST Q03103 HYPOTHETICAL
65.0 KD PROTEIN IN COX14 5'REGION PRECURSOR. ; mRNA sequence.
AA797827
VERSION AA797827
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Merris, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellendberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LINT; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:675493

Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28m13 rev1 Et from Amersham
High quality sequence stop: 1.
Location/Qualifiers

FEATURES

source 1..85
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:1294445"
/issue_type="macrophage"
/dev_stage="WEHI-3 cell line"

/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene mouse macrophage (#937306)"
/note="Organ: blood; Vector: pBluescript SK-; Site 1:
EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. WEHI-3 cell line. Average insert size: 1.5 kb.
Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGACGACG
3' ~3' adaptor sequence: 5' CTCGAGTGTGTGTGTGTGTGT 3'."

ORIGIN

Query Match 76.0%; Score 15.2; DB 1; Length 85;
Best Local Similarity 85.0%; Pred. No. 2.3e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGCCGACGACGACTG 20
|||||
Db 66 GTGCCGACGACGACTG 47

RESULT 3 70 bp mRNA linear GSS 01-OCT-2003
CG552451
LOCUS OST161696 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST161696,
DEFINITION mRNA sequence.
CG552451
ACCESSION CG552451.1 GI:37339038
VERSION GSS.
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Zambrowicz, B.P., Abduln, A., Ramirez-Solis, R., Richter, L.J., Piggett, J., Beltrand, R., Buxton, E.C., Edwards, J., Finch, R.A., Fridde, C.O., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jiang, C., Key, B.W., Ut, K., Kipp, P., Kohlhauf, B., Ma, Z.-Q., Matresich, D., Payne, R., Potter, D.G., Qian, N., Shaw, J., Schick, J., Shi, Z.-Z., Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, Q., Person, C. and Sands, A.T.
TITLE Mnk1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
PUBMED 14610273
COMMENT Contact: Zambrowicz BP
Omnibank

Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature, 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.
Location/Qualifiers

FEATURES
source 1..70
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST161696"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"

ORIGIN

Query Match 75.0%; Score 15; DB 10; Length 70;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CAGCCAGACGACTG 20
|||||
Db 20 CAGCCAGACGACTG 34

RESULT 4
CG476131/c

LOCUS CG476131 94 bp mRNA linear GSS 01-OCT-2003
 DEFINITION OST5407 Mus musculus 129sv/Ev Mus musculus cDNA clone OST5407, mRNA
 sequence.
 ACCESSION CG476131
 VERSION CG476131.1 GI:37227020
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 94)
 Zambrowicz, B.P., Abuh, A., Ramirez-Solis, R., Richter, L.J.,
 Piggott, J., Beltrande-Rio, H., Buxton, E.C., Edwards, J., Finch, R.A.,
 Fridele, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jains, C.,
 Key, B.W., Jr., Kipp, P., Kohlhauf, B., Ma, Z.-Q., Markesich, D.,
 Payne, R., Porter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
 Sparks, M.J., Van Slichtenhorst, I., Vogel, P., Walke, W., Xu, N.,
 Zhu, Q., Person, C. and Sands, A.T.
 Mnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
 screen to identify potential targets for therapeutic intervention
 Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
 14610273
 CONTACT: Zambrowicz BP
 OMIBank
 Lexicon Genetics Incorporated
 4000 Research Forest Drive, The Woodlands, TX 77381, USA
 Email: materials@lexgen.com
 Gene trap sequence tag generated by 3' RACE from mouse ES cells as
 described in Zambrowicz et al (Nature, 1998 Apr 9;392(6676):608-11)
 Class: Gene Trap.
 Location/Qualifiers
 1..94
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="129sv/Ev"
 /db_xref="taxon:10090"
 /clone="OST5407"
 /cell_type="embryonic stem cell"
 /clone_11b="Mus musculus 129sv/Ev"
 ORIGIN
 Query Match 71.0%; Score 14.2; DB 10; Length 94;
 Best Local Similarity 84.2%; Pred. No. 6.7e+04;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 GTGCCAGCGAGCGACT 19
 |||||
 83 GTGCCAGCGAGCGACT 65
 RESULT 5
 LOCUS DQ045724 51 bp DNA linear GSS 02-JUN-2005
 DEFINITION Pan troglodytes PALM gene, VIRUTAL TRANSCRIPT, partial sequence,
 genomic survey sequence.
 ACCESSION DQ045724
 VERSION DQ045724.1 GI:66896939
 KEYWORDS GSS.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominoidea; Pan.
 1 (bases 1 to 51)
 Nielsen, R., Bustamante, C., Clark, A.G., Gianowski, S., Sackton, T.B.,
 Hubisz, M.J., Fedel-Alon, A., Tanenbaum, D.M., Civeello, D.,
 White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.
 A Scan for Positively Selected Genes in the Genomes of Humans and
 Chimpanzees
 (ex) PLOS Biol. 3 (6), E170 (2005)
 15869325
 REFERENCE 2 (bases 1 to 51)
 JOURNAL
 PUBMED
 REFERENCE

AUTHORS Nielsen, R., Bustamante, C., Clark, A.G., Gianowski, S., Sackton, T.B.,
 Hubisz, M.J., Fedel-Alon, A., Tanenbaum, D.M., Civeello, D.,
 White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.
 TITLE Direct Submission
 JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering
 them based on alignment. Translation starts at the beginning of
 alignment.
 FEATURES
 source
 1..51
 /organism="Pan troglodytes"
 /mol_type="genomic DNA"
 /db_xref="taxon:9598"
 <1..>51
 /gene="PALM"
 /locus_tag="HC11484"
 ORIGIN
 Query Match 69.0%; Score 13.8; DB 11; Length 51;
 Best Local Similarity 88.2%; Pred. No. 1e+05;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 4 CCCAGCAGCGCGCTG 20
 |||||
 24 CCCAGCAGCGCGCTG 40
 RESULT 6
 LOCUS AI037190/c 64 bp mRNA linear EST 26-JUN-1998
 DEFINITION udb6a09.y1 Sugano mouse liver mla Mus musculus cDNA clone
 IMAGE:1450264 5' similar to SW:YHLL_EBV P03181 HYPOTHETICAL BHLF1
 PROTEIN. ; mRNA sequence.
 ACCESSION AI037190
 VERSION AI037190.1 GI:3260881
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 64)
 Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
 Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
 Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
 Waterston, R.
 The WashU-HMNI Mouse EST Project
 UNPUBLISHED (1996)
 CONTACT: Marra M/Mouse EST Project
 WashU-HMNI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LIND; contact the
 IMAGE Consortium (info@image.lind.gov) for further information.
 MGI:923580
 Trace considered overall poor quality
 Possible reversed clone: similarity on wrong strand
 Seq primer: custom primer used
 High quality sequence stop: 1.
 Location/Qualifiers
 1..64
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL"
 /db_xref="taxon:10090"
 /clone="IMAGE:1450264"
 /sex="female"
 /dev_stage="adult"

/lab host="DH10B"
 /clone_lib="Sugano mouse liver mlia"
 /note="Organ: liver; Vector: pMT18s-FL3; Site_1: DraIII
 (CACTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
 was primed with an oligo(dT) primer
 (ATGTGGCTTTTCTTTTCTTTT); double-stranded cDNA was
 ligated to a DraIII adaptor (TGTGGCTTACTGG), digested
 and cloned into distinct DraIII sites of the pMT18s-FL3
 vector (5' site CACTGTG; 3' site CACCATGTG). XhoI should
 be used to isolate the cDNA insert. Size selection was
 performed to exclude fragments <1.5kb. Library
 constructed by Dr. Sumio Sugano (University of Tokyo
 Institute of Medical Science). Custom primers for
 sequencing: 5' end primer CTCTGCTTAAAGCTGGC and 3' end
 primer CCACTGCGAGCTCGACACA."

ORIGIN

Query Match 69.0%; Score 13.8; DB 1; Length 64;
 Best Local Similarity 88.2%; Pred. No. 1e+05;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGCCAGCCAGCGCA 17
 |||
 Db 44 GAGACCGACGACGCGA 28

RESULT 7

CG637147 98 bp mRNA linear GSS 02-OCT-2003
 OST362774 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST362774,
 mRNA sequence.

ACCESSION CG637147
 VERSION CG637147.1 GI:37460996
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 98)

Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
 Piggett, J., BeltrandeRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,
 Fridde, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,
 Key, B.W., Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,
 Payne, R., Potter, D.G., Qian, N., Shaw, J., Schlick, J., Shi, Z.-Z.,
 Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,
 Zhu, Q., Person, C. and Sands, A.T.
 Mnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
 screen to identify potential targets for therapeutic intervention
 Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)

COMMENT 14610273
 Contact: Zambrowicz BP

OmniBank
 Lexicon Genetics Incorporated
 4000 Research Forest Drive, The Woodlands, TX 77381, USA
 Email: materials@lexgen.com
 Gene trap sequence tag generated by 3' RACE from mouse ES cells as
 described in Zambrowicz et al (Nature. 1998 Apr 9;352(6676):608-11)
 Class: Gene Trap.

FEATURES Location/Qualifiers

source

1..98
 /organism="Mus musculus"
 /mol_type="RNA"
 /strain="129Sv/Ev"
 /db_xref="taxon:10090"
 /clone="OST362774"
 /cell_type="embryonic stem cell"
 /clone_lib="Mus musculus 129Sv/Ev"

ORIGIN

Query Match 69.0%; Score 13.8; DB 10; Length 98;
 Best Local Similarity 88.2%; Pred. No. 1e+05;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGCCAGCCAGACGAC 18
 |||
 Db 96 TGCCAGCCAGACGAC 80

RESULT 8
 A2487430 55 bp DNA linear GSS 05-OCT-2000
 LOCUS 1M0317A10F Mouse 10kb plasmid UGCGM library Mus musculus genomic
 DEFINITION clone UGCGM0317A10 F, genomic survey sequence.

ACCESSION A2487430
 VERSION A2487430.1 GI:10655167
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 55)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von
 Niederhausen, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL
 COMMENT Unpublished (2000)

Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: rdunn@genetics.utah.edu
 Insert Length: 1000 Std Error: 0.00
 Plate: 0317 row: A column: 10
 Seq primer: CGTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 55.

FEATURES

Location/Qualifiers

source

1..55
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCGM0317A10"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCGM library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (gi4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 68.0%; Score 13.6; DB 9; Length 55;
 Best Local Similarity 80.0%; Pred. No. 1.2e+05;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTGCCAGCCAGAGCAGCTG 20
 Db 30 GAGCCAGCCAGGCTGAGTG 49

RESULT 9
 B2586465 60 bp DNA linear GSS 17-DEC-2002
 DEFINITION B2586465 3590_1_16_1_H09.2EL_Y_1 3590 - RescueMu Grid M Zea mays genomic,
 genomic survey sequence.
 B2586465
 ACCESSION B2586465 GI:27221526
 VERSION B2586465.1
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoidae; Andropogoneae; Zea.
 1 (bases 1 to 60)

REFERENCE
 AUTHORS Walbot,V.
 TITLE Maize genomic sequences found using engineered RescueMu transposon
 JOURNAL Unpublished (2001)
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Possible ligation site of ends cut by 2 different endonucleases.
 Reverse complemented post-ligation sequence from source sequence.
 Plate: 3590_1_16_1 column: 4
 Class: transposon-tagged.
 Location/Qualifiers
 1..60
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /cultivar="mixed Backgroud W23/Al88/B73/K55"
 /db_xref="taxon:4577"
 /tissue_type="leaf"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="3590 - RescueMu Grid M"
 /note="Organ: leaf; Vector: RescueMu (engineered from
 pBluescript backbone); Site 1: BamHI; Site 2: BglII;
 RescueMu is a 4.9 kb, modified maize Mu transposon
 designed to allow plasmid rescue from total genomic DNA.
 Mu elements insert preferentially into transcription
 units. For more information on RescueMu, go to the web
 site 'www.zmdb.iastate.edu' and follow the links for
 'RescueMu.' Grid M was grown at University of Arizona in
 2001. DNA was extracted from leaf punches, double digested
 using BamHI and BglII, and ligated to form circular
 plasmids. DH10B cells were transformed and then screened
 on LB plates with ampicillin."

ORIGIN
 Query Match 68.0%; Score 13.6; DB 9; Length 60;
 Best Local Similarity 80.0%; Pred. No. 1.2e+05;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTGCCAGCCAGAGCAGCTG 20
 Db 14 GTGCCAGCTGAGCCCTG 33

RESULT 10
 AK197036/c 76 bp mRNA linear HTC 23-NOV-2004
 LOCUS AK197036
 DEFINITION Mus musculus cDNA, clone:YIG0123M15, strand:minus,
 reference:ENSEMBL:Mouse-Transcript-ENST:ENSMUST0000040111, based

on BLAT search.

ACCESSION AK197036
 VERSION AK197036.1 GI:56021213
 KEYWORDS HTC; ASSETS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Watahiki,A., Waki,K., Hayatsu,N., Shiraki,T., Kondo,S.,
 1 Nakamura,M., Sasaki,D., Arakawa,T., Kawai,J., Harbers,M.,
 Hayashizaki,Y. and Carninci,P.
 Title Libraries enriched for alternatively spliced exons reveal splicing
 patterns in melanocytes and melanomas
 Nat. Methods 1, 233-239 (2004)
 2 (bases 1 to 76)

JOURNAL
 AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Harbers,M., Hayatsu,N.,
 REFERENCE Arakawa,T., Carninci,P., Fukuda,S., Harbers,M., Hayatsu,N.,
 Hori,F., Imotani,K., Kawai,J., Kondo,S., Murata,M., Nakamura,M.,
 Nomura,K., Ohno,M., Sasaki,D., Shiraki,T., Waki,K., Watahiki,A. and
 Hayashizaki,Y.
 Title Direct Submission
 Submitted (15-SEP-2004) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa, 230-0045, Japan (E-mail:genome-res@gc.riken.jp,
 URL:http://genome.gsc.riken.jp, Tel:81-45-503-9222,
 Fax:81-45-503-9216)
 Alternative Splicing Libraries (ASLs) are prepared by: Preparing
 of single-stranded DNA using a RNA template from full length cDNA
 libraries, hybridizing of
 single-stranded DNAs, removing of remaining single-stranded DNA,
 digesting of regions comprising double-stranded DNA by a set of 4
 bp-cutters, capturing of DNA hybrids with loop structures
 (alternative spliced exon), ligation of Y-shaped primers to
 isolated DNA hybrids with loop structures, PCR amplification of
 ligation products and their cloning into pFIC1 vector. (Reference).
 Location/Qualifiers
 1..76
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone_lib="YIG0123M15"
 /cell_line="mixture of B16-F10Y and melan-C"
 /cell_type="mixture of melanoma cell and melanocyte cell"
 /clone_lib="Alternative Splicing Library L1"
 /note="strand:minus, reference:ENSEMBL:Mouse-Transcript-
 ENST:ENSMUST0000040111, based on BLAT search"

ORIGIN
 Query Match 68.0%; Score 13.6; DB 4; Length 76;
 Best Local Similarity 80.0%; Pred. No. 1.3e+05;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTGCCAGCCAGAGCAGCTG 20
 Db 52 GTGCTGTGCCAGAGCAGCTG 33

RESULT 11
 A2946089/c 20 bp DNA linear GSS 27-APR-2001
 LOCUS A2946089
 DEFINITION 2M0207A13R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
 clone UUGC2M0207A13 R, genomic survey sequence.
 A2946089
 ACCESSION A2946089 GI:13812898
 VERSION A2946089.1
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 JOURNAL Mouse whole genome scaffolding with paired end reads from 10kb
 COMMENT Unpublished (2000)
 CONTACT: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0207 row: A column: 13
 Seq primer: CACACAGGAACAGCTATGAC
 Class: plasmid ends
 High quality sequence stop: 20.
 Location/Qualifiers
 1..20
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGGCM0207A13"
 /sex="Female"
 /lab_host="E. coli strain XL10-Gold, TI-resistant, F-"
 /note="Vector: pMD42nv. Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gii4732114|gb|AF129072.1) a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
 Query Match 67.0%; Score 13.4; DB 9; Length 20;
 Best Local Similarity 93.3%; Pred. No. 1.5e+05;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 CCAGCCGAGCGACT 19
 |||||
 Db 18 CCAGCCGAGCGATT 4
 |||||

RESULT 12
 DN460399/c 73 bp mRNA linear EST 09-MAR-2005
 LOCUS DN460399 Sequencing ESTs from loblolly pine embryos Pinus taeda
 DEFINITION CNA clone RPIHY11 5' end, mRNA sequence.
 ACCESSION DN460399
 VERSION DN460399.1 GI:60666823
 KEYWORDS EST.
 SOURCE Pinus taeda (loblolly pine)
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.

REFERENCE 1 (bases 1 to 73)
 AUTHORS Buell, C.R., Zheng, L., Cowles, A. and Cairney, J.
 TITLE Sequencing of ESTs from loblolly pine embryonic libraries
 JOURNAL Unpublished (2004)
 COMMENT Contact: C. Robin Buell
 Plant Genomes Group
 The Institute for Genomic Research
 9712 Medical Center Dr, Rockville, MD 20850, USA
 Email: rbuell@tigr.org
 This clone is available through TIGR. Please contact pine@tigr.org for further information
 Seq primer: ATT TAG GTG ACA CTA TAG.
 Location/Qualifiers
 1..73
 /organism="Pinus taeda"
 /mol_type="mRNA"
 /cultivar="7-56 mother tree, open-pollinated tree from, Lyons, Georgia, USA"
 /db_xref="taxon:3352"
 /clone="RPIHY11"
 /lab_host="E.coli DH10B-Tona"
 /clone_lib="Sequencing ESTs from loblolly pine embryos"
 /note="Organ: Zygotic Embryo and Megagametophyte. Somatic Embryo; Vector: pCMV-SPORT 6.1; Site_1: NotI; Site_2: EcoRV; tissue: whole megagametophytes isolated from pine seeds, whole embryos excised from these megagametophytes, whole somatic embryos and suspensor tissue from tissue culture, isolated from cell line A12. Pooled RNA from zygotic embryos, megagametophytes, and somatic embryos was used for library construction. Pine cones were harvested weekly from open-pollinated 7-56 mother trees, collections megagametophytes were first isolated from pine seeds, and whole embryos excised from these megagametophytes each was flash frozen. Embryo development was assessed using the system of Pullman et al (Pullman GS, Johnson S, Peter G, Cairney J, Xu N. 2003. Loblolly pine somatic embryogenesis: development of a maturation medium and resulting embryo quality. Plant Cell Reports 21:747-758 (<http://link.springer.de/link/service/journals/00299/content/03/05/056/>). For photographs see Clavatta et al 2001. (Clavatta VE, Morillon R, Pullman GS, Christophs M, Cairney J. 2001. An aquaglyceroporin is abundantly expressed early in the development of the suspensor and the embryo proper of loblolly pine (Pinus taeda L.). Plant Physiol. 127: 1556-1567 (<http://www.plantphysiol.org/cgi/content/full/127/4/1556>))."

ORIGIN
 Query Match 67.0%; Score 13.4; DB 8; Length 73;
 Best Local Similarity 93.3%; Pred. No. 1.6e+05;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 TGCCGAGCGAGCG 16
 |||||
 Db 50 TGCCGAGCGAGG 36
 |||||

RESULT 13
 A2475290 86 bp DNA linear GSS 04-OCT-2000
 LOCUS A2475290 1M0293H07F Mouse 10kb plasmid UGGCM library Mus musculus genomic
 DEFINITION clone UGGCM0293H07 F, genomic survey sequence.
 ACCESSION A2475290
 VERSION A2475290.1 GI:10633415
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 86)

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niedermaier, A., and Wright, D., Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10Kb
plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

FEATURES

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0293 ROW: H Column: 07
Seq primer: CGTTGTAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 86.
Location/Qualifiers

1..86

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0293H07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10Kb plasmid UUCG1M library"
/note="Vector: PWD42uv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 67.0%; Score 13.4; DB 9; Length 86;
Best Local Similarity 93.3%; Pred. No. 1.6e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGCCAGCCAGAGC 15
Db 34 GTGCCAGCCAGTGC 48

RESULT 14

CL271491/c

LOCUS

CL271491 89 bp DNA linear GSS 08-FEB-2005
Ggal_73c_PR_C06, genomic survey sequence.

DEFINITION

Ggal_73c_PR_C06, genomic survey sequence.

ACCESSION

CL271491

VERSION

CL271491.1 GI:58748833

KEYWORDS

GSS
Gallus gallus (chicken)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

REFERENCE

1 (bases 1 to 89)

AUTHORS

Wicker, T., Robertson, J. S., Schulze, S. R., Fellus, F. A., Magrini, V.,
Morrison, V. A., Mardis, E. R., Wilson, R. K., Peterson, D. G.,
Paterson, A. H., and Ivatt, R.

TITLE

The repetitive landscape of the chicken genome
Genome Res. 15 (1), 126-136 (2005)

JOURNAL

PUBMED
15256510

COMMENT

Contact: Paterson AH
Plant Genome Mapping Laboratory
University of Georgia, Center for Applied Genetic Technologies
Riverbend Research Laboratory, Room 162, 110 Riverbend Road,
Athens, GA 30602 USA
Tel: 7065830169
Fax: 7065830160
Email: paterson@ga.edu
Sequence from middle repetitive (MR) Cot fraction, Cot 10-100
Class: Hydroxyapatite-fractionated DNA.
Location/Qualifiers

FEATURES

source

1..89

/organism="Gallus gallus"
/mol_type="genomic DNA"
/db_xref="taxon:9031"
/clone="Ggal_73c_PR_C06"
/sex="female"
/clone_lib="Ggal_PR-1"
/note="Produced by Cot-based cloning and sequencing
(CBCS)"

ORIGIN

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Best Local Similarity 93.3%; Pred. No. 1.6e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGCCAGCCAGAGC 15
Db 38 GTGCCAGCCAGTGC 24

RESULT 15

CB884871

CB884871

LOCUS

DEFINITION

Ma15038 Hamster Bluescript Dp11 library Mesocricetus auratus cDNA
similar to outer dense fibre of sperm tails 2 (ODF2), mRNA
sequence.

CB884871

CB884871

ACCESSION

CB884871

CB884871

EST.

EST.

KEYWORDS

KEYWORDS

ORGANISM

Mesocricetus auratus (golden hamster)

Mesocricetus auratus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Cricetidae; Cricetinae; Mesocricetus.
1 (bases 1 to 94)

Oduru, S., Campbell, J. L., Karr, S., Hendry, W. J., Khan, S. A. and
Williams, S. C.

Gene discovery in the hamster: a comparative genomics approach for
gene annotation by sequencing of hamster testis cDNAs

BMC Genomics 4 (1), 22 (2003)

12783626

Contact: Simon C. Williams

Department of Cell Biology and Biochemistry

Texas Tech University Health Science Center

3601 4th Street, Lubbock, TX 79430, USA

Tel: 806 743 2524

Fax: 806 743 2990

Email: simon.williams@ttu.edu

Insert Length: 94 Std Error: 0.00

Seq primer: T7

High quality sequence stop: 94.

Location/Qualifiers

1..94

/organism="Mesocricetus auratus"

/mol_type="mRNA"

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/db_xref="taxon:10036"
/bex="male"
/tissue_type="testis"
/dev_stage="adult"
/clone_lib="Hamster Bluescript Dpni1 library"
/notes="library prepared by insertion of Dpni1
digested hamster testis cDNA into pbluescript, BamHI digested
vector."

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ORIGIN

Query Match	67.0%	Score 13.4	DB 6	Length 94
Best Local Similarity	93.3%	Pred. No. 1.6e+05		
Matches	14; Conservative	0; Mismatches	1; Indels	0; Gaps
QY	2 TGGCCAGCCAGAGCG 16			
Db	58 TGGCCAGCTAGAGCG 72			

Search completed: December 24, 2005, 18:28:36
Job time : 1576 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 11:34:25 ; Search time 48.1 Seconds
(without alignments)
739.111 Million cell updates/sec

Title: US-09-296-264-8
Perfect score: 20
Sequence: 1 gggccagcagcagcagcactg 20

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1134872

Minimum DB seq length: 20
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents NA: *
1: /cgn2_6/prodata/1/ina/1/COMB.seq:*
2: /cgn2_6/prodata/1/ina/5/COMB.seq:*
3: /cgn2_6/prodata/1/ina/6/COMB.seq:*
4: /cgn2_6/prodata/1/ina/6/COMB.seq:*
5: /cgn2_6/prodata/1/ina/6/COMB.seq:*
6: /cgn2_6/prodata/1/ina/6/COMB.seq:*
7: /cgn2_6/prodata/1/ina/6/COMB.seq:*
8: /cgn2_6/prodata/1/ina/6/COMB.seq:*
9: /cgn2_6/prodata/1/ina/6/COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	15.8	79.0	25	3	US-09-396-196G-16399	Sequence 16399, A
C 2	14.4	72.0	25	3	US-09-396-196G-42233	Sequence 42233, A
C 3	14.4	72.0	25	3	US-09-396-196G-42233	Sequence 42233, A
C 4	13.8	69.0	25	3	US-09-396-196G-16382	Sequence 16382, A
C 5	13.8	69.0	25	3	US-09-396-196G-16382	Sequence 16382, A
C 6	13.6	66.0	25	3	US-09-443-199C-1187	Sequence 1187, A
C 7	13.2	66.0	28	3	US-08-658-034-2	Sequence 2, Appl
C 8	13.2	66.0	28	3	US-09-358-052-2	Sequence 2, Appl
C 9	13.2	66.0	76	3	US-09-348-578-31	Sequence 31, Appl
C 10	13.2	66.0	76	3	US-09-699-684-31	Sequence 31, Appl
C 11	13.2	66.0	25	3	US-09-396-196G-43628	Sequence 43628, A
C 12	13.2	66.0	25	3	US-09-396-196G-43628	Sequence 43628, A
C 13	13.2	66.0	25	3	US-09-396-196G-43628	Sequence 43628, A
C 14	12.8	64.0	25	3	US-09-396-196G-61456	Sequence 61456, A
C 15	12.8	64.0	25	3	US-09-396-196G-20714	Sequence 20714, A
C 16	12.8	64.0	27	2	US-07-749-446-6	Sequence 6, Appl
C 17	12.8	64.0	31	2	US-08-360-841-19	Sequence 19, Appl
C 18	12.8	64.0	50	3	US-10-131-827-1137	Sequence 1137, Ap
C 19	12.8	64.0	55	2	US-07-826-928A-16	Sequence 16, Appl
C 20	12.8	64.0	58	3	US-09-339-913B-54	Sequence 54, Appl
C 21	12.8	64.0	58	3	US-09-339-904A-54	Sequence 54, Appl
C 22	12.8	64.0	58	3	US-08-769-062B-54	Sequence 54, Appl
C 23	12.8	64.0	58	3	US-09-344-002B-54	Sequence 54, Appl
C 24	12.8	64.0	58	3	US-09-559-565C-54	Sequence 54, Appl

25	12.8	64.0	58	3	US-09-693-350-54	Sequence 54, Appl
26	12.8	64.0	58	3	US-09-693-389-54	Sequence 54, Appl
27	12.8	64.0	58	3	US-09-559-671A-54	Sequence 54, Appl
28	12.8	64.0	58	3	US-09-339-926A-54	Sequence 54, Appl
29	12.8	64.0	58	3	US-09-954-692-54	Sequence 54, Appl
30	12.8	64.0	59	3	US-09-462-941-32	Sequence 32, Appl
31	12.8	64.0	60	2	US-08-325-243A-14	Sequence 14, Appl
32	12.8	64.0	60	3	US-09-101-272G-5	Sequence 5, Appl
33	12.8	64.0	62	3	US-09-462-941-31	Sequence 31, Appl
34	12.8	64.0	63	2	US-07-842-089E-5	Sequence 5, Appl
35	12.8	64.0	63	2	US-08-264-485-5	Sequence 5, Appl
36	12.8	64.0	63	2	US-09-003-081-7	Sequence 7, Appl
37	12.8	64.0	63	3	US-08-648-262-7	Sequence 7, Appl
38	12.8	64.0	63	3	US-08-648-262-7	Sequence 7, Appl
39	12.8	64.0	63	3	US-09-904-196B-4	Sequence 4, Appl
40	12.8	64.0	63	3	US-09-230-232A-6	Sequence 6, Appl
41	12.8	64.0	63	3	US-09-760-008A-4	Sequence 4, Appl
42	12.8	64.0	63	3	US-10-192-294-4	Sequence 4, Appl
43	12.8	64.0	64	2	US-08-325-243A-13	Sequence 13, Appl
44	12.8	64.0	64	3	US-09-101-272G-5	Sequence 5, Appl
45	12.8	64.0	65	3	US-09-875-494-20	Sequence 20, Appl

ALIGNMENTS

```
RESULT 1
US-09-396-196G-16399/c
; Sequence 16399, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16399
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-16399

Query Match      79.0%; Score 15.8; DB 3; Length 25;
Best Local Similarity 89.5%; Pred. No. 4.7e+02;
Matches 17; Conservativity 0; Mismatches 2; Indels 0; Gaps 0;

Db      1 GTGCCAGCAGCGACT 19
      20 GTGCCAGCAGCGACT 2

RESULT 2
US-09-396-196G-42233
; Sequence 42233, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
```

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; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42233
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-42233
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Query Match          72.0%; Score 14.4; DB 3; Length 25;
Best Local Similarity 93.8%; Pred. No. 2e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      4 CCCAGCCAGAGCGACT 19
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Db      1 CCCACCAAGAGCGACT 16
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RESULT 3

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US-09-396-196G-62691/c
; Sequence 62691, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 62691
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-62691
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Query Match          72.0%; Score 14.4; DB 3; Length 25;
Best Local Similarity 93.8%; Pred. No. 2e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db      18 CCAGCCAGAGCGACTG 3
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RESULT 4

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US-09-396-196G-16382/c
; Sequence 16382, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16382
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-16382
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Query Match          69.0%; Score 13.8; DB 3; Length 25;
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```
Best Local Similarity 88.2%; Pred. No. 3.7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
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Db      17 GTGCCAAGAGAGAGCGA 1
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RESULT 5

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; Sequence 105272, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 105272
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-105272
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```
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Best Local Similarity 88.2%; Pred. No. 3.7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      3 GCCCAGCCAGAGCGACT 19
          |||||
Db      19 GCCCAGCCAGAGCGACT 3
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RESULT 6

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US-09-443-199C-1187/c
; Sequence 1187, Application US/09443199C
; Patent No. 6670464
; GENERAL INFORMATION:
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Leach, Martin
; TITLE OF INVENTION: Nucleic Acids Containing Single Nucleotide
; FILE REFERENCE: 15966-534A
; CURRENT APPLICATION NUMBER: US/09/443,199C
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/109,024
; PRIOR FILING DATE: 1998-11-17
; NUMBER OF SEQ ID NOS: 1272
; SOFTWARE: Curagen Patent Formatter Version 0.9
; SEQ ID NO 1187
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (26)...(0)
; OTHER INFORMATION: 1 of 2 allelic variants (1188 is other entry)
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Accession number CG44931270
US-09-443-199C-1187
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Best Local Similarity 80.0%; Pred. No. 4.7e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GCCCAGCCAGGACTG 20

Db 25 GCCCAGCCAGACGCGCTG 8

RESULT 10

US-09-699-684-31/C

; Sequence 31, Application US/09699684

; Patent No. 643674

; GENERAL INFORMATION:

; APPLICANT: HONJO, Masaru

; APPLICANT: NAITOH, Naokazu

; APPLICANT: UCHIDA, Hiroshi

; APPLICANT: MOCHIZUKI, Daiuke

; APPLICANT: MATSUMOTO, Kazuya

; TITLE OF INVENTION: METHOD FOR SECRETORY PRODUCTION OF HUMAN GROWTH HORMONE

; FILE REFERENCE: 029430-421

; CURRENT APPLICATION NUMBER: US/09/699,684

; PRIOR FILING DATE: 2000-10-31

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/348,578

; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-07

; NUMBER OF SEQ ID NOS: 41

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 31

; LENGTH: 76

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; LOCATION: (1)..(76)

; OTHER INFORMATION: Description of Artificial Sequence: Designed DNA sequence to

; OTHER INFORMATION: act as a primer for PCR to produce the latter half of Oppa

; OTHER INFORMATION: secretion signal

US-09-699-684-31

Query Match 66.0%; Score 13.2; DB 3; Length 76;

Best Local Similarity 83.3%; Pred. No. 7.2e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GCCCAGCCAGGACTG 20

Db 25 GCCCAGCCAGACGCGCTG 8

RESULT 11

US-09-396-196G-43628

; Sequence 43628, Application US/09396196G

; Patent No. 6821724

; GENERAL INFORMATION:

; APPLICANT: Michael Miltmann

; APPLICANT: David Mack

; APPLICANT: David Lockhart

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis

; FILE REFERENCE: 3101.1

; CURRENT APPLICATION NUMBER: US/09/396,196G

; CURRENT FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: 60/100,678

; PRIOR FILING DATE: 1998-09-17

; NUMBER OF SEQ ID NOS: 127806

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 43628

; LENGTH: 25

; TYPE: DNA

; ORGANISM: mus musculus

US-09-396-196G-43628

Query Match 65.0%; Score 13; DB 3; Length 25;

Best Local Similarity 100.0%; Pred. No. 8.5e+03;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCAGCCAGA 13

Db 4 GTGCCAGCCAGA 16

RESULT 12

US-09-396-196G-43629

; Sequence 43629, Application US/09396196G

; Patent No. 6821724

; GENERAL INFORMATION:

; APPLICANT: Michael Miltmann

; APPLICANT: David Mack

; APPLICANT: David Lockhart

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis

; FILE REFERENCE: 3101.1

; CURRENT APPLICATION NUMBER: US/09/396,196G

; CURRENT FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: 60/100,678

; PRIOR FILING DATE: 1998-09-17

; NUMBER OF SEQ ID NOS: 127806

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 43629

; LENGTH: 25

; TYPE: DNA

; ORGANISM: mus musculus

US-09-396-196G-43629

Query Match 65.0%; Score 13; DB 3; Length 25;

Best Local Similarity 100.0%; Pred. No. 8.5e+03;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCAGCCAGA 13

Db 2 GTGCCAGCCAGA 14

RESULT 13

US-09-396-196G-61456

; Sequence 61456, Application US/09396196G

; Patent No. 6821724

; GENERAL INFORMATION:

; APPLICANT: Michael Miltmann

; APPLICANT: David Mack

; APPLICANT: David Lockhart

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis

; FILE REFERENCE: 3101.1

; CURRENT APPLICATION NUMBER: US/09/396,196G

; CURRENT FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: 60/100,678

; PRIOR FILING DATE: 1998-09-17

; NUMBER OF SEQ ID NOS: 127806

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 61456

; LENGTH: 25

; TYPE: DNA

; ORGANISM: mus musculus

US-09-396-196G-61456

Query Match 65.0%; Score 13; DB 3; Length 25;

Best Local Similarity 100.0%; Pred. No. 8.5e+03;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCAGCCAGA 13

Db 7 GTGCCAGCCAGA 19

RESULT 14

US-09-396-196G-20714/C

; Sequence 20714, Application US/09396196G

; Patent No. 6821724

; GENERAL INFORMATION:

US-09-396-196G-20714/C

APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Alzymetric, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 20714
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-09-396-196G-20714

Query Match 64.0%; Score 12.8; DB 3; Length 25;
Best Local Similarity 87.5%; Pred. No. 1e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CCAGCCAGAGCACTG 20
Db 24 CCAGCCAGAGCACTG 9

RESULT 15

US-07-749-446-6/c
Sequence 6, Application US/07749446
Patent No. 5593857

GENERAL INFORMATION:

APPLICANT: Higaki, Jeffrey N.
APPLICANT: Tischer, Edmund G.
APPLICANT: Cordell, Barbara
APPLICANT: Thompson, Stewart A.
TITLE OF INVENTION: PRODUCTION OF HOMOGENEOUS CILARY
TITLE OF INVENTION: NEUROTROPHIC FACTOR
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: California Biotechnology Inc.
STREET: 2450 Bayshore Parkway
CITY: Mountain View
STATE: California
COUNTRY: USA
ZIP: 94043
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/749,446
FILING DATE: 19911008
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Shearer, Peter R.
REGISTRATION NUMBER: 28,117
REFERENCE/DOCKET NUMBER: PC43:US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-962-5860
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-07-749-446-6

Query Match 64.0%; Score 12.8; DB 2; Length 27;
Best Local Similarity 87.5%; Pred. No. 1e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CCAGCCAGAGCACT 19
Db 27 CCAGCCAGAGCACT 12

Search completed: December 24, 2005, 18:36:29
Job time: 49.1 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 14:06:30 ; Search time 337.6 Seconds
(without alignments) 489.892 Million cell updates/sec

Title: US-09-296-264-8

Perfect score: 20

Sequence: 1 GTGCCAGCAGCAGCAGCTG 20

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 9793542 seqs, 413468905 residues

Total number of hits satisfying chosen parameters: 9887334

Minimum DB seq length: 20

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Published Applications NA Main:*

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- 2: /cgn2_6/ptodata/1/pubpna/us08_PUBCOMB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/us09_PUBCOMB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/us09B_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/us10_PUBCOMB.seq:*
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- 8: /cgn2_6/ptodata/1/pubpna/us10D_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/us10E_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/us11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3	US-09-296-264-8
2	15.8	79.0	25	8	US-10-719-900-39761
3	15.8	79.0	25	9	US-10-809-189-16399
4	15.4	77.0	25	8	US-10-719-900-814778
5	15	75.0	25	7	US-10-719-956-24643
6	15	75.0	25	8	US-10-719-900-871237
7	15	75.0	25	10	US-11-036-317-9133
8	15	75.0	25	10	US-11-036-317-435107
9	15	75.0	25	10	US-11-036-317-42520
10	14.8	74.0	25	7	US-10-719-956-400453
11	14.8	74.0	25	10	US-11-036-317-456571
12	14.4	72.0	25	8	US-10-719-900-44301
13	14.4	72.0	25	8	US-10-719-900-960417
14	14.4	72.0	25	9	US-10-809-189-42233
15	14.4	72.0	25	9	US-10-809-189-62691
16	14.4	72.0	25	10	US-11-036-317-777729
17	14.4	72.0	25	10	US-11-036-317-854970
18	14.4	72.0	25	10	US-11-036-317-879103
19	14.4	72.0	25	10	US-11-036-317-886387
20	14.4	72.0	25	10	US-11-036-317-932924
21	14.4	72.0	25	10	US-11-036-317-987167
22	14.4	72.0	25	7	US-10-719-956-193314
23	14.2	71.0	25	7	US-10-719-956-193314

c	24	14.2	71.0	25	7	US-10-719-956-552832	Sequence 552832,
c	25	14.2	71.0	25	7	US-10-719-956-616700	Sequence 616700,
c	26	14.2	71.0	25	8	US-10-719-900-39762	Sequence 39762, A
c	27	14.2	71.0	25	8	US-10-719-900-495245	Sequence 495245,
c	28	14.2	71.0	25	10	US-11-036-317-400663	Sequence 400663,
c	29	14.2	71.0	25	10	US-11-036-317-789908	Sequence 789908,
c	30	14.2	71.0	42	3	US-09-791-378-664	Sequence 664, App
c	31	14.2	71.0	42	3	US-09-791-393-305	Sequence 306, App
c	32	14.2	71.0	42	3	US-09-791-389-306	Sequence 306, App
c	33	14.2	71.0	42	3	US-09-791-377-664	Sequence 664, App
c	34	14	70.0	25	8	US-10-719-900-479264	Sequence 479264,
c	35	14	70.0	25	10	US-11-036-317-15574	Sequence 15574, A
c	36	13.8	69.0	25	7	US-10-719-956-564652	Sequence 564652,
c	37	13.8	69.0	25	8	US-10-719-900-344999	Sequence 344999,
c	38	13.8	69.0	25	8	US-10-719-900-814777	Sequence 814777,
c	39	13.8	69.0	25	8	US-10-719-900-881264	Sequence 881264,
c	40	13.8	69.0	25	9	US-10-809-189-16382	Sequence 16382, A
c	41	13.8	69.0	25	9	US-10-809-189-105272	Sequence 105272,
c	42	13.8	69.0	25	10	US-11-036-317-576898	Sequence 576898,
c	43	13.8	69.0	36	6	US-10-259-226-10	Sequence 10, Appl
c	44	13.8	69.0	36	6	US-10-200-002-10	Sequence 10, Appl
c	45	13.6	68.0	25	7	US-10-719-956-125172	Sequence 125172,

ALIGNMENTS

```

RESULT 1
US-09-296-264-8
; Sequence 8, Application US/09296264
; Publication No. US20030083274A1
; GENERAL INFORMATION:
; APPLICANT: WRIGHT, Jim A.
; APPLICANT: YOUNG, Aiping H.
; APPLICANT: LEE, Yoon S.
; TITLE OF INVENTION: NEUROFILIN ANTISENSE OLIGONUCLEOTIDE SEQUENCES AND
; TITLE OF INVENTION: METHODS OF USING SAME TO MODULATE CELL GROWTH
; FILE REFERENCE: 032396-043
; CURRENT APPLICATION NUMBER: US/09/296,264
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 60/082,791
; EARLIER FILING DATE: 1998-04-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; TYPE: DNA
; LENGTH: 20
; ORGANISM: Human
; US-09-296-264-8

Query Match      100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCAGCAGCAGCAGCTG 20
Db 1 GTGCCAGCAGCAGCAGCTG 20

RESULT 2
US-10-719-900-39761
; Sequence 39761, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1.1

```

```
; SEQ ID NO 39761
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-39761

Query Match          79.0%; Score 15.8; DB 8; Length 25;
Best Local Similarity 89.5%; Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGCCCGAGCCAGCGACTG 20
Db 4 TGCCCGAGCCAGCGACTG 22

RESULT 3
US-10-809-189-16399/c
; Sequence 16399, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: PaacSeq for Windows Version 4.0
; SEQ ID NO 16399
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-809-189-16399

Query Match          79.0%; Score 15.8; DB 9; Length 25;
Best Local Similarity 89.5%; Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTGCCGAGCCAGCGACT 19
Db 20 GTGCCGAGCCAGCGACT 2

RESULT 4
US-10-719-900-814778
; Sequence 814778, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 814778
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-814778

Query Match          77.0%; Score 15.4; DB 8; Length 25;
Best Local Similarity 94.1%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 2 TGCCCGAGCCAGCGAC 18
Db 1 TGCCCGAGCCAGCGAC 17

RESULT 5
US-10-719-956-247643
; Sequence 247643, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 247643
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-247643

Query Match          75.0%; Score 15; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCCAGCCAGAGCGAC 18
Db 1 CCCAGCCAGAGCGAC 15

RESULT 6
US-10-719-900-871237
; Sequence 871237, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 871237
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-871237

Query Match          75.0%; Score 15; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCGAGCCAGCGC 15
Db 4 GTGCCGAGCCAGCGC 18

RESULT 7
US-11-036-317-9133/c
; Sequence 9133, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
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;; CURRENT FILING DATE: 2005-01-13
;; PRIOR APPLICATION NUMBER: US 60/536,639
;; PRIOR FILING DATE: 2004-01-13
;; NUMBER OF SEQ ID NOS: 991174
;; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
;; SEQ ID NO: 9133
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Mus musculus
US-11-036-317-9133

Query Match 75.0%; Score 15; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CAGCCAGAGCGACTG 20
DB 19 CAGCCAGAGCGACTG 5

RESULT 8
US-11-036-317-39107/c
;; Sequence 39107, Application US/11036317
;; Publication No. US20050214823A1
;; GENERAL INFORMATION:
;; APPLICANT: Williams, Alan
;; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
;; FILE REFERENCE: 3654.1
;; CURRENT APPLICATION NUMBER: US/11/036,317
;; CURRENT FILING DATE: 2005-01-13
;; PRIOR APPLICATION NUMBER: US 60/536,639
;; PRIOR FILING DATE: 2004-01-13
;; NUMBER OF SEQ ID NOS: 991174
;; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
;; SEQ ID NO: 39107
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Mus musculus
US-11-036-317-39107

Query Match 75.0%; Score 15; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CAGCCAGAGCGACTG 20
DB 23 CAGCCAGAGCGACTG 9

RESULT 9
US-11-036-317-42520/c
;; Sequence 42520, Application US/11036317
;; Publication No. US20050214823A1
;; GENERAL INFORMATION:
;; APPLICANT: Williams, Alan
;; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
;; FILE REFERENCE: 3654.1
;; CURRENT APPLICATION NUMBER: US/11/036,317
;; CURRENT FILING DATE: 2005-01-13
;; PRIOR APPLICATION NUMBER: US 60/536,639
;; PRIOR FILING DATE: 2004-01-13
;; NUMBER OF SEQ ID NOS: 991174
;; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
;; SEQ ID NO: 42520
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Mus musculus
US-11-036-317-42520

Query Match 75.0%; Score 15; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 CAGCCAGAGCGACTG 20
DB 21 CAGCCAGAGCGACTG 7

RESULT 10
US-11-036-317-43628/c
;; Sequence 43628, Application US/11036317
;; Publication No. US20050214823A1
;; GENERAL INFORMATION:
;; APPLICANT: Williams, Alan
;; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
;; FILE REFERENCE: 3654.1
;; CURRENT APPLICATION NUMBER: US/11/036,317
;; CURRENT FILING DATE: 2005-01-13
;; PRIOR APPLICATION NUMBER: US 60/536,639
;; PRIOR FILING DATE: 2004-01-13
;; NUMBER OF SEQ ID NOS: 991174
;; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
;; SEQ ID NO: 43628
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Mus musculus
US-11-036-317-43628

Query Match 75.0%; Score 15; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CAGCCAGAGCGACTG 20
DB 24 CAGCCAGAGCGACTG 10

RESULT 11
US-10-719-956-400453/c
;; Sequence 400453, Application US/10719956
;; Publication No. US20040146910A1
;; GENERAL INFORMATION:
;; APPLICANT: Xue Mei Zhou
;; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
;; FILE REFERENCE: 3527.1
;; CURRENT APPLICATION NUMBER: US/10/719,956
;; CURRENT FILING DATE: 2003-11-20
;; PRIOR APPLICATION NUMBER: 60/427,836
;; PRIOR FILING DATE: 2002-11-20
;; NUMBER OF SEQ ID NOS: 699466
;; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
;; SEQ ID NO: 400453
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Rattus norvegicus
US-10-719-956-400453

Query Match 74.0%; Score 14.8; DB 7; Length 25;
Best Local Similarity 88.9%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGCCAGAGCGACT 19
DB 24 TGCCAGAGCGCGCT 7

RESULT 12
US-11-036-317-456571
;; Sequence 456571, Application US/11036317
;; Publication No. US20050214823A1
;; GENERAL INFORMATION:
;; APPLICANT: Williams, Alan
US-11-036-317-456571

TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 456571
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-456571

Query Match 74.0%; Score 14.8; DB 10; Length 25;
Best Local Similarity 88.9%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTGCCGAGCAGCG 18
DB 1 GTGCCGAGCAGCG 18

RESULT 13
US-10-719-900-44301
Sequence 44301, Application US/10719900
Publication No. US20050026164A1
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 44301
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-10-719-900-44301

Query Match 72.0%; Score 14.4; DB 8; Length 25;
Best Local Similarity 93.8%; Pred. No. 5.9e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGCCGAGCAGCG 16
DB 7 GTGCCGAGCAGCG 22

RESULT 14
US-10-719-900-960417/c
Sequence 960417, Application US/10719900
Publication No. US20050026164A1
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 960417
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-10-719-900-960417

Query Match 72.0%; Score 14.4; DB 8; Length 25;

Best Local Similarity 93.8%; Pred. No. 5.9e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCAGCCAGGCGACTG 20
DB 24 CCAGCCAGGCGACTG 9

RESULT 15
US-10-809-189-42233
Sequence 42233, Application US/10809189
Publication No. US20050048531A1
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/10/809,189
CURRENT FILING DATE: 2004-03-25
PRIOR APPLICATION NUMBER: US/09/396,196
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 42233
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-10-809-189-42233

Query Match 72.0%; Score 14.4; DB 9; Length 25;
Best Local Similarity 93.8%; Pred. No. 5.9e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCAGCCAGGCGACT 19
DB 1 CCAGCCAGGCGACT 16

Search completed: December 25, 2005, 04:14:23
Job time : 338.6 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 18:29:07 ; Search time 135.3 Seconds
(without alignments)
76.712 Million cell updates/sec

Title: US-09-296-264-8

Perfect score: 20

Sequence: 1 gggccagccagcagcagcgcg 20

Scoring table:

IDENTITY_NUC
Gapop 10.0, Gapect 1.0

Searched: 4168288 seqs, 259477437 residues

Total number of hits satisfying chosen parameters: 1608458

Minimum DB seq length: 20
Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA New:*
1: /cgn2_6/prodata/2/pubphn/US08_NEW_PUB.seq:*
2: /cgn2_6/prodata/2/pubphn/US06_NEW_PUB.seq:*
3: /cgn2_6/prodata/2/pubphn/US07_NEW_PUB.seq:*
4: /cgn2_6/prodata/2/pubphn/US09_NEW_PUB.seq:*
5: /cgn2_6/prodata/2/pubphn/US10_NEW_PUB.seq:*
6: /cgn2_6/prodata/2/pubphn/US11_NEW_PUB.seq:*
7: /cgn2_6/prodata/2/pubphn/US11_NEW_PUB.seq2:*
8: /cgn2_6/prodata/2/pubphn/US11_NEW_PUB.seq3:*
9: /cgn2_6/prodata/2/pubphn/US11_NEW_PUB.seq4:*
10: /cgn2_6/prodata/2/pubphn/US60_NEW_PUB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15.8	79.0	25	US-11-121-849-444117	Sequence 444117, A
2	15.2	76.0	25	US-11-121-849-28342	Sequence 28342, A
3	15.2	76.0	25	US-11-121-849-548725	Sequence 548725, A
4	14.2	71.0	25	US-11-121-849-548692	Sequence 548692, A
5	14	70.0	25	US-11-121-849-429927	Sequence 429927, A
6	13.8	69.0	25	US-11-121-849-248643	Sequence 248643, A
7	13.8	69.0	25	US-11-121-849-313084	Sequence 313084, A
8	13.8	69.0	25	US-11-121-849-340873	Sequence 340873, A
9	13.8	69.0	25	US-11-121-849-340915	Sequence 340915, A
10	13.8	69.0	25	US-11-121-849-340916	Sequence 340916, A
11	13.6	68.0	25	US-11-121-849-195011	Sequence 195011, A
12	13.6	68.0	25	US-11-121-849-195074	Sequence 195074, A
13	13.6	68.0	25	US-11-121-849-485677	Sequence 485677, A
14	13.4	67.0	25	US-11-121-849-94049	Sequence 94049, A
15	13.4	67.0	25	US-11-121-849-593181	Sequence 593181, A
16	13.2	66.0	25	US-11-121-849-452270	Sequence 452270, A
17	13.2	66.0	25	US-11-121-849-520368	Sequence 520368, A
18	13	65.0	25	US-11-121-849-83263	Sequence 83263, A
19	13	65.0	25	US-11-121-849-83264	Sequence 83264, A
20	13	65.0	25	US-11-121-849-280576	Sequence 280576, A
21	13	65.0	25	US-11-121-849-291424	Sequence 291424, A
22	13	65.0	25	US-11-121-849-438663	Sequence 438663, A
23	13	65.0	25	US-11-121-849-474629	Sequence 474629, A

C 24	13	65.0	25	US-11-121-849-474630	Sequence 474630, A
C 25	13	65.0	25	US-11-121-849-474631	Sequence 474631, A
C 26	13	65.0	25	US-11-121-849-489362	Sequence 489362, A
C 27	12.8	64.0	25	US-11-121-849-42175	Sequence 42175, A
C 28	12.8	64.0	25	US-11-121-849-112602	Sequence 112602, A
C 29	12.8	64.0	25	US-11-121-849-131719	Sequence 131719, A
C 30	12.8	64.0	25	US-11-121-849-131720	Sequence 131720, A
C 31	12.8	64.0	25	US-11-121-849-132378	Sequence 132378, A
C 32	12.8	64.0	25	US-11-121-849-132379	Sequence 132379, A
C 33	12.8	64.0	25	US-11-121-849-457604	Sequence 457604, A
C 34	12.8	64.0	25	US-11-121-849-518332	Sequence 518332, A
C 35	12.8	64.0	25	US-11-121-849-538982	Sequence 538982, A
C 36	12.8	64.0	25	US-11-121-849-647201	Sequence 647201, A
C 37	12.8	64.0	32	US-10-939-294A-17166	Sequence 17166, A
C 38	12.6	63.0	25	US-11-121-849-23949	Sequence 23949, A
C 39	12.6	63.0	25	US-11-121-849-31672	Sequence 31672, A
C 40	12.6	63.0	25	US-11-121-849-127447	Sequence 127447, A
C 41	12.6	63.0	25	US-11-121-849-181631	Sequence 181631, A
C 42	12.6	63.0	25	US-11-121-849-191930	Sequence 191930, A
C 43	12.6	63.0	25	US-11-121-849-256169	Sequence 256169, A
C 44	12.6	63.0	25	US-11-121-849-297509	Sequence 297509, A
C 45	12.6	63.0	25	US-11-121-849-297510	Sequence 297510, A

ALIGNMENTS

RESULT 1
US-11-121-849-444117
; Sequence 444117, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 444117
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-444117

Query Match
Best Local Similarity 79.0%; Score 15.8; DB 7; Length 25;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGGCCAGCCAGCAGCAGCTG 20
Db 5 TGGCCAGCCAGCAGCAGCTG 23

RESULT 2
US-11-121-849-28342
; Sequence 28342, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 28342

LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-28342

Query Match 76.0%; Score 15.2; DB 7; Length 25;
Best Local Similarity 85.0%; Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGCCAGCCGAGGACTG 20
|||||
DB 5 GTGCCAGCCGAGGACTG 24

RESULT 3
US-11-121-849-548725

Sequence 548725, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:

APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 548725
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-548725

Query Match 76.0%; Score 15.2; DB 7; Length 25;
Best Local Similarity 85.0%; Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGCCAGCCGAGGACTG 20
|||||
DB 6 GTGCCAGCCGAGGACTG 25

RESULT 4
US-11-121-849-548692

Sequence 548692, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:

APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 548692
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-548692

Query Match 71.0%; Score 14.2; DB 7; Length 25;
Best Local Similarity 84.2%; Pred. No. 7.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGCCAGCCGAGGACT 19
|||||
DB 7 GTGCCAGCCGAGGACT 25

RESULT 5
US-11-121-849-429927

Sequence 429927, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:

APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 429927
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-429927

Query Match 70.0%; Score 14; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGCCAGCCGAGGC 15
|||||
DB 2 TGCCAGCCGAGGC 15

RESULT 6
US-11-121-849-248643/C

Sequence 248643, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:

APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 248643
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-248643

Query Match 69.0%; Score 13.8; DB 7; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGCCAGCCGAGGC 18
|||||
DB 17 TGCCAGCCGAGGC 1

RESULT 7
US-11-121-849-313084/C

Sequence 313084, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:

APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949

Query Match 69.0%; Score 13.8; DB 7; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGCCAGCCGAGGC 18
|||||
DB 17 TGCCAGCCGAGGC 1

RESULT 7
US-11-121-849-313084/C

Sequence 313084, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:

APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949

Query Match 69.0%; Score 13.8; DB 7; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGCCAGCCGAGGC 18
|||||
DB 17 TGCCAGCCGAGGC 1

PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 313084
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-313084

Query Match 69.0%; Score 13.8; DB 7; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CCCAGCCAGAGCACTG 20
Db 25 CACAGCCAGAGCACTG 9

RESULT 8
US-11-121-849-340873

Sequence 340873, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:

APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 340873
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-340873

Query Match 69.0%; Score 13.8; DB 7; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CCCAGCCAGAGCACTG 20
Db 4 CCCAGCCAGAGCACTG 20

RESULT 9
US-11-121-849-340915

Sequence 340915, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 340915
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-340915

Query Match 69.0%; Score 13.8; DB 7; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CCCAGCCAGAGCACTG 20
Db 4 CCCAGCCAGAGCACTG 20

RESULT 10
US-11-121-849-340916

Sequence 340916, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 340916
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-340916

Query Match 69.0%; Score 13.8; DB 7; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CCCAGCCAGAGCACTG 20
Db 2 CCCAGCCAGAGCACTG 18

RESULT 11
US-11-121-849-195011

Sequence 195011, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 195011
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-195011

Query Match 68.0%; Score 13.6; DB 7; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GTGCCAGCCAGAGCACTG 20
Db 2 GTGCCAGCCAGAGCACTG 21

RESULT 12
US-11-121-849-195074

Sequence 195074, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 195074
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-195074

Query Match 69.0%; Score 13.8; DB 7; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 195074
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-195074
```

```
Query Match          68.0%; Score 13.6; DB 7; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1 GTGCCCGAGCGAGCGACTG 20
Db 2 GTGACCGAGCGAGCGCAATG 21
```

```
RESULT 13
US-11-121-849-485677
; Sequence 485677, Application US/11/121,849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 485677
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-485677
```

```
Query Match          68.0%; Score 13.6; DB 7; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1 GTGCCCGAGCGAGCGACTG 20
Db 6 GTCCCGAGCGAGCGCAATG 25
```

```
RESULT 14
US-11-121-849-94049/c
; Sequence 94049, Application US/11/121,849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 94049
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-94049
```

```
Query Match          67.0%; Score 13.4; DB 7; Length 25;
Best Local Similarity 93.3%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 GTGCCCGAGCGAGGC 15
Db 22 GTGCCCGAGCGAGGC 8
```

```
RESULT 15
US-11-121-849-593181
; Sequence 593181, Application US/11/121,849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 593181
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-593181
```

```
Query Match          67.0%; Score 13.4; DB 7; Length 25;
Best Local Similarity 93.3%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 5 CCAGCGAGCGAGACT 19
Db 11 CCAAGCGAGCGAGACT 25
```

Search completed: December 25, 2005, 04:37:03
Job time : 135.3 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 10:28:41 ; Search time 582 Seconds
(without alignments)
1953.383 Million cell updates/sec

Title: US-09-296-264-9

Perfect score: 20

Sequence: 1 tgaagtcgcggtcggaagtcgc 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 1858228

Minimum DB seq length: 20

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

- 1: gb_ba:*
- 2: gb_in:*
- 3: gb_env:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pr:*
- 9: gb_ro:*
- 10: gb_scs:*
- 11: gb_sy:*
- 12: gb_un:*
- 13: gb_vi:*
- 14: gb_hcg:*
- 15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6	BD211666 Antisense
2	15.2	76.0	60	6	CQ552983 Sequence
3	15.2	76.0	100	6	AX999601 Sequence
4	15	75.0	24	6	A57512 Sequence 4
5	15	75.0	24	6	A57514 Sequence 6
6	15	75.0	24	6	AR052978 Sequence
7	15	75.0	24	6	AR052980 Sequence
8	14.8	74.0	48	6	A28016 Sequence
9	14.8	74.0	48	6	A28017 Sequence
10	14.4	72.0	60	6	CQ551412 Sequence
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14	14.2	71.0	30	6	AR126277 Sequence
15	14.2	71.0	30	6	BD075492 Sequence
16	14.2	71.0	50	6	BD172352 Sequence
17	14.2	71.0	50	6	BD172671 Sequence
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26	14.2	71.0	50	6	AR473105 Sequence
27	14.2	71.0	50	6	AR527091 Sequence
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29	14.2	71.0	50	6	AR592142 Sequence
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33	14.2	71.0	50	6	AR635838 Sequence
34	14.2	71.0	50	6	AR650567 Sequence
35	14.2	71.0	50	6	AR657508 Sequence
36	14.2	71.0	50	6	AX697560 Sequence
37	14.2	71.0	51	6	CQ005584 Sequence
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40	14.2	71.0	66	6	CS016537 Sequence
41	14.2	71.0	68	6	BD105319 Method fo
42	14.2	71.0	77	6	BD105318 Method fo
43	14.2	71.0	82	2	AY282610 Symaglit
44	14.2	71.0	82	8	AY270944 Homo sapi
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ALIGNMENTS

RESULT 1
BD211666
LOCUS
DEFINITION
Antisense oligonucleotide sequence of neuropilin and method of using the same for controlling cell proliferation.

ACCESSION
BD211666.1 GI:33021436
VERSION
JP 2002512793-A/9.
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
AUTHORS
Wright,J.A., Young,A.H. and Lee,Y.S.
TITLE
Antisense oligonucleotide sequence of neuropilin and method of using the same for controlling cell proliferation
JOURNAL
Patent: JP 2002512793-A 9 08-MAY-2002;
GENSENSE TECHNOLOGIES INC

COMMENT
OS Homo sapiens (human)
PN JP 2002512793-A/9
PD 08-MAY-2002
PR 23-APR-1999 JP 2000545999

PI JIM A WRIGHT,ALPING H YOUNG,YOON S LEE
PC C12N15/09,A61K31/711,A61K48/00,A61P35/00,C12N15/00 CC
Antisense oligonucleotide sequence of neuropilin and method of using the
CC same for controlling cell proliferation
FH key Location/Qualifiers
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FEATURES

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ORIGIN

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QY 1 TGAGTGGCGGTGAGTGC 20
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Db 1 TGAGTGGCGGTGAGTGC 20

RESULT 2
LOCUS CQ552983 60 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 22618 from Patent WO0210449.
ACCESSION CQ552983
VERSION CQ552983.1 GI:41519410
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE 1
AUTHORS Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Faigler, S.
TITLE Oligonucleotide library for detecting rna transcripts and splice
variants that populate a transcriptome
JOURNAL Patent: WO 0210449-A 22618 07-FEB-2002;
CompuGen Inc. (US)
FEATURES Location/Qualifiers
source 1..60
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 76.0%; Score 15.2; DB 6; Length 60;
Best Local Similarity 85.0%; Pred. No. 2.7e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAGTGGCGGTGAGTGC 20
| | | | | | | | | | | | | | | | | | | | | |
Db 25 TGAGTGGCTGTGATGATCC 44

RESULT 3
LOCUS AX999601 100 bp DNA linear PAT 16-JAN-2004
DEFINITION Sequence 11064 from Patent EP1260592.
ACCESSION AX999601
VERSION AX999601.1 GI:41005947
KEYWORDS
SOURCE Escherichia coli
ORGANISM Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.

REFERENCE 1
AUTHORS Donner, H., Drescher, B., Huber, A. and Weber, J.
TITLE Biochip
JOURNAL Patent: EP 1260592-A 11064 27-NOV-2002;
MMG-Biotech AG (DE)
FEATURES Location/Qualifiers
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/note="B1980 B1981 U00096 complement(2050646__2051350)"

ORIGIN

Query Match 76.0%; Score 15.2; DB 6; Length 100;
Best Local Similarity 85.0%; Pred. No. 2.7e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAGTGGCGGTGAGTGC 20
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Db 31 TGAGTGGCGCGAGGAATGC 50

RESULT 4
LOCUS A57512/c 24 bp DNA linear PAT 03-MAR-1998
DEFINITION Sequence 4 from Patent WO9632483.
ACCESSION A57512
VERSION A57512.1 GI:3713370
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified sequences.

REFERENCE 1
AUTHORS Masucci, M.G.
TITLE IMMUNE-EVADING PROTEINS
JOURNAL Patent: WO 9632483-A 4 17-OCT-1996;
MASUCCI MARIA GRAZIA (SE)
COMMENT Other publication AU 5284296 961030.
FEATURES Location/Qualifiers
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/db_xref="taxon:3264"

ORIGIN

Query Match 75.0%; Score 15; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.5e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGTGGCGGTGGA 16
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Db 15 GAGGTGGCGGTGGA 1

RESULT 5
LOCUS A57514/c 24 bp DNA linear PAT 03-MAR-1998
DEFINITION Sequence 6 from Patent WO9632483.
ACCESSION A57514
VERSION A57514.1 GI:3713372
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified sequences.

REFERENCE 1
AUTHORS Masucci, M.G.
TITLE IMMUNE-EVADING PROTEINS
JOURNAL Patent: WO 9632483-A 6 17-OCT-1996;
MASUCCI MARIA GRAZIA (SE)
COMMENT Other publication AU 5284296 961030.
FEATURES Location/Qualifiers
source 1..24
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/mol_type="unassigned DNA"
/db_xref="taxon:3264"

ORIGIN

Query Match 75.0%; Score 15; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.5e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGTGGCGGTGGA 16
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Db 15 GAGGTGGCGGTGGA 1

RESULT 6
LOCUS AR052978 24 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 7 from patent US 5833991.
ACCESSION AR052978
VERSION AR052978.1 GI:5977840
KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Mauceli, M.G.
TITLE Glycine-containing sequences conferring invisibility to the immune system
JOURNAL Patent: US 5833991-A 7 10-NOV-1998;
FEATURES Location/Qualifiers
source 1..24
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Query Match 75.0%; Score 15; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.5e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GAGGTGCGGGTGAA 16
15 GAGGTGCGGGTGAA 1

RESULT 7
LOCUS AR052980 24 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 10 from patent US 5833991.
ACCESSION AR052980
VERSION AR052980.1 GI:5977842
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Mauceli, M.G.
TITLE Glycine-containing sequences conferring invisibility to the immune system
JOURNAL Patent: US 5833991-A 10 10-NOV-1998;
FEATURES Location/Qualifiers
source 1..24
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/mol_type="unassigned DNA"

ORIGIN
Query Match 75.0%; Score 15; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.5e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GAGGTGCGGGTGAA 16
15 GAGGTGCGGGTGAA 1

RESULT 8
LOCUS A28016 48 bp DNA linear PAT 03-OCT-1995
DEFINITION PC04-FPCD3 construction oligo 2119.
ACCESSION A28016
VERSION A28016.1 GI:1248563
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 48)
AUTHORS Karjalainen, K., Lanzavecchia, A. and Trautnecker, A.
TITLE Chimeric polypeptides
JOURNAL Patent: EP 0505908-A 11 30-SEP-1992;
F. HOFMANN-LA ROCHE AG
FEATURES Location/Qualifiers
source 1..48
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ORIGIN

Query Match 74.0%; Score 14.8; DB 6; Length 48;
Best Local Similarity 88.9%; Pred. No. 4.2e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GAGGTGCGGGTGAAAGTG 19
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RESULT 9
LOCUS A28017 48 bp DNA linear PAT 03-OCT-1995
DEFINITION PC04-FPCD3 construction oligo 2120.
ACCESSION A28017
VERSION A28017.1 GI:1248564
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 48)
AUTHORS Karjalainen, K., Lanzavecchia, A. and Trautnecker, A.
TITLE Chimeric polypeptides
JOURNAL Patent: EP 0505908-A 12 30-SEP-1992;
F. HOFMANN-LA ROCHE AG
FEATURES Location/Qualifiers
source 1..48
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 74.0%; Score 14.8; DB 6; Length 48;
Best Local Similarity 88.9%; Pred. No. 4.2e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GAGGTGCGGGTGAAAGTG 19
37 GAGGTGCGGGTGAAAGTG 20

RESULT 10
LOCUS CQ551412 60 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 21047 from Patent W00210445.
ACCESSION CQ551412
VERSION CQ551412.1 GI:41517839
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)
REFERENCE 1
AUTHORS Shoshan, A., Wasserman, A., Mintz, B., Mintz, L. and Paigler, S.
TITLE Oligonucleotide library for detecting rna transcripts and splice variants that populate a transcriptome
JOURNAL Patent: WO 0210449-A 21047 07-FEB-2002;
Comugen Inc. (US)
FEATURES Location/Qualifiers
source 1..60
/organism="Homo sapiens"
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Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 AGGTGCGGGTGAAAGT 18
6 AGGTGCGGGTGAAAGT 21

DB

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RESULT 11
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DEFINITION AJ008144
ACCESSION AJ008144.1 GI:3873593
VERSION NIK gene.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
AUTHORS Aronson,F.C., Magnusson,P., Andersson,B., Karsten,S.L.,
Shibasaki,Y., Lendon,C.L., Goate,A.M. and Brookes,A.J.
TITLE The NIK protein kinase and C17orf1 genes: chromosomal mapping, gene
structures and mutational screening in frontotemporal dementia and
parkinsonism linked to chromosome 17
JOURNAL Hum. Genet. 103 (3), 340-345 (1998)
PUBMED 9799091
REFERENCE
AUTHORS Brookes,A.
TITLE Direct Submision
JOURNAL Submitted (21-APR-1998) A. Brookes, Department of Genetics and
Pathology, Biomedical Center, Box 589, 751 23 Uppsala, SWEDEN
FEATURES
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Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 AGGTGCGGCTGGAAGT 18
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Db 49 AGGTGCGGCTGGAAGT 64
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ARI06307/c
LOCUS ARI06307 30 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 11 from patent US 6107025.
ACCESSION ARI06307
VERSION ARI06307.1 GI:12820837
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS 1 (bases 1 to 30)
Unclassified.
Caskey,C.Thomas., Nelson,D.L., Pieretti,M., Warren,S.T. and
Oostra,B.A.
TITLE Diagnosis of the fragile X syndrome
JOURNAL Patent: US 6107025-A 11 22-AUG-2000;
FEATURES
Location/Qualifiers
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Query Match 71.0%; Score 14.2; DB 6; Length 30;
Best Local Similarity 84.2%; Pred. No. 8.1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 GAGTGCAGGTGGAAGTGC 20
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Db 25 GAGCTGTGTGTGGAAGTGC 7
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RESULT 13
ARI10116/c
LOCUS ARI10116 30 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 7 from patent US 6114150.
ACCESSION ARI10116
VERSION ARI10116.1 GI:12826392
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS 1 (bases 1 to 30)
Unclassified.
Weissman,S.M. and Baskaran,N.
TITLE Amplification of nucleic acids
JOURNAL Patent: US 6114150-A 7 05-SEP-2000;
FEATURES
Location/Qualifiers
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Best Local Similarity 84.2%; Pred. No. 8.1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 GAGTGCAGGTGGAAGTGC 20
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Db 25 GAGCTGTGTGTGGAAGTGC 7
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LOCUS ARI26277 30 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 11 from patent US 6180337.
ACCESSION ARI26277
VERSION ARI26277.1 GI:14112870
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS 1 (bases 1 to 30)
Unclassified.
Caskey,C.Thomas., Nelson,D.L., Pieretti,M., Warren,S.T.,
Oostra,B.A. and Fu,Y.-h.
TITLE Diagnosis of the fragile X syndrome
JOURNAL Patent: US 6180337-A 11 30-JAN-2001;
FEATURES
Location/Qualifiers
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QY 2 GAGTGCAGGTGGAAGTGC 20
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Db 25 GAGCTGTGTGTGGAAGTGC 7
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RESULT 15
BD075492
LOCUS BD075492 50 bp DNA linear PAT 27-AUG-2002
DEFINITION Secretary and transmembrane polypeptide and nucleic acid encoding
the same.
ACCESSION BD075492
VERSION BD075492.1 GI:22621095

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Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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LOCUS ARI10116 30 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 7 from patent US 6114150.
ACCESSION ARI10116
VERSION ARI10116.1 GI:12826392
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS 1 (bases 1 to 30)
Unclassified.
Weissman,S.M. and Baskaran,N.
TITLE Amplification of nucleic acids
JOURNAL Patent: US 6114150-A 7 05-SEP-2000;
FEATURES
Location/Qualifiers
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Query Match 71.0%; Score 14.2; DB 6; Length 30;
Best Local Similarity 84.2%; Pred. No. 8.1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 GAGTGCAGGTGGAAGTGC 20
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Db 25 GAGCTGTGTGTGGAAGTGC 7
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RESULT 14
ARI26277/c
LOCUS ARI26277 30 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 11 from patent US 6180337.
ACCESSION ARI26277
VERSION ARI26277.1 GI:14112870
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS 1 (bases 1 to 30)
Unclassified.
Caskey,C.Thomas., Nelson,D.L., Pieretti,M., Warren,S.T.,
Oostra,B.A. and Fu,Y.-h.
TITLE Diagnosis of the fragile X syndrome
JOURNAL Patent: US 6180337-A 11 30-JAN-2001;
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Best Local Similarity 84.2%; Pred. No. 8.1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 GAGTGCAGGTGGAAGTGC 20
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Db 25 GAGCTGTGTGTGGAAGTGC 7
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RESULT 15
BD075492
LOCUS BD075492 50 bp DNA linear PAT 27-AUG-2002
DEFINITION Secretary and transmembrane polypeptide and nucleic acid encoding
the same.
ACCESSION BD075492
VERSION BD075492.1 GI:22621095

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KEYWORDS	JP 2001516580-A/125.
SOURCE	synthetic construct
ORGANISM	synthetic construct
REFERENCE	other sequences; artificial sequences.
AUTHORS	1 (bases 1 to 50)
TITLE	Wood, W. I., Gunney, A. L., Goddard, A., Penica, D., Chen, J., and Yuan, J.
JOURNAL	Secretary and transmembrane polypeptide and nucleic acid encoding the same: JP 2001516580-A 125 02-OCT-2001; Patent: JP 2001516580-A 125 02-OCT-2001;

COMMENT

OS Artificial Sequence
PN JP 2001516580-A/125
PD 02-OCT-2001

PF 16-SEP-1998 JP 2000511867
PR 17-SEP-1997 US 60/059115, 17-SEP-1997 US 60/059184 PR

17-SEP-1997	US	60/059122, 17-SEP-1997	US	60/059117	PR
17-SEP-1997	US	60/059113, 17-SEP-1997	US	60/059121	PR

17-SEP-1997	US	60/059119, 18-SEP-1997	US	60/059263	PR
18-SEP-1997	US	60/059266, 15-OCT-1997	US	60/062125	PR

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21-OCT-1997	US	60/063486, 24-OCT-1997	US	60/062816	PR

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24-OCT-1997	US	60/063045, 24-OCT-1997	US	60/063128	PR
27-OCT-1997	US	60/063329, 27-OCT-1997	US	60/063327	PR

28-OCT-1997	US	60/063549, 28-OCT-1997	US	60/063541	PR
28-OCT-1997	US	60/063550, 28-OCT-1997	US	60/063542	PR

28-OCT-1997	US	60/063544, 28-OCT-1997	US	60/063564	PR
29-OCT-1997	US	60/063734, 29-OCT-1997	US	60/063738	PR

29-OCT-1997	US	60/063704, 29-OCT-1997	US	60/063435	PR
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29-OCT-1997	US	60/064103, 31-OCT-1997	US	60/063870	PR
03-NOV-1997	US	60/064248, 07-NOV-1997	US	60/064809	PR

12-NOV-1997	US	60/065186, 17-NOV-1997	US	60/065846	PR
18-NOV-1997	US	60/065693, 21-NOV-1997	US	60/066120	PR

21-NOV-1997	US	60/066364, 24-NOV-1997	US	60/066772	PR
24-NOV-1997	US	60/066466, 24-NOV-1997	US	60/066770	PR

24-NOV-1997	US	60/066511, 24-NOV-1997	US	60/066453	PR
25-NOV-1997	US	60/066840			

PI WILLIAM I WOOD, AUSTIN L GURNEY, AUDLEY GODDARD, DIANE PENICA
JEAN CHEN,

PI JEAN YUAN
PC C12N15/09, C07K14/47, C07K14/705, C07K16/18, C07K16/28, C07K19/
C12N15/09

PC C12N1/19,
PC C12N5/10, C12P21/02, C12P21/08, C12Q1/02// (C12P21/08
C12N1/01)

C12R1:91),
PC C12N15/00, C12N5/00

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Location/Qualifiers		

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Location/Qualifiers
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71.0%; Score 14.2; DB 6; Length 50;

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16; Conservative 0; Mismatches 3; Indels 0; Gaps

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16 TGAAGGGCGGGTGAAGTG 34

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583 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 10:37:31 / Search time 1572 Seconds
(without alignments)
595.256 Million cell updates/sec

Title: US-09-296-264-9

Perfect score: 20
Sequence: 1 tgaagtcgcgcgcgcgaagtcgc 20

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 768474

Minimum DB seq length: 20
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: EST.*

1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	15.8	79.0	100	6	CF648803 3530.1.59
C 2	14.8	74.0	49	10	C2470063 C05523-5P
C 3	14.8	74.0	100	1	A1198185 G151F03.x
C 4	14.4	72.0	75	9	BH790276 SALX 0567
C 5	14.2	71.0	61	2	BF507253 S9235-29
C 6	14.2	71.0	73	2	BE130245 L48-385T3
C 7	14.2	71.0	76	10	BX205183 Danio rer
C 8	14.2	71.0	78	10	BX997035 Forward s
C 9	14.2	71.0	82	1	AA646813 vnt37b09.x
C 10	14.2	71.0	84	10	CG567843 OST194423
C 11	14.2	71.0	86	2	BG402252 602465822
C 12	14.2	71.0	89	8	DT019117 VIT033A04
C 13	14.2	71.0	98	8	CV973314 F06_q444
C 14	14.2	71.0	98	10	C2467313 C01634-3P
C 15	14.2	71.0	98	10	C2467324 C01645-3P
C 16	14.2	71.0	99	1	A1559239 cg32603.x
C 17	13.8	69.0	50	1	AU102737 AU102737
C 18	13.8	69.0	81	10	CG511332 OST63636
C 19	13.8	69.0	84	10	CG637376 OST63947
C 20	13.8	69.0	98	10	CL279855 Ggal_142C
C 21	13.6	66.0	56	5	BU348446 604165925
C 22	13.6	66.0	60	9	AZ982649 2M0263H04

23	13.6	68.0	61	1	AA659447	AA659447 nu24D08.s
24	13.6	68.0	69	11	DR17P21S	AL740955 Danio rer
C 25	13.6	68.0	73	10	BX185949	BX185949 Danio rer
C 26	13.6	68.0	88	1	AA500773	AA500773 vq01b07.t
C 27	13.6	68.0	91	6	CA964627	CA964627 CGLX05a18
C 28	13.6	68.0	92	8	H55398	H55398 CHR220337 C
C 29	13.6	68.0	96	8	Z20250	Z20250 HSAABRW1 P
C 30	13.4	67.0	77	7	CN850437	CN850437 000918AAF
C 31	13.2	66.0	39	9	BH902151	BH902151 SALX 0913
C 32	13.2	66.0	61	6	CA772274	CA772274 i094a11.Y
C 33	13.2	66.0	61	10	CG715138	CG715138 1119040B0
C 34	13.2	66.0	63	7	CV573829	CV573829 oc40G01.Y
C 35	13.2	66.0	68	6	CB365695	CB365695 zF001-P00
C 36	13.2	66.0	70	10	CG400347	CG400347 0180611-1
C 37	13.2	66.0	72	9	AQ248436	AQ248436 T7M22-Sp6
C 38	13.2	66.0	73	2	BG879136	BG879136 iB70n10.Y
C 39	13.2	66.0	76	1	A1221944	A1221944 g001a03.x
C 40	13.2	66.0	76	10	C2442725	C2442725 IBH14G5.f
C 41	13.2	66.0	77	10	BX950521	BX950521 Reverse s
C 42	13.2	66.0	77	10	CG575957	CG575957 OST210254
C 43	13.2	66.0	78	10	CL211282	CL211282 M051B01 G
C 44	13.2	66.0	84	1	AV848064	AV848064 AV848064
C 45	13.2	66.0	87	4	AK190815	AK190815 Mus muscu

ALIGNMENTS

RESULT 1
LOCUS CF648803/c 100 bp mRNA linear EST 02-OCT-2003
DEFINITION 3530.1.59.1 P10.x.2 3530 - Full length cDNA library created by Invitrogen from multiple tissues Zea mays cDNA, mRNA sequence.

ACCESSION CF648803
VERSION CF648803.1 GI:37422195
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 100)
Maize ESTs from various cDNA libraries sequenced at Stanford University

JOURNAL Unpublished (1999)
CONTACT: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu

FEATURES
source 1.100
location/Qualifiers
1..100
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"
/db_xref="taxon:4577"
/ligase_type="multiple"
/dev_stage="varies by tissue"
/lab_host="DH108"
/clone_id="3530 - Full length cDNA library created by Invitrogen from multiple tissues"

/note="Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo; Vector: PCWV-SHORT 6.1; Site_1: BC9V; Site_2: Nott; Maize Gene Discovery Project constructed with Invitrogen to produce a normalized, full length library in a pSport vector. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes."

Details of the vector and sequencing primers are available at zMDB in the EST library description tables. poly(A) + mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. This step effected a 20X to 80X reduction in common transcript types. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in project 3530 will be archived at the University of Arizona along with the unigene clones from the Maize Gene Discovery EST sequencing projects. Clones can be ordered through the zMDB web site or directly from the University of Arizona (<http://www.genome.arizona.edu/orders/>). High density filters containing over 18,000 clones can also be ordered from the University of Arizona."

ORIGIN

Query Match 79.0%; Score 15.8; DB 6; Length 100;
Best Local Similarity 89.5%; Pred. No. 1.8e+04;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGAGTCCGGGTGGAAGTG 19
Db 30 TGAGTCCGGGTGGAAGG 12

RESULT 2
LOCUS CZ470063/c 49 bp DNA linear GSS 29-APR-2005
DEFINITION c05523-Sprine Exelixis piggyBac PB insertions Drosophila melanogaster genomic Sequence recovered from 5' end of piggyBac, genomic survey sequence.
ACCESSION CZ470063 GI:62964076
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS Drosophila melanogaster (fruit fly)
TITLE Drosophila melanogaster
JOURNAL Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 49)

REFERENCE
AUTHORS Thibault, S.T., Singer, M.A., Miyazaki, W.Y., Milash, B., Dompe, N.A., Singh, C.M., Buchholz, R., Demsky, M., Fawcett, R., Francis-Lang, H.L., Ryner, L., Cheung, L.M., Chong, A., Erickson, C., Fisher, W.W., Greer, K., Hartouni, S.R., Howie, E., Jakkula, L., Joo, D., Killpack, K., Laufer, A., Mazzotta, J., Smith, R.D., Stevens, L.M., Stuber, C., Tan, L.R., Ventura, R., Woo, A., Zakrjsek, I., Zhao, L., Chen, R., Swimmer, C., Koczynski, C., Duyk, G., Winberg, M.L., and Margolis, J. A complementary transposon tool kit for Drosophila melanogaster using P and piggyBac
Nat Genet. 36 (3), 283-287 (2004)

JOURNAL
FUTURED 14981521
COMMENT Contact: Roger A Hoskins
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
Tel: 510 486 4015
Fax: 510 486 6798
Email: Rhooskins@lbl.gov

Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5' end of piggyBac element.
The piggyBac insertion position is 46 in the 49 bases. This insertion position refers to the first base of the 4 base TTA

FEATURES
source target recognition sequence.
Class: transposon insertion site.
Location/Qualifiers
1..49

/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/strain="isogenic w- strain"
/db_xref="taxon:7227"
/clone_lib="Exelixis piggyBac PB insertions"
/note="Vector: piggyBac PB (Genbank accession number AY515146); An isogenic w- Drosophila melanogaster strain was mutagenized by remobilization of transposable elements. We remobilized the PB element using Hep70:piggyBac transposase from a single ammunition element on either the X or third chromosome. We induced transposase expression by immersing bottles in a circulating 37°C water bath for a daily (days 3-10 after egg-laying) 1-h heat shock. We outcrossed the resulting dysgenic males to an isogenic w- strain. New insertions were identified on the basis of a change in eye color (third chromosome ammunition) or the appearance of w+ male progeny (X chromosome ammunition). All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability, and used for recovery of flanking genomic sequence by inverse PCR."

ORIGIN

Query Match 74.0%; Score 14.8; DB 10; Length 49;
Best Local Similarity 88.9%; Pred. No. 4.9e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GAGTCCGGGTGGAAGTG 19
Db 33 GAGTCCGGGTGGAAGTG 16

RESULT 3
LOCUS A1198185 100 bp mRNA linear EST 02-DEC-1998
DEFINITION q151f03.X1 NCI CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1660029 3', mRNA sequence.
ACCESSION A1198185
VERSION A1198185.1 GI:3750791
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS Homo sapiens (human)
TITLE Homo sapiens
JOURNAL Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 100)

REFERENCE
AUTHORS NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BRGAP), Tumor Gene Index
JOURNAL Unpublished (1998)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/BLNI at:
www-bio.11nl.gov/bdrrp/image/image.html

Insert length: 1236 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 82.
Location/Qualifiers
1..100

FEATURES
source /organism="Homo sapiens"
/mol_type="mRNA"

ORIGIN

Oy	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
Oy	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
Db	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23

	75 bp	DNA	linear	GSS	02-APR-2002
RESULT 4					
BH790276					
LOCUS					
DEFINITION					
	BH790276				
	SALK_056721.50.40.x	Arabidopsis thaliana	TMDA insertion	lines	
	Arabidopsis thaliana	genomic clone SALK_056721.50.40.x,	genomic		
	survey sequence.				

ACCESSION	BH790276
VERSION	BH790276.1
KEYWORDS	GI:19863374
SOURCE	GSS.
ORGANISM	<i>Arabidopsis thaliana</i> (thale cress)
	<i>Arabidopsis thaliana</i>
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons, core eudicotyledons; rosids; eustroids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE	TITLE	JOURNAL	COMMENT
1 (Pages 1 to 75)			
Alonso, J.M., Leisae, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrin, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J., and Ecker, J.R.	A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome		Unpublished (2001)
Contact: Joseph R. Ecker			

Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
IDNA.

Class: TDNA tagged.

FEATURES

Location/Qualifiers

```

/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_056721.50.40.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/notes="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/dna\_protocols.html"

```

ORIGIN	Query Match	72.0%	Score 14.4	DB 9	Length 75
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Qy 4 GGTGGGGGTGGAAGTC 19
|||
Db 45 GGTGGGGGTGGAAGTC 60

RESULT 5	LOCUS	DEFINITION
BF507253	BF507253	61 bp mRNA linear EST 07-DEC-2000 5923P-29 Pooled green leaf and root tissue Sorghum bicolor cDNA clone 5923P-29, mRNA sequence.

ACCESSION	BF507253
VERSION	BF507253.1
KEYWORDS	GI:11590551
SOURCE	EST.
ORGANISM	Sorghum bicolor (sorghum)
	Sorghum bicolor

**REFERENCE
AUTHORS
TITLE**

Childs, K.L., Klein, R.R., Klein, P.E., Mortishige, D.T. and Mullet, J.E.
Mapping Genes on an Integrated sorghum Genetic and Physical Map
Using cDNA Selection Technology

1 (bases 1 to 61)

clade; Panicoidae; Andropogoneae; Sorghum.

Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

JOURNAL COMMENT
Unpublished (2001)
Contact: Kevin Childs
Department of Biochemistry and Biophysics
Texas A&M University
College Station, TX 77843, USA
Tel: 979 845 0832
Fax: 979 862 4778
Email: kchilds@unix.tamu.edu

FEATURES	Location/Qualifiers
source	1. .61

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/organism="Sorghum bicolor"
/mol_type="mRNA"
/cultivar="BTx623"
/db_xref="taxon:4558"
/clone="S923p-29"
/tissue_type="green leaf and root tissue"
/clone_id="Pooled green leaf and root tissue"
/notes="Vector: pBluescript II (SK); Site_1: EcoRI; Site_2
EcoRI"

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Query Match	71.0%;	Score 14.2;	DB 2;	length 61;
Best Local Similarity	84.2%;	Pred. No. 9.1e+04;		
Matches 16; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0

QY	1	TGAGGTGCCGGTGAAGTG	19
Db	13	TGTGCTGGGTGTGAAGTG	31

RESULT 6	LOCUS	DEFINITION
BE130245	73 bp	RNA
BE130245	L48-38T3	Ice plant lambda Uni-Lap XR expression library, 48 hours
	NaCl treatment	Mesembryanthemum crystallinum cDNA clone L48-385 5',
	RNA sequence.	

ACCESSION	BE130245	
VERSION	BE130245.1	GI:8577608
KEYWORDS	EST.	
SOURCE	Mesembryanthemum crystallinum	(common iceplant)
ORGANISM	Mesembryanthemum crystallinum	

REFERENCE
AUTHORS

Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta
Spermatophyta: Magnoliophyta, eudicotyledons, core eudicotyledons
Caryophyllales, Alzooaceae: *Meibomiaanthemum*.
1 (bases 1 to 73)
Cushman, J.C.

Mesembryanthemum crystallinum

JOURNAL
COMMENT

Unpublished (1997)
Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR Primers
FORWARD: T7
BACKWARD: T3
Plate: L48-4 row: H column: 1
Seq primer: T3
High quality sequence stop: 73
POLYA=No.

FEATURES

source Location/Qualifiers

1. 73
/organism="Mesembryanthemum crystallinum"
/mol_type="rRNA"
/db_xref="taxon:3544"
/clone="L48-385"
/tissue_type="Leaf, 48 h 0.4M NaCl"
/dev_stage="Six week old"
/clone_lib="Ice plant lambda Uni-Zap XR expression library, 48 hours NaCl treatment"
/note="Vector: lambda Uni-Zap XR, Bluescript SK-, Site_1: EcoRI, Site_2: XhoI"

ORIGIN

Query Match 71.0%; Score 14.2; DB 2; Length 73;
Best Local Similarity 84.2%; Pred. No. 9.1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAGTGGCGGTGGAAGTG 19
|||||
Db 42 TGAAGTGAAGGTGAATTTG 60

RESULT 7 76 bp DNA linear GSS 29-JAN-2003
BX205183
LOCUS BX205183
DEFINITION Danio rerio genomic clone DKEX-223N20, genomic survey sequence.
ACCESSION BX205183
VERSION BX205183.1 GI:28037069
KEYWORDS GSS:
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio

REFERENCE
AUTHORS Humphray, S.J., Huckle, E. and Durham, J.L.
TITLE Direct Submission
JOURNAL Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humphray@sanger.ac.uk Unpublished

COMMENT This sequence was generated from the S66 end of BAC 223N20. 223N20 is part of the Daniokey BAC library created by R. Plasterik and N.V. Keygene. Further details:
http://www.sanger.ac.uk/projects/D_rerio/.

FEATURES
source Location/Qualifiers

1. 76
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEX-223N20"
/tissue_type="Testis"
/note="Vector pindigobAC-536"

ORIGIN

Query Match 71.0%; Score 14.2; DB 10; Length 76;
Best Local Similarity 84.2%; Pred. No. 9.1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGTGGCGGTGGAAGTGC 20
|||||
Db 10 GAGCGCCAGAGAGAACTGC 28

RESULT 8 78 bp DNA linear GSS 05-JUL-2004
BX997035
LOCUS BX997035
DEFINITION Forward strand read from insert in 3'HPT insertion targeting and chromosome engineering clone MHP294c05, genomic survey sequence.
ACCESSION BX997035.1 GI:49728493
VERSION BX997035.1
KEYWORDS GSS; genome survey sequence; MICEP.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 78)

ADAMS, D.J., BIGGS, P.J., COX, A.V., DAVIES, R.M., VAN DER WEYDEN, L., JONKERS, J., SMITH, J.J., PLUMB, R.W., TAYLOR, R.G., NISHIJIMA, I., YU, Y., ROGERS, J., and BRADLEY, A.
TITLE Direct Submission
JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. http://www.sanger.ac.uk/MICEP

FEATURES

source Location/Qualifiers

1. 78
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHP294c05"
/clone_lib="MHPP"

ORIGIN

Query Match 71.0%; Score 14.2; DB 10; Length 78;
Best Local Similarity 84.2%; Pred. No. 9.1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAGTGGCGGTGGAAGTG 19
|||||
Db 60 TGGGTTACGGGTGAGAGTG 78

RESULT 9 82 bp mRNA linear EST 28-OCT-1997
AA646813
LOCUS AA646813
DEFINITION vnt37b09.r1 StrataGene mouse skin (#937313) Mus musculus cDNA clone IMAGE:1023353 5' similar to SW:ANXA_RABIT P33477 ANNEXIN XI ;, mRNA sequence.
ACCESSION AA646813
VERSION AA646813.1 GI:2573242
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 82)

MARRA, M., HILLIER, L., ALLEN, M., BOWLES, M., DIETRICH, N., DUBUQUE, T., GEISEL, S., KUCABA, T., LACY, M., LE, M., MARTIN, J., MORRIS, M., SCHELLENBERG, K., STEPTOE, M., TAN, F., UNDERWOOD, K., MOORE, B., THEISING, B., WYLIE, T., LEMMON, G., SOARES, B., WILSON, R. and WATERSTON, R.
TITLE The WashU-HMIT Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Maria M/Mouse EST Project
WashU-HMIT Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

MG1:574129

Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 rev1 RT from Amersham
High quality sequence stop: 1.

FEATURES

source

1.82
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:1023353"
/sex="female"
/issue_type="whole skin"
/dev_stage="11 weeks old"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene mouse skin (#937313)"
/note="Organ: skin; Vector: pBluescript SK-; Site: 1;
ECORI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dt: whole skin from 11 week old C57BL/6 female mice.
Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5'
adaptor sequence: 5' GAAATTCGGCAGCAG 3' -3' adaptor
sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3' "

ORIGIN

Query Match 71.0%; Score 14.2; DB 1; Length 82;
Best Local Similarity 84.2%; Pred. No. 9.1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TGAGGTGCGGTGGAAGTG 19
|||||
41 TGAGGAGCCGCTGGAAGTG 23

RESULT 10
CG567843

LOCUS OST194423 Mus musculus 1295v/5v Mus musculus cDNA clone OST194423,
DEFINITION mRNA sequence.
ACCESSION CG567843
VERSION CG567843.1 GI:37354430
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

Zambrowicz, B.P., Abujin, A., Ramirez-Solis, R., Richter, L.J.,
Piggott, J., Beltranderio, H., Buxton, E.C., Edwards, J., Finch, R.A.,
Fridde, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jai, C.,
Key, B.W., Jr., Kipp, P., Kohlschut, B., Ma, Z.-Q., Markesich, D.,
Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
Zhao, Q., Person, C., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,
Wink, K. Kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
14610273
Contact: Zambrowicz BP
OmniBank

JOURNAL

PUBMED

COMMENT

TITLE

JOURNAL

PUBMED

COMMENT

TITLE

JOURNAL

PUBMED

COMMENT

TITLE

JOURNAL

PUBMED

COMMENT

/db_xref="taxon:10090"
/clone="OST194423"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 1295v/5v"

ORIGIN

Query Match 71.0%; Score 14.2; DB 10; Length 84;
Best Local Similarity 84.2%; Pred. No. 9.1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GAGGTGCGGTGGAAGTG 20
|||||
1 GAGGTGCGGTGGAAGTG 19

RESULT 11
BG402252

LOCUS 602465822F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4593941 5',
DEFINITION mRNA sequence.
ACCESSION BG402252 GI:13295700
VERSION BG402252.1 GI:13295700
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 86)
NIH-MGC http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contract: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: ILGM1334 row: 1 column: 06
High quality sequence stop: 42.

FEATURES

source

1.86
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4593941"
/lab_host="DH10B (TI phage-resistant)"
/clone_lib="NIH_MGC_75"
/note="Organ: Kidney; Vector: pDNR-LIB (Clontech); Site: 1;
SfiI (ggcgccggcgcc); Site 2: SfiI (ggcgccggcgcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCATTATGGC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCCGAGGCGCGGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.65
kb (range 0.5-4.0 kb). 15/15 clones contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC library."

ORIGIN

Query Match 71.0%; Score 14.2; DB 2; Length 86;
Best Local Similarity 84.2%; Pred. No. 9.1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TGAGGTGCGGTGGAAGTG 19
|||||
45 TGAGGTGCGGTGGAAGTG 63

RESULT 12

DT019117 89 bp mRNA linear EST 05-AUG-2005
 LOCUS DT019117
 DEFINITION VV1033A04.588074 CabSau Flower Stage 12 (FLOU0012) Vitis vinifera
 accession VV1033A04 5, mRNA sequence.
 DT019117
 VERSION DT019117.1 GI:71870062
 KEYWORDS EST.
 SOURCE Vitis vinifera
 ORGANISM Vitis vinifera
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; Vitaceae; Vitis.
 1 (bases 1 to 89)
 Iocco, P., Hua, C., Davies, C. and Thomas, M. R.
 Expressed sequence tags from the grapevine cultivar Cabernet
 Sauvignon
 Unpublished (2003)
 JOURNAL Contact: Cushman JC
 COMMENT Department of Biochemistry
 University of Nevada
 MS200, Reno, NV 89557-0014, USA
 Tel: 775-784-1918
 Fax: 775-784-1650
 Email: jcushman@unr.edu
 PCR Primers
 FORWARD: T7 20mer (forward)
 BACKWARD: SP6 18mer
 Plate: 033 row: A column: 04
 Seq primer: T7 20mer (forward)
 High quality sequence stop: 89.
 Location/Qualifiers
 1..89
 /organism="Vitis vinifera"
 /mol_type="mRNA"
 /cultivar="Cabernet Sauvignon"
 /db_xref="taxon:29760"
 /clone="VV1033A04"
 /sex="Hermaphrodite"
 /dev_stage="12 - modified E-L system"
 /clone_lib="CabSau Flower Stage 12 (FLOU0012)"
 /note="Organ: Inflorescence including flowers; Vector:
 pZL; A cDNA library from immature inflorescences at stage
 12 of the modified E-L system. Tissue collected from
 field grown plants. A description of the modified E-L
 system can be found in the paper by B. G. Coombe
 'Adoption of a system for identifying grapevine growth
 stages' (1995) Aust. J. Grape and Wine Res. 1: 104-110."

ORIGIN
 Query Match 71.0%; Score 14.2; DB 8; Length 89;
 Best Local Similarity 84.2%; Pred. No. 9.1e+04;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGGTGCGGCTGGAAGTGC 20
 |||||
 13 GCGGTGCAAGTGCAGTGC 31

Db 13 GCGGTGCAAGTGCAGTGC 31

RESULT 13
 CV973314 98 bp mRNA linear EST 30-NOV-2004
 LOCUS CV973314
 DEFINITION R06.444.4 q:444 Triticum aestivum cDNA, mRNA sequence.
 accession CV973314
 VERSION CV973314.1 GI:56134217
 KEYWORDS EST.
 SOURCE Triticum aestivum (bread wheat)
 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Triticum.
 1 (bases 1 to 98)
 Sprunck, S., Baumann, U., Edwards, K., Langridge, P. and Dresselhaus, T.
 The transcript composition of egg cells changes significantly

JOURNAL
 PUBMED 15703054
 COMMENT Contact: Sprunck S
 Developmental Biology and Biotechnology
 University of Hamburg, Biocenter Klein Flottbek
 Ohnhorststrasse 18, D-22609 Hamburg, Germany
 Email: sprunck@botanik.uni-hamburg.de
 Sequenced as part of the BBSRC Investigating Gene Function program;
 Wilson I., Bewick R., Shepherd S., Barker G., Parker J., Owen P.,
 Edwards D., Coghill J., Holdsworth M., Lenton J., Shewry P.,
 Edwards K. A BBSRC-funded wheat EST resource for the academic
 community. Unpublished.
 Location/Qualifiers
 1..98
 /organism="Triticum aestivum"
 /mol_type="mRNA"
 /cultivar="Florida"
 /db_xref="taxon:4565"
 /cell_type="2-cell proembryo"
 /dev_stage="24 hours after fertilization"
 /clone_lib="q:444"

ORIGIN
 Query Match 71.0%; Score 14.2; DB 8; Length 98;
 Best Local Similarity 84.2%; Pred. No. 9.1e+04;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGGTGCGGCTGGAAGTGC 20
 |||||
 19 GAGGCGGGGTGGAAGTGC 1

Db 19 GAGGCGGGGTGGAAGTGC 1

RESULT 14
 CZ467313 98 bp DNA linear GSS 29-APR-2005
 LOCUS CZ467313
 DEFINITION C01634-3prime Exelixis piggyBac PB insertions Drosophila
 melanogaster genomic Sequence recovered from 3' end of piggyBac,
 genomic survey sequence.
 CZ467313 GI:62961326
 GSS.
 accession CZ467313.1 GI:62961326
 VERSION GSS.
 KEYWORDS Drosophila melanogaster (fruit fly)
 SOURCE Drosophila melanogaster
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 98)
 Thibault, S. T., Singer, M. A., Miyazaki, W. Y., Milash, B., Dompe, N. A.,
 Singh, C. M., Buchholz, R., Demsky, M., Fawcett, R., Francis-Lang, H. L.,
 Ryner, L., Cheung, L. M., Chong, A., Erickson, C., Fisher, W. W.,
 Greer, K., Hartouni, S. R., Howie, E., Jakkula, J., Joo, D., Killpack, K.,
 Laufer, A., Mazzotta, D., Smith, R. D., Stevens, L. M., Stuber, C.,
 Tan, L. R., Ventura, R., Woo, A., Zakrjsek, I., Zhao, L., Chen, F.,
 Swimmer, C., Kopczyński, C., Duyk, G., Winberg, M. L. and Margolis, J.
 A complementary transposon tool kit for Drosophila melanogaster
 using P and piggyBac
 Nat. Genet. 36 (3), 283-287 (2004)
 14981521
 JOURNAL
 PUBMED 14981521
 COMMENT Contact: Roger A Hoskins
 Berkeley Drosophila Genome Project
 Lawrence Berkeley National Laboratory
 Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
 Tel: 510 486 4015
 Fax: 510 486 6798
 Email: Rhooskins@lbl.gov
 Sequence recovery method was inverse PCR.
 Sequence orientation is forward strand relative to 5' end of
 piggyBac element.
 The piggyBac insertion position is 1 in the 98 bases. This
 insertion position refers to the first base of the 4 base TTA
 target recognition sequence.
 Class: transposon insertion site.

FEATURES					
source					
Location/Qualifiers					
1..98					
/organism="Drosophila melanogaster"					
/mol_type="genomic DNA"					
/strain="isogenic w- strain"					
/db_xref="caxon:7227"					
/clone_lib="Exelixis piggyBac PB insertions"					
/note="Vector: piggyBac PB (GenBank accession number AY515146); An isogenic w- Drosophila melanogaster strain was mutagenized by remobilization of transposable elements. We remobilized the PB element using Hsp70:piggyBac transposase from a single ammunition element on either the X or third chromosome. We induced transposase expression by immersing bottles in a circulating 37°C water bath for a daily (days 3-10 after egg-laying) 1-h heat shock. We outcrossed the resulting dysgenic males to an isogenic w- strain. New insertions were identified on the basis of a change in eye color (third chromosome ammunition) or the appearance of w+ male progeny (X chromosome ammunition). All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability, and used for recovery of flanking genomic sequence by inverse PCR."					
ORIGIN					
Query Match	71.0%;	Score 14.2;	DB 10;	Length 98;	
Best Local Similarity	84.2%;	Pred. No. 9.1e+04;			
Matches	16;	Conservative	0;	Mismatches	3;
				Indels	0;
				Gaps	0;
Oy	2	GAGGCGCGGTGGGAAGTGC	20		
Dd	24	GAA GTG GAG GTG GAAG TGC	42		
RESULT 15					
CZ467324					
LOCUS					
DEFINITION	CZ467324	98 bp	DNA	linear	GSS 29-Apr-2005
	c01645-3prime Exelixis piggyBac PB insertions Drosophila melanogaster genomic Sequence recovered from 3' end of piggyBac, genomic survey sequence.				
ACCESSION	CZ467324				
VERSION	CZ467324.1	GI:62961337			
KEYWORDS	GSS.				
SOURCE	Drosophila melanogaster (fruit fly)				
ORGANISM	Drosophila melanogaster				
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.				
REFERENCE	1 (bases 1 to 98)				
AUTHORS	Thibault,S.T., Singer,M.A., Miyazaki,W.Y., Mliah,B., Domepe,N.A., Singh,C.M., Bucholtz,R., Demeky,M., Fawcett,R., Francis-Lang,H.L., Ryner,L., Cheung,L.M., Chong,A., Erickson,C., Fisher,W.W., Greer,K., Hartoni,S.R., Howie,E., Jakula,L., Joo,D., Killpack,K., Laufer,A., Mazzotta,J., Smith,R.D., Stevens,L.M., Stuber,C., Tan,L.R., Ventura,R., Woo,A.C., Zakradsek,I., Zhao,L., Chen,F., Swammer,C., Koczynski,C., Duyk,G., Winberg,M.L. and Margolis,J.				
TITLE	A complementary transposon tool kit for Drosophila melanogaster using P and piggyBac				
JOURNAL	Nat. Genet.	36 (3),	283-287	(2004)	
PUBMED	14981521				
COMMENT	Contact: Roger A Hoskins Berkeley Drosophila Genome Project Lawrence Berkeley National Laboratory Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA Tel: 510 486 4015 Fax: 510 486 6798 Email: Rhooskin@lbl.gov Sequence recovery method was inverse PCR. Sequence orientation is forward strand relative to 5' end of piggyBac element. The piggyBac insertion position is 1 in the 98 bases. This insertion position refers to the first base of the 4 base TTAA target recognition sequence				

```

Class: transposon insertion site.
Location/Qualifiers
1..98
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/strain="isogenic w- strain"
/db_xref="taxon:7227"
/clone_lib="Exelixis piggyBac PB insertions"
/notes="Vector: piggyBac PB (GenBank accession number AY515146). An isogenic w- Drosophila melanogaster strain was mutagenized by remobilization of transposable elements. We remobilized the PB element using Hep70.piggyBac transposase from a single amuntion element on either the X or third chromosome. We induced transposase expression by immersing bottles in a circulating 37°C water bath for a daily (days 3-10 after egg-laying) 1-h heat shock. We outcrossed the resulting dysgenic males to an isogenic w- strain. New insertions were identified on the basis of a change in eye color (third chromosome amuntion) or the appearance of w+ male progeny (X chromosome amuntion). All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability, and used for recovery of flanking genomic sequence by inverse PCR."

```

ORIGIN

Query Match	71.0%;	Score 14.2;	DB 10;	Length 98;
Best Local Similarity	84.2%;	Pred. No. 9.1e+04;		
Matches 16;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;

```

OY      2 GAGGTGGCGGTGAAGTGC 20
        |||||
DB      24 GAAATGGAGTGGAGATGC 42

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Search completed: December 24, 2005, 18:28:39
Job time : 1575 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 11:34:25 ; Search time 48.1 Seconds
(without alignments)
739.111 Million cell updates/sec

Title: US-09-296-264-9

Perfect score: 20

Sequence: 1 tgaagtcgcggcggaagtcgc 20

Scoring table: IDENTITY_NUC

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1134872

Minimum DB seq length: 20
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*

1: /cgn2_6/prodata/1/ina/1 COMB.seq:*\n2: /cgn2_6/prodata/1/ina/5 COMB.seq:*\n3: /cgn2_6/prodata/1/ina/8 COMB.seq:*\n4: /cgn2_6/prodata/1/ina/9 COMB.seq:*\n5: /cgn2_6/prodata/1/ina/10 COMB.seq:*\n6: /cgn2_6/prodata/1/ina/11 COMB.seq:*\n7: /cgn2_6/prodata/1/ina/12 COMB.seq:*\n8: /cgn2_6/prodata/1/ina/13 COMB.seq:*\n9: /cgn2_6/prodata/1/ina/14 COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	15	75.0	24	2	US-08-529-190B-7	Sequence 7, Appl
C 2	15	75.0	24	2	US-08-529-190B-10	Sequence 10, Appl
C 3	14.8	74.0	25	3	US-09-396-196G-56226	Sequence 56226, A
C 4	14.8	74.0	25	3	US-09-396-196G-56227	Sequence 56227, A
C 5	14.2	71.0	21	6	PCT-US93-12600-10	Sequence 10, Appl
C 6	14.2	71.0	30	3	US-07-705-490-11	Sequence 11, Appl
C 7	14.2	71.0	30	3	US-08-758-662-7	Sequence 7, Appl
C 8	14.2	71.0	30	3	US-07-751-891B-11	Sequence 11, Appl
C 9	14.2	71.0	50	3	US-09-907-794A-151	Sequence 151, App
C 10	14.2	71.0	50	3	US-09-905-125A-151	Sequence 151, App
C 11	14.2	71.0	50	3	US-09-902-775A-151	Sequence 151, App
C 12	14.2	71.0	50	3	US-09-906-700-151	Sequence 151, App
C 13	14.2	71.0	50	3	US-09-903-603A-151	Sequence 151, App
C 14	14.2	71.0	50	3	US-09-904-920A-151	Sequence 151, App
C 15	14.2	71.0	50	3	US-09-909-064-151	Sequence 151, App
C 16	14.2	71.0	50	3	US-09-905-381A-151	Sequence 151, App
C 17	14.2	71.0	50	3	US-09-906-618-151	Sequence 151, App
C 18	14.2	71.0	50	3	US-09-906-646-151	Sequence 151, App
C 19	14.2	71.0	50	3	US-09-904-462-151	Sequence 151, App
C 20	14.2	71.0	50	3	US-09-902-736A-151	Sequence 151, App
C 21	14.2	71.0	50	3	US-09-906-722A-151	Sequence 151, App
C 22	14	70.0	24	2	US-08-529-190B-4	Sequence 4, Appl
C 23	14	70.0	24	2	US-08-529-190B-13	Sequence 13, Appl
C 24	14	70.0	24	2	US-08-529-190B-16	Sequence 16, Appl

C 25	13.8	69.0	27	3	US-09-435-327A-22	Sequence 22, Appl
C 26	13.8	69.0	48	2	US-07-917-034A-20	Sequence 20, Appl
C 27	13.6	68.0	65	3	US-09-744-931-57	Sequence 57, Appl
C 28	13.6	68.0	65	3	US-09-744-931-58	Sequence 58, Appl
C 29	13.4	67.0	47	3	US-09-422-978-2497	Sequence 2497, Ap
C 30	13.4	67.0	97	2	US-08-399-412A-79	Sequence 79, Appl
C 31	13.2	66.0	24	3	US-10-167-528-1	Sequence 1, Appl
C 32	13.2	66.0	25	3	US-09-733-042-4	Sequence 4, Appl
C 33	13.2	66.0	25	3	US-09-396-196G-67637	Sequence 67637, A
C 34	13.2	66.0	30	3	US-08-506-296B-34	Sequence 34, Appl
C 35	13.2	66.0	30	3	US-09-119-507B-10	Sequence 10, Appl
C 36	13.2	66.0	30	3	US-09-119-507B-38	Sequence 38, Appl
C 37	13.2	66.0	30	3	US-09-119-507B-39	Sequence 39, Appl
C 38	13.2	66.0	30	3	US-08-897-556A-10	Sequence 10, Appl
C 39	13.2	66.0	30	3	US-08-897-556A-38	Sequence 38, Appl
C 40	13.2	66.0	30	3	US-08-897-556A-39	Sequence 39, Appl
C 41	13.2	66.0	30	3	US-09-547-693-10	Sequence 10, Appl
C 42	13.2	66.0	30	3	US-09-547-693-38	Sequence 38, Appl
C 43	13.2	66.0	30	3	US-09-547-693-39	Sequence 39, Appl
C 44	13.2	66.0	51	2	US-08-285-936-44	Sequence 44, Appl
C 45	13.2	66.0	51	2	US-08-285-936-45	Sequence 45, Appl

ALIGNMENTS

RESULT 1
US-08-529-190B-7/c
; Sequence 7, Application US/08529190B
; Patent No. 5833991
; GENERAL INFORMATION:
; APPLICANT: Masucci, Maria G.
; TITLE OF INVENTION: GLYCINE-CONTAINING SEQUENCES
; NUMBER OF SEQUENCES: 76
; TITLE OF INVENTION: CONFERRING INVISIBILITY TO THE IMMUNE SYSTEM
; CORRESPONDENCE ADDRESS:
; ADDRESS: Banner & Witcoff, Ltd.
; STREET: One Financial Center
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/529,190B
; FILING DATE: 15-SEP-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE9501324-9
; FILING DATE: 10-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US08/522,595
; FILING DATE: 01-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Ph.D., Kathleen A
; REGISTRATION NUMBER: 34,380
; REFERENCE/DOCKET NUMBER: 3255/53015
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-9110
; TELEFAX: 617-345-9111
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; US-08-529-190B-7

Query Match 75.0%; Score 15; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGTGCGGGTGGA 16
|||||
Db 15 GAGGTGCGGGTGGA 1

RESULT 2

US-08-529-190B-10/C
; Sequence 10, Application US/08529190B
; Patent No. 5833991

GENERAL INFORMATION:
; APPLICANT: Masucci, Maria G.
; TITLE OF INVENTION: GLYCINE-CONTAINING SEQUENCES
; TITLE OF INVENTION: CONFERRING INVISIBILITY TO THE IMMUNE SYSTEM
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: One Financial Center
; CITY: Boston
; STATE: MA
; COUNTRY: USA

ZIP: 02111

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: Wordperfect 6.1

CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/529,190B
; FILING DATE: 15-SEP-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE9501324-9
; FILING DATE: 10-APR-1995

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US08/522,595
; FILING DATE: 01-SEP-1995

ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Ph.D., Kathleen A

REGISTRATION NUMBER: 34,380

REFERENCE/DOCKET NUMBER: 3255/53015

TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-9100

TELEFAX: 617-345-9111

INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:

LENGTH: 24 bases

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-529-190B-10

Query Match 75.0%; Score 15; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGTGCGGGTGGA 16
|||||
Db 15 GAGGTGCGGGTGGA 1

RESULT 3

US-09-396-196G-56226
; Sequence 56226, Application US/09396196G
; Patent No. 6821724

GENERAL INFORMATION:

; APPLICANT: Michael Miltmann

; APPLICANT: David Mack

; APPLICANT: David Lockhart

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis

; FILE REFERENCE: 3101.1

; CURRENT APPLICATION NUMBER: US/09/396,196G

; CURRENT FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: 60/100,678

; PRIOR FILING DATE: 1998-09-17

; NUMBER OF SEQ ID NOS: 127806

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 56226

; LENGTH: 25

; TYPE: DNA

; ORGANISM: mus musculus

US-09-396-196G-56226

Query Match 74.0%; Score 14.8; DB 3; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.3e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAGGTGCGGGTGGA 18
|||||
Db 7 TGAGGTGCGGGTGGA 24

RESULT 4

US-09-396-196G-56227
; Sequence 56227, Application US/09396196G
; Patent No. 6821724

GENERAL INFORMATION:

; APPLICANT: Michael Miltmann

; APPLICANT: David Mack

; APPLICANT: David Lockhart

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis

; FILE REFERENCE: 3101.1

; CURRENT APPLICATION NUMBER: US/09/396,196G

; CURRENT FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: 60/100,678

; PRIOR FILING DATE: 1998-09-17

; NUMBER OF SEQ ID NOS: 127806

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 56227

; LENGTH: 25

; TYPE: DNA

; ORGANISM: mus musculus

US-09-396-196G-56227

Query Match 74.0%; Score 14.8; DB 3; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.3e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAGGTGCGGGTGGA 18
|||||
Db 4 TGAGGTGCGGGTGGA 21

RESULT 5

PCT-US93-12600-10/C
; Sequence 10, Application PC/TUS9312600
; GENERAL INFORMATION:

; APPLICANT: Denver, Larry A.

; APPLICANT: Rege, Ajay A.

; APPLICANT: Dixon, Richard A.F.

; TITLE OF INVENTION: ANTISENSE MOLECULES DIRECTED AGAINST A

; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR RECEPTOR GENE FAMILY

; NUMBER OF SEQUENCES: 29

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dressler, Goldsmith, Shore &

; ADDRESSEE: Milamov, Ltd.

; STREET: 180 North Stearns, Suite 4700

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60601

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/12600
; FILING DATE: 28-DEC-1993
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/999,706
; FILING DATE: December 31, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Katz, Martin L.
; REGISTRATION NUMBER: 25,011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)616-5400
; TELEFAX: (312)616-5460
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; PCT-US93-12600-10

Query Match      71.0%; Score 14.2; DB 6; Length 21;
Best Local Similarity 84.2%; Pred. No. 2.3e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 GAGTGGCGGTGAAGTGC 20
Db      19 GATGTGGGCTGGAAGTGC 1

RESULT 6
US-07-705-490-11/c
; Sequence 11, Application US/07705490
; Patent No. 6107025
; GENERAL INFORMATION:
; APPLICANT: Caskey, C. T.
; APPLICANT: Nelson, David L.
; APPLICANT: Pieretti, Maura
; APPLICANT: Warren, Stephen T.
; APPLICANT: Oostra, Ben A.
; TITLE OF INVENTION: Diagnosis of the Fragile X Syndrome
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Thomas D. Paul
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/705,490
; FILING DATE: 19910708
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 762829
; INFORMATION FOR SEQ ID NO: 11:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; US-07-705-490-11

Query Match      71.0%; Score 14.2; DB 3; Length 30;
Best Local Similarity 84.2%; Pred. No. 2.4e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 GAGTGGCGGTGAAGTGC 20
Db      25 GAGCTGGTGTGAAGTGC 7

RESULT 7
US-08-758-662-7/c
; Sequence 7, Application US/08758662
; Patent No. 6114150
; GENERAL INFORMATION:
; APPLICANT: Weissman, Sherman
; APPLICANT: Baskaran, Namadev
; TITLE OF INVENTION: AMPLIFICATION OF NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 701 Fifth Avenue, 6300 Columbia Center
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/758,662
; FILING DATE: 29-NOV-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6114150endurg Ph.D., Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 390036.402C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-758-662-7

Query Match      71.0%; Score 14.2; DB 3; Length 30;
Best Local Similarity 84.2%; Pred. No. 2.4e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 GAGTGGCGGTGAAGTGC 20
Db      25 GAGCTGGTGTGAAGTGC 7

RESULT 8
US-07-751-891B-11/c
; Sequence 11, Application US/07751891B
; Patent No. 6180337
; GENERAL INFORMATION:
; APPLICANT: Caskey, C. T.
```

```

; Nelson, David L.
; pieretti, Maura
; Warren, Stephen T.
; Oostera, Ben A.
; Fu, Ying-hui
;
; TITLE OF INVENTION: Diagnosis of the Fragile X Syndrome
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Thomas D. Paul
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA: US/07/751,891B
; APPLICATION NUMBER: US/07/751,891B
; FILING DATE: 29-Aug-1991
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5350
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; TELEX: 762829
;
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-07-751-891B-11

Query Match      71.0%; Score 14.2; DB 3; Length 30;
Best Local Similarity 84.2%; Pred. No. 2.4e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2  GAGGTGCGGTGGAAGTGC 20
Db      25  GAGCTGTGCTGGAAGTGC 7

RESULT 9
US-09-907-794A-151
; Sequence 151, Application US/09907794A
; Patent No. 6635468
;
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavlin, Ivar J.
```

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; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
;
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 151
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-907-794A-151

Query Match      71.0%; Score 14.2; DB 3; Length 50;
Best Local Similarity 84.2%; Pred. No. 2.5e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1  TGAGTGGCGGTGGAAGTGTG 19
Db      16  TGAGGCGCGGTGGAAGTGTG 34

RESULT 10
US-09-905-125A-151
; Sequence 151, Application US/09905125A
; Patent No. 6664376
;
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
```

APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Thomas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,125A
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 151
LENGTH: 50
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-905-125A-151
Query Match 71.0%; Score 14.2; DB 3; Length 50;

Best Local Similarity 84.2%; Pred. No. 2.5e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 TGAGGTGCGGTGGAATG 19
Db 16 TGAGGCGCGGTGGAATG 34
RESULT 11
US-09-902-775A-151
Sequence 151, Application US/09902775A
Patent No. 6686451
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Thomas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,775A
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20

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; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 151
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide probe
US-09-902-775A-151

Query Match
Best Local Similarity 84.2%; Score 14.2; DB 3; Length 50;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TGAGGTGCGGTGGAAGTG 19
Db 16 TGAAGGCGGCGTGAGAGTG 34

RESULT 12
US-09-906-700-151
; Sequence 151, Application US/09906700
; Patent No. 6723535
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Guiney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,700
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
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; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 151
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide probe
US-09-906-700-151

Query Match
Best Local Similarity 84.2%; Score 14.2; DB 3; Length 50;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TGAGGTGCGGTGGAAGTG 19
Db 16 TGAAGGCGGCGTGAGAGTG 34

RESULT 13
US-09-903-603A-151
; Sequence 151, Application US/09903603A
; Patent No. 6767995
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Guiney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: GNE.1618P2C12
; CURRENT APPLICATION NUMBER: US/09/903,603A
; CURRENT FILING DATE: 2001-07-11
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1      PRIOR APPLICATION NUMBER: PCT/US00/04414
2      PRIOR FILING DATE: 2000-02-22
3      PRIOR APPLICATION NUMBER: US 60/143,048
4      PRIOR FILING DATE: 1999-07-07
5      PRIOR APPLICATION NUMBER: US 60/145,698
6      PRIOR FILING DATE: 1999-07-26
7      PRIOR APPLICATION NUMBER: US 60/146,222
8      PRIOR FILING DATE: 1999-07-28
9      PRIOR APPLICATION NUMBER: PCT/US99/20594
10     PRIOR FILING DATE: 1999-09-08
11     PRIOR APPLICATION NUMBER: PCT/US99/20944
12     PRIOR FILING DATE: 1999-09-13
13     PRIOR APPLICATION NUMBER: PCT/US99/21090
14     PRIOR FILING DATE: 1999-09-15
15     PRIOR APPLICATION NUMBER: PCT/US99/21547
16     PRIOR FILING DATE: 1999-09-15
17     PRIOR APPLICATION NUMBER: PCT/US99/23089
18     PRIOR FILING DATE: 1999-10-05
19     PRIOR APPLICATION NUMBER: PCT/US99/28214
20     PRIOR FILING DATE: 1999-11-29
21     PRIOR APPLICATION NUMBER: PCT/US99/28313
22     PRIOR FILING DATE: 1999-11-30
23     PRIOR APPLICATION NUMBER: PCT/US99/28564
24     PRIOR FILING DATE: 1999-12-02
25     PRIOR APPLICATION NUMBER: PCT/US99/28565
26     PRIOR FILING DATE: 1999-12-02
27     PRIOR APPLICATION NUMBER: PCT/US99/30095
28     PRIOR FILING DATE: 1999-12-16
29     PRIOR APPLICATION NUMBER: PCT/US99/30911
30     PRIOR FILING DATE: 1999-12-20
31     PRIOR APPLICATION NUMBER: PCT/US99/30999
32     PRIOR FILING DATE: 1999-12-20
33     PRIOR APPLICATION NUMBER: PCT/US00/00219
34     PRIOR FILING DATE: 2000-01-05
35     NUMBER OF SEQ ID NOS: 423
36     SEQ ID NO 151
37     LENGTH: 50
38     TYPE: DNA
39     ORGANISM: Artificial Sequence
40     FEATURE:
41     OTHER INFORMATION: Description of Artificial Sequence: Synthetic
42     US-09-903-603A-151

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Query Match      71.0%; Score 14.2; DB 3; Length 50;
Best Local Similarity 84.2%; Pred. NO.2.5e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0.

QY      1 TGAGTGGCGGTGGAAGTG 19
      ||| ||| ||| ||| |||
Db      16 TGAAGCGCGGTGGAAGTG 34

RESULT 14
US-09-904-920A-151
: Sequence 151, Application US/0904920A
: Patent No. 6806352
: GENERAL INFORMATION:
: APPLICANT: Genentech, Inc.
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Baton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, A.
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, Christopher J.
: APPLICANT: Gurney, Austin L.

```

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APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Machner, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/904,920A
CURRENT FILING DATE: 2001-07-13
PRIORITY APPLICATION NUMBER: PCT/US00/04414
PRIORITY FILING DATE: 2000-02-22
PRIORITY APPLICATION NUMBER: US 60/143,048
PRIORITY FILING DATE: 1999-07-07
PRIORITY APPLICATION NUMBER: US 60/145,698
PRIORITY FILING DATE: 1999-07-26
PRIORITY APPLICATION NUMBER: US 60/146,222
PRIORITY FILING DATE: 1999-07-28
PRIORITY APPLICATION NUMBER: PCT/US99/20554
PRIORITY FILING DATE: 1999-09-08
PRIORITY APPLICATION NUMBER: PCT/US99/20944
PRIORITY FILING DATE: 1999-09-13
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PRIORITY FILING DATE: 1999-09-15
PRIORITY APPLICATION NUMBER: PCT/US99/21547
PRIORITY FILING DATE: 1999-09-15
PRIORITY APPLICATION NUMBER: PCT/US99/23089
PRIORITY FILING DATE: 1999-10-05
PRIORITY APPLICATION NUMBER: PCT/US99/28214
PRIORITY FILING DATE: 1999-11-29
PRIORITY APPLICATION NUMBER: PCT/US99/28313
PRIORITY FILING DATE: 1999-11-30
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PRIORITY FILING DATE: 1999-12-02
PRIORITY APPLICATION NUMBER: PCT/US99/28565
PRIORITY FILING DATE: 1999-12-02
PRIORITY APPLICATION NUMBER: PCT/US99/30095
PRIORITY FILING DATE: 1999-12-16
PRIORITY APPLICATION NUMBER: PCT/US99/30911
PRIORITY FILING DATE: 1999-12-20
PRIORITY APPLICATION NUMBER: PCT/US99/30999
PRIORITY FILING DATE: 1999-12-20
PRIORITY APPLICATION NUMBER: PCT/US00/00219
PRIORITY FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 151
LENGTH: 50
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-904-920A-151
Query Match      71.0%; Score 14.2; DB 3; Length 50;
Best Local Similarity 84.2%; Pred. No. 2.5e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY      1 TGAGTGC GGCGGTGGAAGTG 19
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DB      16 TGAAGCG CGGTGGAAGTG 34

RESULT 15
US-09-909-064--151
Sequence 151, Application US/09909064
Patent No. 6818449
GENERAL INFORMATION:
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APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/909,064
CURRENT FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
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PRIOR APPLICATION NUMBER: PCT/US99/21547
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PRIOR APPLICATION NUMBER: PCT/US99/23089
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PRIOR APPLICATION NUMBER: PCT/US99/28214
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PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 151
LENGTH: 50
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-909-064-151

Query Match 71.0%; Score 14.2; DB 3; Length 50;
Best Local Similarity 84.2%; Pred. No. 2.5e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 TGAAGTCCGGGTGGAAGTG 19
||| |
DB 16 TGAAGGCGGGGTGAGAGTG 34

Search completed: December 24, 2005, 18:36:29
Job time : 48.1 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using ew model

Run on: December 24, 2005, 14:06:30 ; Search time 337.6 Seconds
(without alignments)
489.892 Million cell updates/sec

Title: US-09-296-264-9
Perfect score: 20
Sequence: 1 tgaagtcgcgggagagtcgc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 9887334

Minimum DB seq length: 20
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA Main:

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- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
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- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
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- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	20	100.0	20	3	US-09-296-264-9	Sequence 9, Appli
2	15.2	76.0	25	8	US-10-719-900-855558	Sequence 855558,
3	15.2	76.0	60	3	US-09-908-975-22618	Sequence 22618, A
4	14.8	74.0	25	5	US-10-098-263B-45504	Sequence 45504, A
5	14.8	74.0	25	9	US-10-809-189-56226	Sequence 56226, A
6	14.8	74.0	25	9	US-10-809-189-56227	Sequence 56227, A
7	14.4	72.0	25	5	US-10-215-112-8648	Sequence 8648, Ap
8	14.4	72.0	25	5	US-10-098-263B-86887	Sequence 86887, A
9	14.4	72.0	25	8	US-10-719-900-932959	Sequence 932959,
10	14.4	72.0	60	3	US-09-908-975-21047	Sequence 21047, A
11	14.2	71.0	25	10	US-11-036-317-61324	Sequence 61324, A
12	14.2	71.0	25	10	US-11-036-317-61324	Sequence 61324, A
13	14.2	71.0	25	10	US-11-036-317-61324	Sequence 61324, A
14	14.2	71.0	30	5	US-10-073-353-7	Sequence 597647,
15	14.2	71.0	50	3	US-09-909-320-151	Sequence 7, Appli
16	14.2	71.0	50	3	US-09-909-320-151	Sequence 151, App
17	14.2	71.0	50	3	US-09-905-291A-151	Sequence 151, App
18	14.2	71.0	50	3	US-09-902-853-151	Sequence 151, App
19	14.2	71.0	50	3	US-09-907-824-151	Sequence 151, App
20	14.2	71.0	50	3	US-09-907-824-151	Sequence 151, App
21	14.2	71.0	50	3	US-09-904-011-151	Sequence 151, App
22	14.2	71.0	50	3	US-09-903-640-151	Sequence 151, App
23	14.2	71.0	50	3	US-09-908-093-151	Sequence 151, App

24	14.2	71.0	50	3	US-09-906-742-151	Sequence 151, App
25	14.2	71.0	50	3	US-09-906-838-151	Sequence 151, App
26	14.2	71.0	50	3	US-09-907-613-151	Sequence 151, App
27	14.2	71.0	50	3	US-09-907-942-151	Sequence 151, App
28	14.2	71.0	50	3	US-09-904-859-151	Sequence 151, App
29	14.2	71.0	50	3	US-09-909-204-151	Sequence 151, App
30	14.2	71.0	50	3	US-09-904-820-151	Sequence 151, App
31	14.2	71.0	50	3	US-09-904-786-151	Sequence 151, App
32	14.2	71.0	50	3	US-09-906-646-151	Sequence 151, App
33	14.2	71.0	50	3	US-09-906-700-151	Sequence 151, App
34	14.2	71.0	50	3	US-09-903-786-151	Sequence 151, App
35	14.2	71.0	50	3	US-09-902-903-151	Sequence 151, App
36	14.2	71.0	50	3	US-09-903-749A-151	Sequence 151, App
37	14.2	71.0	50	3	US-09-904-119-151	Sequence 151, App
38	14.2	71.0	50	3	US-09-904-956-151	Sequence 151, App
39	14.2	71.0	50	3	US-09-902-736-151	Sequence 151, App
40	14.2	71.0	50	3	US-09-907-794-151	Sequence 151, App
41	14.2	71.0	50	3	US-09-903-943-151	Sequence 151, App
42	14.2	71.0	50	3	US-09-904-462-151	Sequence 151, App
43	14.2	71.0	50	3	US-09-907-925-151	Sequence 151, App
44	14.2	71.0	50	3	US-09-902-692-151	Sequence 151, App
45	14.2	71.0	50	3	US-09-903-520-151	Sequence 151, App

ALIGNMENTS

RESULT 1
US-09-296-264-9
; Sequence 9, Application US/09296264
; Publication No. US20030083274A1
; GENERAL INFORMATION:
; APPLICANT: WRIGHT, Jim A.
; APPLICANT: YOUNG, Aiping H.
; APPLICANT: LEE, Yoon S.
; TITLE OF INVENTION: NEUROFILIN ANTISENSE OLIGONUCLEOTIDE SEQUENCES AND
; TITLE OF INVENTION: METHODS OF USING SAME TO MODULATE CELL GROWTH
; FILE REFERENCE: 033396-043
; CURRENT APPLICATION NUMBER: US/09/296,264
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 60/082,791
; EARLIER FILING DATE: 1998-04-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-09-296-264-9
Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAAGTCGGGAGAGTC 20
DB 1 TGAAGTCGGGAGAGTC 20
RESULT 2
US-10-719-900-855558
; Sequence 855558, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 855558
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-10-719-900-855558

Query Match 76.0%; Score 15.2; DB 8; Length 25;
Best Local Similarity 85.0%; Pred. No. 3.7e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAGTGGCGGTGAAGTGC 20
Db 1 TGAGTGGCGGTGAAGTGC 20

RESULT 3
US-09-908-975-22618
Sequence 22618, Application US/09908975
Publication NO. US20030165843A1
GENERAL INFORMATION:
APPLICANT: SHOSHAN, Avi
APPLICANT: WASSERMAN, Alon
APPLICANT: MINTZ, Eli
APPLICANT: MINTZ, Liat
APPLICANT: RAIGER, Simchon
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
FILE REFERENCE: 36688-0005
CURRENT APPLICATION NUMBER: US/09/908,975
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/221,607
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 32337
SOFTWARE: PatentIn version 3.0
SEQ ID NO 22618
LENGTH: 60
TYPE: DNA
ORGANISM: Homo sapiens
US-09-908-975-22618

Query Match 76.0%; Score 15.2; DB 3; Length 60;
Best Local Similarity 85.0%; Pred. No. 3.5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAGTGGCGGTGAAGTGC 20
Db 25 TGAGTGGCGGTGAAGTGC 44

RESULT 4
US-10-098-263B-45504/C
Sequence 45504, Application US/10098263B
Publication NO. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 45504
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-10-098-263B-45504

Query Match 74.0%; Score 14.8; DB 5; Length 25;
Best Local Similarity 88.9%; Pred. No. 5.6e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAGTGGCGGTGAAGT 18
Db 24 TGAGTGGCGGTGAAGT 7

RESULT 5
US-10-809-189-56226
Sequence 56226, Application US/10809189
Publication NO. US20050048531A1
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/10/809,189
CURRENT FILING DATE: 2004-03-25
PRIOR APPLICATION NUMBER: US/09/396,196
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 56226
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-10-809-189-56226

Query Match 74.0%; Score 14.8; DB 9; Length 25;
Best Local Similarity 88.9%; Pred. No. 5.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAGTGGCGGTGAAGT 18
Db 7 TGAGTGGCGGTGAAGT 24

RESULT 6
US-10-809-189-56227
Sequence 56227, Application US/10809189
Publication NO. US20050048531A1
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/10/809,189
CURRENT FILING DATE: 2004-03-25
PRIOR APPLICATION NUMBER: US/09/396,196
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 56227
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-10-809-189-56227

Query Match 74.0%; Score 14.8; DB 9; Length 25;
Best Local Similarity 88.9%; Pred. No. 5.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGAGTGGCGGTGAAGT 18
Db 4 TGAGTGGCGGTGAAGT 21

```
RESULT 7
US-10-215-112-8648/c
; Sequence 8648, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltman
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE OF INVENTION: Test3
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 8648
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-8648

Query Match          72.0%; Score 14.4; DB 5; Length 25;
Best Local Similarity 93.8%; Pred. No. 8.5e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GAGTGCGGGTGAAG 17
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Db      24 GAGTGCGGGTGAAG 9

RESULT 8
US-10-098-263B-86887
; Sequence 86887, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 86887
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-86887

Query Match          72.0%; Score 14.4; DB 5; Length 25;
Best Local Similarity 93.8%; Pred. No. 8.5e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 GTGCGGGTGAAGTGC 20
      |||||
Db      4 GTGCGGGTGAAGTGC 19

RESULT 9
US-10-719-900-932959/c
; Sequence 932959, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
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; NUMBER OF SEQ ID NOS: 982314
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 932959
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-932959

Query Match          72.0%; Score 14.4; DB 8; Length 25;
Best Local Similarity 93.8%; Pred. No. 8.5e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 TGAGGTGCGGTGA 16
      |||||
Db      16 TGAGGTGCGGTGA 1

RESULT 10
US-09-908-975-21047
; Sequence 21047, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21047
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-21047

Query Match          72.0%; Score 14.4; DB 3; Length 60;
Best Local Similarity 93.8%; Pred. No. 7.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 AGTGCGGGTGAAGT 18
      |||||
Db      6 AGTGCGGGTGAAGT 21

RESULT 11
US-11-036-317-61324
; Sequence 61324, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 61324
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-61324
```

Query Match 71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAGGTGCGGTGGAAGTG 19
DB 1 TGACGTGCTGTGTGAGAG 19

RESULT 12

US-11-036-317-319797
; Sequence 319797, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 319797
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-319797

Query Match 71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAGGTGCGGTGGAAGTG 19
DB 7 TTAGGTGAGGTGGAAGTG 25

RESULT 13

US-11-036-317-597647
; Sequence 597647, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 597647
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-597647

Query Match 71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGGTGCGGTGGAAGTG 20
DB 6 GAGGTGCGAGTGAGAGAGC 24

RESULT 14

US-10-073-353-7/C
; Sequence 7, Application US/10073353

; Publication No. US20020168658A1

; GENERAL INFORMATION:
; APPLICANT: Sherman M. Weisman

; TITLE OF INVENTION: Amplification of Nucleic Acids

; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan, Lewis & Bockius LLP

; STREET: 1111 Pennsylvania Ave., NW
; CITY: Washington

; STATE: D.C.
; COUNTRY: USA

; ZIP: 20004

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0. Version #1.30

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/073,353

; FILING DATE: 03-May-2002

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/758,662

; FILING DATE: 1996-12-07

; APPLICATION NUMBER: US 08/758,662 (CPA)

; FILING DATE: 1999-02-17

; APPLICATION NUMBER: US 09/585,437

; FILING DATE: 2000-06-02

; ATTORNEY/AGENT INFORMATION:
; NAME: Michael S. Tuscan

; REGISTRATION NUMBER: 43,210

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-739-3000

; TELEFAX: 202-739-3001

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs

; TYPE: nucleic acid
; STRANDEDNESS: single

; TOPOLOGY: linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-10-073-353-7

Query Match 71.0%; Score 14.2; DB 5; Length 30;
Best Local Similarity 84.2%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGGTGCGGTGGAAGTG 20
DB 25 GAGCTGTGTGTGGAAGTGC 7

RESULT 15

US-09-909-320-151
; Sequence 151, Application US/09909320
; Patent No. US20020132240A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerilsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.

```

; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,320
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 151
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide probe
US-09-909-320-151

Query Match      71.0%; Score 14.2; DB 3; Length 50;
Best Local Similarity 84.2%; Pred. No. 9.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 TGAGGTGCGGCTGGAAGTG 19
      ||| ||| ||| ||| |||
Db      16 TGAGGCGCGGCTGGAAGTG 34
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Job time : 338.6 secs

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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 10:28:41 ; Search time 582 Seconds
(without alignments)
1953.383 Million cell updates/sec

Title: US-09-296-264-10

Perfect score: 20
Sequence: 1 gtgcgcagcgtgagccaccaga 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 1858228

Minimum DB seq length: 20
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sbs:*
11: gb_ey:*
12: gb_un:*
13: gb_vl:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6	BD211667 Antisense
2	17.6	88.0	21	6	ARS31240 Sequence
3	17.6	88.0	21	6	AX097265 Sequence
4	14.2	71.0	60	6	ARS61935 Sequence
5	13.8	69.0	27	6	AX188785 Sequence
6	13.8	69.0	50	6	CO009079 Sequence
7	13.8	69.0	65	6	CO532692 Sequence
8	13.8	69.0	72	4	AY604639 Sequence
9	13.6	68.0	27	6	AY8650 Sequence
10	13.6	68.0	51	6	AX162818 Sequence
11	13.6	68.0	65	6	CO532435 Sequence
12	13.6	68.0	65	6	CO532930 Sequence
13	13.4	67.0	30	6	AX611417 Sequence
14	13.4	67.0	50	6	CO008762 Sequence
15	13.2	66.0	27	6	AX002713 Sequence
16	13.2	66.0	33	6	AR127237 Sequence
17	13.2	66.0	33	6	AR127238 Sequence
18	13.2	66.0	33	6	BD130578 Controlle

C 19	13.2	66.0	33	6	BD130579	BD130579 Controlle
C 20	13.2	66.0	35	6	AX358674	AX358674 Sequence
C 21	13.2	66.0	35	6	AX358675	AX358675 Sequence
C 22	13.2	66.0	44	6	AR143578	AR143578 Sequence
C 23	13.2	66.0	44	6	AR168947	AR168947 Sequence
C 24	13.2	66.0	44	6	AR232695	AR232695 Sequence
C 25	13.2	66.0	44	6	AR262637	AR262637 Sequence
C 26	13.2	66.0	44	6	AR316574	AR316574 Sequence
C 27	13.2	66.0	65	6	CO534393	CO534393 Sequence
C 28	13.2	66.0	83	6	BD040906	BD040906 Sequence
C 29	13.2	66.0	83	6	AX905373	AX905373 Sequence
C 30	13.2	66.0	90	8	HSEXTX2	X99574 H. sapiens e
C 31	12.8	64.0	22	6	E11187	E11187 Probe, 9/19
C 32	12.8	64.0	24	6	BD131726	BD131726 Method fo
C 33	12.8	64.0	24	6	AR606669	AR606669 Sequence
C 34	12.8	64.0	24	6	AX019309	AX019309 Sequence
C 35	12.8	64.0	25	6	AR065111	AR065111 Sequence
C 36	12.8	64.0	25	6	E09880	E09880 Primer, 9/1
C 37	12.8	64.0	30	8	HUMPLTP12	U37819 Human phosp
C 38	12.8	64.0	35	6	AX756529	AX756529 Sequence
C 39	12.8	64.0	48	6	AY7298	AY7298 Sequence, 15
C 40	12.8	64.0	51	6	CO002980	CO002980 Sequence
C 41	12.8	64.0	53	6	E11189	E11189 Probe, 9/19
C 42	12.8	64.0	62	6	AR127979	AR127979 Sequence
C 43	12.8	64.0	62	6	AR408324	AR408324 Sequence
C 44	12.8	64.0	68	8	AY805392	AY805392 Homo sapi
C 45	12.8	64.0	70	6	E03982	E03982 Probe for d

ALIGNMENTS

RESULT 1
BD211667
LOCUS BD211667 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Antisense oligonucleotide sequence of neupopilin and method of using the same for controlling cell proliferation.
ACCESSION BD211667
VERSION BD211667.1 GI:33021437
KEYWORDS JP 2002512793-A/10.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 20)
Wright,J.A., Young,A.H. and Lee,Y.S.
TITLE Antisense oligonucleotide sequence of neupopilin and method of using the same for controlling cell proliferation
JOURNAL GENESENSE TECHNOLOGIES INC
COMMENT OS Homo sapiens (human)
PN JP 2002512793-A/10
PD 08-MAY-2002
PF 23-APR-1999 JP 2000545999
PR 23-APR-1998 US 60/082791
PI JIM A WRIGHT,ALPING H YOUNG,YOON S LEE
PC C12N15/09,A61K31/711,A61K48/00,A61P35/00,C12N15/00 CC
Antisense oligonucleotide sequence of neupopilin and method of using the same for controlling cell proliferation
CC same for controlling cell proliferation
FT Key location/Qualifiers
FT source 1..20 /organism='Homo sapiens (human)'.
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source location/Qualifiers
1..20 /organism='Homo sapiens (human)'
/mol_type='genomic DNA'
/db_xref='taxon:9606'
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCGACGTGGACCCAGA 20
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Db 1 GTGCCGACGTGGACCCAGA 20

RESULT 2
ARS31240/c
LOCUS ARS31240 21 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 2443 from patent US 6727063.
ACCESSION ARS31240
VERSION ARS31240.1 GI:53919677
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Lander,E.S., Cargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
McCarthy,J.J.
TITLE Single nucleotide polymorphisms in genes
JOURNAL Patent: US 6727063-A 2443 27-APR-2004;
Millennium Pharmaceuticals, Inc. and Whitehead Institute for
Biomedical Research; Cambridge, MA
FEATURES
source 1..21
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 88.0%; Score 17.6; DB 6; Length 21;
Best Local Similarity 94.4%; Pred. No. 4.1e+02;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCGACGTGGACCCCA 18
|||||
Db 18 GTGCCGAYGTGGACCCCA 1

RESULT 3
AX097265/c
LOCUS AX097265 21 bp DNA linear PAT 30-MAR-2001
DEFINITION Sequence 2443 from Patent WO0118250.
ACCESSION AX097265
VERSION AX097265.1 GI:13513682
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Carchinh;
Homnidae; Homo.
REFERENCE 1
AUTHORS Lander,E.S., Cargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
McCarthy,J.J.
TITLE Single nucleotide polymorphisms in genes
JOURNAL Patent: WO 0118250-A 2443 15-MAR-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
Pharmaceuticals, Inc. (US)
FEATURES
source 1..21
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 88.0%; Score 17.6; DB 6; Length 21;
Best Local Similarity 94.4%; Pred. No. 4.1e+02;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCGACGTGGACCCCA 18
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Db 18 GTGCCGAYGTGGACCCCA 1

RESULT 4
ARS61935/c
LOCUS ARS61935 60 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 162 from patent US 6759198.
ACCESSION ARS61935
VERSION ARS61935.1 GI:53975586
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 60)
AUTHORS Kris,R.M. and Felder,S.
TITLE High throughput assay system
JOURNAL Patent: US 6759198-A 162 06-JUL-2004;
High Throughput Genomics, Inc.; Tucson, AZ
FEATURES
source 1..60
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 71.0%; Score 14.2; DB 6; Length 60;
Best Local Similarity 84.2%; Pred. No. 2.2e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGCCGACGTGGACCCAG 19
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Db 48 GTGCTTACGTGGACCTCAG 30

RESULT 5
AX188785
LOCUS AX188785 27 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 32 from Patent WO0148228.
ACCESSION AX188785
VERSION AX188785.1 GI:15142326
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Chater,K.F., Bruton,C.J., O'Rourke,S.J. and Wietzorrek,A.W.
TITLE Methods and materials relating to gene expression
JOURNAL Patent: WO 0148228-A 32 05-JUL-2001;
Plant Bioscience Limited (GB)
FEATURES
source 1..27
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide primer"

ORIGIN
Query Match 69.0%; Score 13.8; DB 6; Length 27;
Best Local Similarity 88.2%; Pred. No. 3.7e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GCCGACGTGGACCCAG 19
|||||
Db 3 GCCGACGCGGACCCCG 19

RESULT 6
CQ009079/c
LOCUS CQ009079 50 bp DNA linear PAT 16-JAN-2004
DEFINITION Sequence 7719 from Patent WO0147944.
ACCESSION CQ009079
VERSION CQ009079.1 GI:41015805
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.

REFERENCE 1
AUTHORS Shimkete, R.A. and Leach, M.
TITLE Nucleic acid containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0147944-A 7719 05-JUL-2001;
Curagen Corporation (US)
FEATURES
SOURCE Location/Qualifiers
1..50 /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
25..26 /note="Nucleotide deleted between bases 25 and 26"
Accession number CG43931874"

ORIGIN
Query Match 69.0%; Score 13.8; DB 6; Length 50;
Best Local Similarity 88.2%; Pred. No. 3.6e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GCCGACGTGGAGCCAG 19
|||
26 GCCCAGTGGAGCCAG 10
|||

Db

RESULT 7
CQ532692 65 bp DNA linear PAT 30-JAN-2004
LOCUS Sequence 2327 from Patent WO0210449.
DEFINITION CQ532692
ACCESSION CQ532692
VERSION CQ532692.1 GI:41498956
KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Rattus.
REFERENCE 1
AUTHORS Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Faigler, S.
TITLE Oligonucleotide library for detecting rna transcripts and splice variants that populate a transcriptome
JOURNAL Patent: WO 0210449-A 2327 07-FEB-2002;
Compugen Inc. (US)
FEATURES
SOURCE Location/Qualifiers
1..65 /organism="Rattus norvegicus"
/mol_type="unassigned DNA"
/db_xref="taxon:10116"

ORIGIN
Query Match 69.0%; Score 13.8; DB 6; Length 65;
Best Local Similarity 88.2%; Pred. No. 3.6e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GCCGACGTGGAGCCAG 19
|||
23 GCAGACGTGGAGCCAG 39
|||

Db

RESULT 8
AY604639 72 bp mRNA linear MAM 09-JUN-2004
LOCUS Sus scrofa clone 8413-11 T-cell receptor delta chain CDR3 region
DEFINITION (TCRD) mRNA, partial cds.
ACCESSION AY604639
VERSION AY604639.1 GI:48249576
KEYWORDS
SOURCE Sus scrofa (pig)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae;

Sus.
1 (bases 1 to 72)
REFERENCE 1
AUTHORS Holtmeier, W., Geisel, W., Bernert, K., Butler, J.E., Sinkora, M., Renakova, Z., Sinkora, J., and Caspar, W.F.
TITLE Prenatal development of the porcine TCR delta repertoire: Dominant expression of an invariant T cell receptor Vdelta3-Jdelta3 chain
JOURNAL Eur. J. Immunol. (2004) In press
REFERENCE 2 (bases 1 to 72)
AUTHORS Holtmeier, W., Geisel, W., Bernert, K., Butler, J.E., Sinkora, M., Renakova, Z., Sinkora, J., and Caspar, W.F.
TITLE Direct Submision
JOURNAL Submitted (22-APR-2004) Medizinische Klinik II, Department of Gastroenterology, Johann Wolfgang Goethe-Universitaet, Theodor-Stern-Kai 7, Frankfurt am Main 60590, Germany
FEATURES
SOURCE Location/Qualifiers
1..72 /organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="8413-11"
/dev_stage="fetal"
1..572 /gene="TCRD"
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1..572 /gene="TCRD"
/note="TRDV3DJ1"
/codon_start=1
/product="T-cell receptor delta chain CDR3 region"
/protein_id="AA141037.1"
/db_xref="GI:48249577"
/translation="ADSAARYFCAFWLGRGDKLFGKG"

ORIGIN
Query Match 69.0%; Score 13.8; DB 4; Length 72;
Best Local Similarity 88.2%; Pred. No. 3.6e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CCACGTGGAGCCAGA 20
|||
45 CCACGTGGAGCCAGA 29
|||

Db

RESULT 9
A98650 27 bp DNA linear PAT 26-JAN-2000
LOCUS Sequence 6 from Patent WO9910500.
DEFINITION A98650
ACCESSION A98650
VERSION A98650.1 GI:6781694
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified sequences.
REFERENCE 1 (bases 1 to 27)
AUTHORS Schlichter, U. and Steinbiss, H.
TITLE NUCLEIC ACID MOLECULES CODING FOR A CYSTEINE PROTEINASE OF PLANT ORIGIN AND THEIR REGULATING REGIONS
JOURNAL Patent: WO 9910500-A 6 04-MAR-1999;
MAX PLANCK GESELLSCHAFT (DE); SCHLICHTER URSULA (DE)
FEATURES
SOURCE Location/Qualifiers
1..27 /organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

ORIGIN
Query Match 68.0%; Score 13.6; DB 6; Length 27;
Best Local Similarity 80.0%; Pred. No. 4.7e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTGCCGACGTGGAGCCAGA 20
|||
6 GTGTGGACGTGGAGCCAGA 25
|||

Db

RESULT 10
AX162818/c
LOCUS AX162818 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 6146 from Patent WO0140521.
ACCESSION AX162818
VERSION AX162818.1 GI:14544149
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 6146 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source
1..51
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="2 of 2 allelic variants (6145 is other entry)"
Accession number CG44914955"
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68.0%; Score 13.6; DB 6; Length 51;
Query Match
Best Local Similarity 80.0%; Pred. No. 4.6e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 GTGCCGACGTGGAGCCAGCA 20
DB 45 GTTCAGACGTGGAGCCAGCA 26
RESULT 11
CQ532435
LOCUS CQ532435 65 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 2070 from Patent WO0210449.
ACCESSION CQ532435
VERSION CQ532435.1 GI:41498699
KEYWORDS
SOURCE
ORGANISM Rattus norvegicus (Norway rat)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Rattus.
REFERENCE
AUTHORS Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Faigler, S.
TITLE Oligonucleotide library for detecting rna transcripts and splice
variance that populate a transcriptome
JOURNAL Patent: WO 0210449-A 2070 07-FEB-2002;
Comugen Inc. (US)
FEATURES
source
1..65
/organism="Rattus norvegicus"
/mol_type="unassigned DNA"
/db_xref="taxon:10116"
ORIGIN
Query Match
Best Local Similarity 68.0%; Score 13.6; DB 6; Length 65;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 GTGCCGACGTGGAGCCAGCA 20
DB 5 GTCCAGACGTGGAGCCAGCA 24

RESULT 12
CQ532930/c
LOCUS CQ532930 65 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 2565 from Patent WO0210449.
ACCESSION CQ532930
VERSION CQ532930.1 GI:41499194
KEYWORDS
SOURCE
ORGANISM Rattus norvegicus (Norway rat)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Rattus.
REFERENCE
AUTHORS Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Faigler, S.
TITLE Oligonucleotide library for detecting rna transcripts and splice
variants that populate a transcriptome
JOURNAL Patent: WO 0210449-A 2565 07-FEB-2002;
Comugen Inc. (US)
FEATURES
source
1..65
/organism="Rattus norvegicus"
/mol_type="unassigned DNA"
/db_xref="taxon:10116"
ORIGIN
Query Match
Best Local Similarity 68.0%; Score 13.6; DB 6; Length 65;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 GTGCCGACGTGGAGCCAGCA 20
DB 20 GTGCCGACGTGGAGCCAGCA 1
RESULT 13
AX611417/c
LOCUS AX611417 30 bp DNA linear PAT 17-FEB-2003
DEFINITION Sequence 2442 from Patent WO02072882.
ACCESSION AX611417
VERSION AX611417.1 GI:28406846
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Cullen, P. and Seedorf, U.
TITLE Coronary chip
JOURNAL Patent: WO 02072882-A 2442 19-SEP-2002;
OGHAM GmbH (DE)
FEATURES
source
1..30
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match
Best Local Similarity 67.0%; Score 13.4; DB 6; Length 30;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 TGCCGACGTGGAGCC 16
DB 18 TGCCGACGTGGAGCC 4
RESULT 14
CQ008762/c
LOCUS CQ008762 50 bp DNA linear PAT 16-JAN-2004
DEFINITION Sequence 7402 from Patent WO0147944.
ACCESSION CQ008762
VERSION CQ008762.1 GI:41015477

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Shimkova, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
JOURNAL methods of use thereof
Patent: WO 0147944-A 7402 05-JUL-2001;
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
25..26
/note="Nucleotide deleted between bases 25 and 26
Accession number cg43922182"

ORIGIN
Query Match 67.0%; Score 13.4; DB 6; Length 50;
Best Local Similarity 93.3%; Pred. No. 5.8e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGCCGACGTGGAC 15
DB 29 GTGCCGACGTGGAC 15

RESULT 15
AX002713/c 27 bp DNA linear PAT 21-AUG-2000
LOCUS AX002713
DEFINITION Sequence 5 from Patent WO9900490.
ACCESSION AX002713
VERSION AX002713.1 GI:3885040

KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE
1
AUTHORS Weinberg, M.A.
TITLE Attenuated human immunodeficiency virus vaccine
JOURNAL Patent: WO 9800490-A 5 07-JAN-1999;
WEINBERG MARK A (CA); SIR MORTIMER B DAVIS JEWISH GE (CA)
FEATURES
source Location/Qualifiers
1..27
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 66.0%; Score 13.2; DB 6; Length 27;
Best Local Similarity 83.3%; Pred. No. 7.5e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GCCGACGTGGAGCCAG 20
DB 26 GCCGACGTGGAGCCAG 9

Search completed: December 24, 2005, 14:06:15
Job time : 584 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 01:41:40 ; Search time 171.4 Seconds
(without alignments)
777.677 Million cell updates/sec

Title: US-09-296-264-10

Perfect score: 20

Sequence: 1 gtccgcagctgagaccacaga 20

Scoring table: IDENTITY_NUC

Searched: 4596997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 3390896

Minimum DB seq length: 20

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : N Geneseq_21:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
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- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*
- 14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3	AAZ31440
2	20	100.0	20	9	ADA74692
3	18	90.0	21	4	AA97678
4	15.2	76.0	25	9	ACI90367
5	14.2	71.0	25	9	ACK25958
6	14.2	71.0	60	8	AB272759
7	13.8	69.0	25	9	ACK26420
8	13.8	69.0	25	9	ACT182748
9	13.8	69.0	27	4	AA507631
10	13.8	69.0	28	4	AA83785
11	13.8	69.0	50	4	AA134511
12	13.8	69.0	55	12	ADN00075
13	13.8	69.0	65	6	ABN29579
14	13.6	68.0	25	9	ACT190366
15	13.6	68.0	27	2	AAK23277
16	13.6	68.0	51	4	AA179205
17	13.6	68.0	65	6	ABN29817
18	13.6	68.0	65	6	ABN29322
19	13.4	67.0	25	9	ACI35533

C	20	13.4	67.0	50	4	AA134194	AA134194 Human SNP
C	21	13.2	66.0	20	10	AB298158	AB298158 Human CD2
C	22	13.2	66.0	20	11	ABD31189	ABD31189 Human CD2
C	23	13.2	66.0	20	12	ADU60023	ADU60023 Oligonuc1
C	24	13.2	66.0	20	12	ADU45513	ADU45513 Human o11
C	25	13.2	66.0	21	13	ADU43138	ADU43138 Knock-dow
C	26	13.2	66.0	21	13	ADU45352	ADU45352 Knock-dow
C	27	13.2	66.0	25	9	ACT15240	ACT15240 Human m1c
C	28	13.2	66.0	25	9	ACK09387	ACK09387 Human m1c
C	29	13.2	66.0	27	2	AAK03341	AAK03341 PCR prime
C	30	13.2	66.0	33	2	AAK89941	AAK89941 Sequence
C	31	13.2	66.0	33	2	AAK89942	AAK89942 Sequence
C	32	13.2	66.0	35	6	ABL32002	ABL32002 Dihydroxy
C	33	13.2	66.0	44	2	AAT38282	AAT38282 Murine 10
C	34	13.2	66.0	44	3	AAA51915	AAA51915 Reverse p
C	35	13.2	66.0	44	4	AAK03383	AAK03383 3' primer
C	36	13.2	66.0	44	4	AAK23475	AAK23475 Mouse 103
C	37	13.2	66.0	44	4	AAK23475	AAK23475 3' Oligon
C	38	13.2	66.0	44	4	AA170278	AA170278 Mouse 103
C	39	13.2	66.0	44	4	AAK82626	AAK82626 Murine TH
C	40	13.2	66.0	44	6	AB553332	AB553332 Mouse 103
C	41	13.2	66.0	44	8	ABQ77055	ABQ77055 Murine 10
C	42	13.2	66.0	44	9	ADB37507	ADB37507 Mouse Th-
C	43	13.2	66.0	44	11	ADM68648	ADM68648 Mouse try
C	44	13.2	66.0	50	14	ADW98969	ADW98969 Human her
C	45	13.2	66.0	51	10	ADP92437	ADP92437 PCR prime

ALIGNMENTS

RESULT 1	AAZ31440	AAZ31440 standard; DNA; 20 BP.
ID	AAZ31440;	
AC	AAZ31440;	
XX	07-FEB-2000	(first entry)
DT	Human neuropilin mRNA specific antisense oligo GTT3610.	
DE	Neuropilin; human; growth; metastasis; tumor; neovascularisation; cancer;	
XX	papilloma; diabetic retinopathy; antisense; ss.	
KW	Synthetic.	
XX	Homo sapiens.	
OS	MO9955855-A2.	
XX	04-NOV-1999.	
PD	23-APR-1999;	99WO-CA000324.
XX	23-APR-1998;	98US-0082791P.
PR	(GENE-) GENESENSE TECHNOLOGIES INC.	
XX	Wright JA, Young AH, Lee YS;	
PI	WPI; 2000-023357/02.	
XX	Antisense oligonucleotides that inhibit neuropilin expression, useful for	
PT	treating cancer.	
FT	Claim 4; Page 16; 57pp; English.	
PS	Sequences AAZ31431-460 represent antisense oligonucleotides which inhibit	
XX	human neuropilin expression. The antisense oligonucleotides can be used	
CC	to inhibit the growth or metastasis of a mammalian tumor and inhibit	
CC	neovascularisation. The oligonucleotides may be used to treat various	
CC	forms of cancers or tumors, such as sarcomas, melanomas, adenomas,	
CC	carcinomas of solid tissue, hypoxic tumors, squamous cell carcinomas of	
CC	the mouth, throat, larynx and lung, genitourinary cancers such as	

CC cervical and bladder cancer, hematopoietic cancers, colon cancer, breast
 CC cancer, pancreatic cancer, renal cancer, brain cancer, skin cancer, liver
 CC cancer, head and neck cancers, and nervous system cancers, as well as
 CC benign lesions such as papillomas. The methods may be used to treat
 CC neovascularisation disorders such as diabetic retinopathy, and
 CC retinopathy of prematurity and age related macular degeneration
 XX
 SQ Sequence 20 BP; 4 A; 6 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 20;
 Best Local Similarity 100.0%; Pred. No. 8.4;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCGACGTGGAGCCGAGA 20
 DB 1 GTGCCGACGTGGAGCCGAGA 20

RESULT 2
 ADA74692

ID ADA74692 standard; DNA; 20 BP.

AC ADA74692;

DT 20-NOV-2003 (first entry)

DE GT13610 antisense oligonucleotide targeted to human neuropilin mRNA.

XX neuropilin; VEGF165R; vascular endothelial growth factor receptor;
 KM cytosolic; growth; tumour metastasis; angiogenesis; gene therapy;
 KW GT13610; antisense; human; ss.

OS Homo sapiens.

PN US2003083274-A1.

PD 01-MAY-2003.

PF 22-APR-1999; 99US-00296264.

PR 23-APR-1998; 98US-0082791P.

PA (WRIGHT) WRIGHT J A.

PA (YOUNG) YOUNG A H.

PA (LEBY) LEE Y S.

PI Wright JA, Young AH, Lee YS;

XX WPI; 2003-576622/54.

PT New antisense oligonucleotide that inhibits neuropilin expression, useful
 PT for inhibiting growth of mammalian tumor or inhibiting metastasis of a
 PT mammalian tumor.

PS Claim 1, Page 5; 27pp; English.

CC The invention relates to a novel antisense oligonucleotide that inhibits
 CC the expression of neuropilin, also known as VEGF165R (vascular
 CC endothelial growth factor receptor). The oligonucleotide of the invention
 CC demonstrates cytostatic activity and may be useful for inhibiting the
 CC growth or metastasis of a mammalian tumour and to inhibit angiogenesis in
 CC mammals. Furthermore, the oligonucleotide may be utilised during gene
 CC therapy. The current sequence is that of the GT13610 antisense
 CC oligonucleotide of the invention which is targeted to human neuropilin
 CC mRNA.

SQ Sequence 20 BP; 4 A; 6 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 9; Length 20;
 Best Local Similarity 100.0%; Pred. No. 8.4;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCGACGTGGAGCCGAGA 20

DB 1 GTGCCGACGTGGAGCCGAGA 20

RESULT 3

ID AAF97678/c

AAAF97678 standard; DNA; 21 BP.

DT 18-NOV-2004 (revised)

DT 06-JUN-2001 (first entry)

DE Human gene single nucleotide polymorphism #2439.

XX Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
 KW polymorphism; vascular disease; coronary artery disease; forensics;
 KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
 KW pulmonary embolism; paternity test; ds.

OS Homo sapiens.
 OS Unidentified.

XX Key Location/Qualifiers

FT variation 11 /tag= a
 FT /standard_name= "Single nucleotide polymorphism"

PN W0200118250-A2.

PD 15-MAR-2001.

PF 07-SEP-2000; 2000WO-US024503.

PR 10-SEP-1999; 99US-0153357P.

PR 26-JUL-2000; 2000US-0220947P.

PR 16-AUG-2000; 2000US-0225724P.

PA (MHED) WHITEHEAD INST BIOMEDICAL RES.

PA (MILL-) MILLENNIUM PHARM INC.

PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JI;

XX WPI; 2001-226749/23.

PT Nucleic acids comprising single nucleotide polymorphisms, useful in
 PT applications such as forensics, paternity testing, medicine, genetic
 PT analysis and phenotype correlations to diseases such as diabetes and
 PT atherosclerosis.

PS Example; Page 213; 242pp; English.

CC The present invention provides a method of diagnosing a vascular disease
 CC in an individual, involving determining the sequence at various
 CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
 CC genes. The sequences at a number of polymorphic sites are also provided
 CC in the specification. In particular, the method can be used in the
 CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
 CC disease, stroke, peripheral vascular diseases, venous thromboembolism and
 CC pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
 CC useful in forensics, paternity testing, genetic analysis and phenotype
 CC correlations to diseases. The present sequence is an example of one of
 CC the human gene SNPs shown in the specification

CC Revised record issued on 18-NOV-2004 : The variation feature was
 CC incorrectly given a capital V

SQ Sequence 21 BP; 3 A; 8 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 90.0%; Score 18; DB 4; Length 21;
 Best Local Similarity 100.0%; Pred. No. 76;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCCGACGTGGACCCA 18
|||
DB 18 GTGCCGACGTGGACCCA 1

RESULT 4

ID AC190367/c
AC190367 standard; DNA; 25 BP.

AC AC190367;

DT 14-OCT-2003 (first entry)

DE Human microarray DNA oligonucleotide SEQ ID NO 90358.

KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; diallelic marker; polymorphism; human;
KW cross-species comparison.

OS Homo sapiens.

PN US2003104410-A1.

PD 05-JUN-2003.

PF 15-MAR-2002; 2002US-00098263.

PR 16-MAR-2001; 2001US-0276759P.

PA (AFY-) AFFYMETRIX INC.

PI Miltmann MP;

DR WPI; 2003-567953/53.

PT New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.

PS Claim 1; SEQ ID NO 90358; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridization to a DNA library,
CC in analysis of genetic variation or in hybridization of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridizing at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridization. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying diallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in in situ hybridization, in Southern, Northern or dot-
CC blot hybridization to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX

SQ Sequence 25 BP; 6 A; 8 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 76.0%; Score 15.2; DB 9; Length 25;

Best Local Similarity 85.0%; Pred. No. 1.6e+03;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGCCGACGTGGACCCA 20
|||
DB 1 GTGCCGACGTGGACCCA 20

DB 23 GTGCCGACGTGTACCGAGA 4

RESULT 5

ID ACK25958/c
ACK25958 standard; DNA; 25 BP.

AC ACK25958;

DT 14-OCT-2003 (first entry)

DE Human microarray DNA oligonucleotide SEQ ID NO 125939.

KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; diallelic marker; polymorphism; human;
KW cross-species comparison.

OS Homo sapiens.

PN US2003104410-A1.

PD 05-JUN-2003.

PF 15-MAR-2002; 2002US-00098263.

PR 16-MAR-2001; 2001US-0276759P.

PA (AFY-) AFFYMETRIX INC.

PI Miltmann MP;

DR WPI; 2003-567953/53.

PT New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.

PS Claim 1; SEQ ID NO 125939; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridization to a DNA library,
CC in analysis of genetic variation or in hybridization of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridizing at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridization. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying diallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in in situ hybridization, in Southern, Northern or dot-
CC blot hybridization to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX

SQ Sequence 25 BP; 4 A; 6 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 9; Length 25;

Best Local Similarity 84.2%; Pred. No. 4.9e+03;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGCCGACGTGGACCCA 20
|||
DB 25 TGACGACGTGAGACCCA 7

RESULT 6
 ABZ72759/C
 ID ABZ72759 standard; DNA, 60 BP.
 XX
 AC
 XX ABZ72759;
 DT 09-APR-2003 (first entry)
 DE Linker oligonucleotide SEQ ID NO:162.
 XX
 XX High throughput assay system; nucleic acid detection; anchor; target;
 KW linker; ss.
 OS Synthetic.
 PN WO2003002750-A2.
 PD 09-JAN-2003.
 PE 26-JUN-2002; 2002MO-US020039.
 PR 26-JUN-2001; 2001US-00888413.
 PS (HIGH-) HIGH THROUGHPUT GENOMICS INC.
 PI Kris RM, Felder S;
 DR WPI: 2003-201508/19.
 PT
 PT Detecting nucleic acid target in sample by using combination comprising
 PT multiple regions each of which has two different loci of anchors in
 PT association with a bifunctional linker that has portion specific for
 PT anchor.
 PS
 PS Example 30; Page 116; 129pp; English.
 PS
 PS The present invention describes a method for detecting a nucleic acid
 CC target (T) in a sample (S). The method involves: (a) contacting (S) which
 CC may comprise the target(s) with a nuclease protection fragment(s) (I)
 CC specific for and which binds to the target(s), exposing the (S) to a
 CC nuclease effective to digest remaining single stranded nucleic acid, and
 CC then contacting the resultant (S) with a combination (II) which
 CC comprises, before addition of (S), a surface comprising multiple
 CC spatially discrete regions, at least two of which are substantially
 CC identical, each region comprising at least two different loci of anchors,
 CC the anchors at each locus, each in association with a bifunctional linker
 CC portion that comprises a probe which is specific for the anchor, and a second
 CC under conditions effective for the (I) to bind to the combination, where
 CC two or more of the anchors located at a first locus of a region are in
 CC association with different bifunctional linkers, having different target
 CC specificities; and (b) detecting the bound protection fragment(s), and
 CC where the regions are tubes, and the loci of anchors are arranged in a
 CC linear array in the tubes. Such an assay can be termed a multi array
 CC plate screen (MAPS) method or assay. When the probes are
 CC oligonucleotides, the MAPS can be used for diagnosing or specific mutations
 CC genetic variations or defects e.g. polymorphisms or pathogenic organisms.
 CC associated with disease such as cystic fibrosis or pathogenic organisms.
 CC When the probes are antigen binding molecules, the assays can be used for
 CC screening variant proteins or protein expression patterns. The assay can
 CC also be used for mapping expressed sequence tags (ESTs). ABZ72599 to
 CC ABZ72762, and ABP56911, represent sequences used in the exemplification
 CC of the present invention
 XX
 SQ Sequence 60 BP; 16 A; 14 C; 19 G; 11 T; 0 U; 0 Other;
 Query Match 71.0%; Score 14.2; DB 8; Length 60;
 Best Local Similarity 84.2%; Pred. No. 4.9e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0
 1 GTGGCGACGTGGAGCCAG 19
 ||||| ||||| || |||

DB	48	GTGCTACGTGCACTAG	30
		RESULT 7	
ID	ACK26420	standard; DNA; 25 BP.	
AC	ACK26420;		
DT	14-OCT-2003	(first entry)	
XX			
DE	Human microarray DNA oligonucleotide SEQ ID NO 126401.		
XX			
KM	EST; ss; probe; expressed sequence tag; microarray; gene expression;		
KW	genetic variation; diallelic marker; polymorphism; human;		
XX	cross-species comparison.		
OS	Homo sapiens.		
XX			
PN	US2003104410-A1.		
PD	05-JUN-2003.		
XX			
PF	15-MAR-2002; 2002US-00098263.		
XX			
PR	16-MAR-2001; 2001US-0276759P.		
PA	(AFYY-) AFFYMETRIX INC.		
PI	Miltmann MP;		
XX			
DR	WPI; 2003-567953/53.		
XX			
PT	New array of nucleic acid probes, useful for in situ hybridization, in		
PR	Southern, Northern or dot-blot hybridization to identify or detect the		
PI	sequence or specific mutations of any gene.		
PS	Claim 1; SEQ ID NO 126401; 9pp; English.		
XX			
CC	The invention discloses a microarray comprising a plurality of nucleic		
CC	acid probes including one of 2,018,500 fully defined sequences, or its		
CC	perfect match, perfect mismatch, antisense match or antisense mismatch.		
CC	Also disclosed is a method of gene expression analysis. The array is used		
CC	in monitoring gene expression levels by hybridisation to a DNA library,		
CC	in analysis of genetic variation or in hybridisation of tag-labelled		
CC	compounds. The nucleic acid probes are specifically designed for analysis		
CC	of at least one target sequence. The method of analysis comprises		
CC	hybridising at least one or more nucleic acids to at least two or more		
CC	nucleic acid probes and detecting the hybridisation. The nucleic acid		
CC	probes are attached to a solid support. The analysis comprises monitoring		
CC	gene expression levels, identifying diallelic markers or polymorphisms,		
CC	or family members of a gene and a cross-species comparison. Each of the		
CC	nucleic acids further comprises a tag sequence. The array of nucleic acid		
CC	probes is useful in in situ hybridisation, in Southern, Northern or dot-		
CC	blot hybridisation to identify or detect the sequence or specific		
CC	mutations of any gene, in mapping the 5' terminus of mRNA molecules by		
CC	primer extensions or in screening cDNA or genomic libraries or subclones		
CC	for additional subclones containing segments of DNA that have been		
CC	isolated and previously sequenced. The sequence presented is one of the		
CC	nucleic acid probes incorporated in the microarray. Note: The sequence		
CC	data for this patent can also be obtained in electronic format directly		
CC	from USPTO at seqdata.uspto.gov/sequence.html		
XX			
SQ	Sequence 25 BP; 5 A; 9 C; 9 G; 2 T; 0 U; 0 Other;		
Query Match	69.0%; Score 13.8; DB 9; Length 25;		
Best Local Similarity	86.2%; Pred. 7.7e+03;		
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0			
4	CCGACGTGGAGCCGAGA 20		
4			
4	CGAGCTGAGACCCAGA 20		

RESULT 8

ACI82748 standard; DNA; 25 BP.

ACI82748;

14-OCT-2003 (first entry)

Human microarray DNA oligonucleotide SEQ ID NO 82739.

EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human; cross-species comparison.

Homo sapiens.

US2003104410-A1.

05-JUN-2003.

15-MAR-2002; 2002US-00098263.

16-MAR-2001; 2001US-0276759P.

(AFFY-) AFFYMETRIX INC.

Miltmann MP;

WPI; 2003-567953/53.

New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.

Claim 1; SEQ ID NO 82739; 9pp; English.

The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridization to a DNA library, in analysis of genetic variation or in hybridization of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridizing at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridization. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html

Sequence 25 BP; 5 A; 7 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 69.0%; Score 13.8; DB 9; Length 25;

Best Local Similarity 88.2%; Pred. No. 7.7e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

4 CCGAGCTGGGAGCCAGA 20

7 CCGAGCTGGGAGCCAGA 23

RESULT 9

AAS07631 standard; DNA; 27 BP.

AAS07631;

11-SEP-2003 (revised)

23-OCT-2001 (first entry)

Streptococcus coelicolor mmyTOG promoter PCR primer CR344.

SCP1; ss; methylenomycin cluster; mmc; MmyR; Mmf; MmfH; mmyTOG; MmfL; MmyR; MmyT; MmyO; MmyG; MmyJ; Mmr; heterologous gene expression; PCR primer; CR344.

Streptomyces coelicolor.

WO200148228-A1.

05-JUL-2001.

20-DEC-2000; 2000WO-GB004972.

23-DEC-1999; 99GB-00030477.

(PLAN-) PLANT BIOSCIENCE LTD.

Chater KF, Bruton CJ, O'rouke SJ, Wietzorrek AW;

WPI; 2001-425675/45.

Novel expression cassette for expressing a nucleic acid of interest, derived from the regulatory region of methylenomycin gene cluster of SCP1 plasmid of Streptomyces coelicolor A3(2).

Example 11; Page 75; 142pp; English.

The sequence represents a PCR primer used to amplify the promoter mmyTOG from an expression cassette SCP1 (the regulatory region of the methylenomycin cluster (mmc) from Streptomyces coelicolor A3(2)), which encodes the MmyR, Mmf, MmfH, MmfL, MmyR, MmyT, MmyO, MmyG, MmyJ and partial Mmr polypeptides) for use as a strong promoter for heterologous gene expression. The expression cassette is useful for expressing a nucleic acid of interest, substantially only when the host cell culture reaches high cell density at or close to the stationary phase of host cell culture. In particular the system is useful in regulating methylenomycin production. Reduced or no expression of the nucleic acid of interest is observed earlier in growth, avoiding toxic effects of some gene products on growth and the system does not require addition of exogenous inducer. The methylenomycin cluster naturally present on a highly transmissible plasmid permits properly regulated expression in diverse Streptomyces host and the expression is driven by a strong promoter, leading to high yield of the desired end product. (Updated on 11-SEP-2003 to standardise OS field)

Sequence 27 BP; 3 A; 12 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 69.0%; Score 13.8; DB 4; Length 27;

Best Local Similarity 88.2%; Pred. No. 7.7e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

3 GCCGAGCTGGGAGCCAG 19

3 GCCGAGCTGGGAGCCAG 19

RESULT 10

AAX83785 standard; DNA; 28 BP.

AAX83785;

06-SEP-1999 (first entry)

```
DE PmeI restriction endonuclease PCR primer PmeI-IP1.
XX
XX PmeI: restriction endonuclease; modification methylase;
KW recombinant DNA technique; molecular cloning; gene characterization;
KW Pseudomonas mendocina; PCR primer; ss.
XX
OS Synthetic.
OS Pseudomonas mendocina.
XX
XX EP91835-A2.
XX
XX 28-JUL-1999.
XX
XX 24-NOV-1998; 98EP-00309629.
XX
XX 24-NOV-1997; 97US-00976703.
XX
XX (NEW) NEW ENGLAND BIOLABS INC.
XX
XX Chang Z, Morgan RD;
PI
XX WPI, 1999-397163/34.
XX
XX New restriction endonuclease useful in recombinant DNA techniques.
XX
XX Example 1; Page 9; 28pp; English.
XX
XX The present sequence represents a PCR primer for the 27 kD Pseudomonas
CC mendocina PmeI restriction endonuclease protein. The PmeI restriction
CC endonuclease is used to cut DNA in the middle of the site GTTAAAC
CC between the third T and the first A, to produce blunt ends. The PmeI
CC restriction endonuclease is therefore useful in recombinant DNA
CC techniques such as molecular cloning and gene characterization
XX
XX Sequence 28 BP; 5 A; 7 C; 10 G; 6 T; 0 U; 0 Other;
SQ
Query Match 69.0%; Score 13.8; DB 2; Length 28;
Best Local Similarity 88.2%; Pred. No. 7.7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 2 TGCCGACGTGGAGCCCA 18
DB 19 TGCCGACGTGGAGCCCA 3
RESULT 11
AAL34511/c
ID AAL34511 standard; DNA; 50 BP.
XX
XX AAL34511;
AC
XX
XX 24-JAN-2002 (first entry)
DE
XX
XX Human SNP oligonucleotide #7719.
XX
XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200147944-A2.
XX
XX 05-JUL-2001.
XX
XX 28-DEC-2000; 2000WO-US035498.
XX
XX 28-DEC-1999; 99US-0173419P.
XX
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PR 27-DEC-2000; 2000US-00173419.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Shimkova RA, Leach M;
XX
XX WPI, 2001-465210/50.
XX
XX Polymorphic nucleic acids encoding e.g. amyloses, cyclins, polymerases,
XX oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
XX autoimmune diseases and infections.
XX
XX Claim 1; Page 3620; 4143pp; English.
XX
XX The present invention relates to oligonucleotides encoding polymorphic
XX variants of proteins related to amyloses, amyloid proteins, angiotensin,
XX apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
XX histones, kinases, colony stimulating factors, complement related
XX proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-
XX protein coupled receptors and thioesterases. The present sequence is one
XX such oligonucleotide. The oligonucleotides and the peptides encoded by
XX them may be used in the prevention, diagnosis and treatment of diseases
XX associated with inappropriate expression of the proteins listed above.
XX Disorders that may be prevented, diagnosed and/or treated include
XX multifactorial diseases with a genetic component, such as autoimmune
XX diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
XX systemic lupus erythematosus and Grave's disease), inflammation, cancer
XX (e.g. cancers of the bladder, brain, breast, colon and kidney,
XX leukemia), diseases of the nervous system and an infection of pathogenic
XX organisms
XX
XX Sequence 50 BP; 7 A; 15 C; 17 G; 11 T; 0 U; 0 Other;
SQ
Query Match 69.0%; Score 13.8; DB 4; Length 50;
Best Local Similarity 88.2%; Pred. No. 7.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 3 GCCGACGTGGAGCCAG 19
DB 26 GCCGACGTGGAGCCAG 10
RESULT 12
ADN00075
ID ADN00075 standard; DNA; 55 BP.
XX
XX ADN00075;
AC
XX
XX 15-JUL-2004 (first entry)
XX
XX Human FCER2 (CD23) single nucleotide polymorphism-containing DNA 24.
XX
XX variation; drug sensitivity; chronic obstructive pulmonary disease; COPD;
KW asthma; depression; corticosteroid; beta-agonist; human; SNP;
KW single nucleotide polymorphism; ds; FCER2; CD23.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
XX variation 26
XX FT /*tag= a
XX FT /label= Single nucleotide polymorphism (SNP)
XX
XX WO2004033650-A2.
XX
XX 22-APR-2004.
XX
XX 08-OCT-2003; 2003WO-US031917.
XX
XX 08-OCT-2002; 2002US-0416969P.
XX
XX (BGM) BRIGHAM & WOMEN'S HOSPITAL INC.
XX
```

XX Wetes ST, Tantistira K;
XX
XX WPI; 2004-364864/34.
XX
XX Use of sequence variations in candidate pathway genes for assessing
PT sensitivity to therapeutic agents, e.g. corticosteroids or beta-agonists,
PT in a subject with chronic obstructive pulmonary disease, asthma or
PT depression.
XX
XX Claim 54; SEQ ID NO 256; 212pp; English.
XX
XX The invention relates to a novel use for sequence variations in candidate
CC pathway genes for assessing sensitivity to a therapeutic agent in a
CC subject with chronic obstructive pulmonary disease (COPD), asthma or
CC depression. The sequence variations in candidate pathway genes of the
CC invention may be useful for assessing sensitivity to a therapeutic
CC agents, such as corticosteroids or beta-agonists, in a subject with COPD,
CC asthma or depression. The current sequence is that of a human FCER2
CC (CD23) SNP (single nucleotide polymorphism)-containing DNA of the
CC invention.
XX
XX Sequence 55 BP; 6 A; 11 C; 24 G; 12 T; 0 U; 2 Other;
SQ
Query Match 69.0%; Score 13.8; DB 12; Length 55;
Best Local Similarity 78.9%; Pred. No. 7.6e+03;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
OY 2 TGCCGACGTGGAGCCAG 20
DB 18 TGCAGCGCGGAGCTCAGA 36
RESULT 13
ABN29579
ID ABN29579 standard; DNA; 65 BP.
XX
XX ABN29579;
AC
XX
XX 15-JUL-2002 (first entry)
DT
XX
XX Rat spliced transcript detection oligonucleotide SEQ ID NO:2327.
DE
XX Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
XX Rattus norvegicus.
OS
XX
XX WO200210449-A2.
PN
XX
XX 07-FEB-2002.
PD
XX
XX 20-JUL-2001; 2001WO-IB001903.
PF
XX
XX 28-JUL-2000; 2000US-0221607P.
PR
XX 02-MAY-2001; 2001US-0287724P.
XX
XX (COMP-) COMPUGEN INC.
PA
XX
XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
PI
XX WPI; 2002-257383/30.
DR
XX
XX New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of a
PT genome, useful for detecting tissue-, pathology-, and developmental-
PT specific genes.
XX
XX Example 1; SEQ ID NO 2327; 47pp; English.
XX
XX The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-
CC)transcriptome comprises messenger RNAs transcribed from multiple

CC transcription units that populate a genome. The library comprises several
CC oligonucleotides, each capable of hybridizing selectively to a set of
CC messenger RNAs transcribed from a given transcription unit of the genome,
CC which encodes one or more messenger RNA splice variants. The
CC oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterizing the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a particular
CC biological or pathological state, and so allowing the detection of tissue
CC - and pathology-specific genes such as those genes only expressed in
CC specific tissue under a specific pathological condition; to detect
CC developmental specific genes; and to detect RNA transcripts and splice
CC variants of a transcriptome of a patient suffering from a particular
CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
CC rats, humans and mice, which are used in the exemplification of the
CC present invention. N.B. The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 65 BP; 14 A; 14 C; 18 G; 19 T; 0 U; 0 Other;
SQ
Query Match 69.0%; Score 13.8; DB 6; Length 65;
Best Local Similarity 88.2%; Pred. No. 7.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 3 GCCGACGTGGAGCCAG 19
DB 23 GCAGACGTGGAGCCAG 39
RESULT 14
ACT190366/c
ID ACT190366 standard; DNA; 25 BP.
XX
XX ACT190366;
AC
XX
XX 14-OCT-2003 (first entry)
DT
XX
XX Human microarray DNA oligonucleotide SEQ ID NO 90357.
DE
XX
XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; diallelic marker; polymorphism; human;
KW cross-species comparison.
XX
XX Homo sapiens.
OS
XX
XX US2003104410-A1.
PN
XX
XX 05-JUN-2003.
PD
XX
XX 15-MAR-2002; 2002US-00098263.
PF
XX
XX 16-MAR-2001; 2001US-0276759P.
PR
XX
XX (AEFY-) AEFYMETRIX INC.
PA
XX
XX Miltmann MP;
PI
XX
XX WPI; 2003-567953/53.
DR
XX
XX New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
XX Claim 1; SEQ ID NO 90357; 9pp; English.
XX
XX The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,

CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying allelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' terminus of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX
SQ Sequence 25 BP; 6 A; 7 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 68.0%; Score 13.6; DB 9; Length 25;
Best Local Similarity 80.0%; Pred. No. 9.6e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GTGCCGACGTGGAGCCGAGA 20
Db 23 GTGCCGACGTGGAGCCGAGA 4

RESULT 15

AAK23277 standard; DNA; 27 BP.

AAK23277;

11-JUN-1999 (first entry)

H. vulgare cysteine protease PCR primer GSPI.

Cysteine protease; barley; transgenic plant; disease resistance;
KW prevention; treatment; infection; stress; temperature; drought; salt;
KW wound; root-specific expression; antimicrobial; antistress;
KW anti-wounding; PCR primer; ss.

OS Synthetic.

OS Hordeum vulgare.

PN WO9910500-A1.

PD 04-MAR-1999.

PF 21-AUG-1998; 98WO-EP005339.

PR 26-AUG-1997; 97DE-01037118.

PR 22-JAN-1998; 98DE-01002384.

PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

PI Schlichter U, Steinbiss H, Antoniw J;

DR WPI; 1999-204668/17.

PT Nucleic acid encoding plant cysteine protease - that increases resistance
XX to injury and infection.

PS Example 5; Page 71; 81pp; German.

CC This invention describes a novel Hordeum vulgare cysteine protease which
CC is used to produce transgenic plants with (a) increased or reduced
CC expression of protease or (b) increased resistance to disease
CC (particularly prevention of infection) or other stress
CC factors such as extreme temperatures, drought, salt or wounding. The

CC invention also describes a regulatory region which is used to provide
CC root-specific expression of heterologous DNA following infection/injury
CC of roots. The products of the invention have antimicrobial, antistress
CC and anti-wounding activity in plants

SQ Sequence 27 BP; 6 A; 6 C; 11 G; 4 T; 0 U; 0 Other;

Query Match 68.0%; Score 13.6; DB 2; Length 27;
Best Local Similarity 80.0%; Pred. No. 9.6e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GTGCCGACGTGGAGCCGAGA 20
Db 6 GTGTGACCTGCGACCCGAGA 25

Search completed: December 24, 2005, 12:29:04
Job time : 173.4 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 10:37:31 ; Search time 1572 Seconds

(without alignments)
595.256 Million cell updates/sec

Title: US-09-296-264-10

Perfect score: 20
Sequence: 1 gtgcgcagctgtgaccacaga 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 2339354128 residues

Total number of hits satisfying chosen parameters: 768474

Minimum DB seq length: 20
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST:
1: gb_ests1.*
2: gb_ests2.*
3: gb_ests3.*
4: gb_hic.*
5: gb_ests4.*
6: gb_ests5.*
7: gb_ests6.*
8: gb_ests7.*
9: gb_gsa1.*
10: gb_gsa2.*
11: gb_gsa3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.2	71.0	74	9	BH215436
2	14.2	71.0	82	11	CR056878
3	13.8	69.0	57	10	CG718544
4	13.8	69.0	91	1	AA837667
5	13.6	68.0	49	10	CL520524
6	13.6	68.0	75	10	CG627915
7	13.6	68.0	91	1	AA930982
8	13.4	67.0	60	9	AZ776503
9	13.2	66.0	49	10	CL520524
10	13.2	66.0	50	1	AU103727
11	13.2	66.0	51	9	AZ438521
12	13.2	66.0	67	10	CG503103
13	13.2	66.0	68	9	CG326401
14	13.2	66.0	75	10	BX287246
15	13.2	66.0	79	10	CL903354
16	13.2	66.0	83	10	CM882832
17	13.2	66.0	84	10	CM509348
18	13.2	66.0	88	5	BQ756506
19	13.2	66.0	89	9	CC325628
20	13.2	66.0	93	9	CC325627
21	13.2	66.0	95	9	AZ653293
22	12.8	64.0	67	2	BG327801

23	12.8	64.0	67	10	CG506889	CG506889 OST56627
24	12.8	64.0	76	6	CD028849	CD028849 mgmy005xc
25	12.8	64.0	77	10	CG733899	CG733899 1119160G0
26	12.8	64.0	88	1	AU077180	AU077180 AU077180
27	12.8	64.0	89	1	AA094815	AA094815 cpl650..se
28	12.8	64.0	93	4	AK211710	AK211710 Mus muscu
29	12.6	63.0	25	8	CK001203	CK001203 iv39f11.b
30	12.6	63.0	39	1	AJ922836	AJ922836 AJ922836
31	12.6	63.0	44	10	CZ471572	CZ471572 d00396-3p
32	12.6	63.0	45	10	AG218255	AG218255 Drosoph11
33	12.6	63.0	50	1	AU106651	AU106651 AU106651
34	12.6	63.0	50	1	AU106652	AU106652 AU106652
35	12.6	63.0	50	1	AU106653	AU106653 AU106653
36	12.6	63.0	50	1	AU106654	AU106654 AU106654
37	12.6	63.0	50	1	AU106655	AU106655 AU106655
38	12.6	63.0	50	1	AU106659	AU106659 AU106659
39	12.6	63.0	50	1	AU106661	AU106661 AU106661
40	12.6	63.0	50	1	AU106662	AU106662 AU106662
41	12.6	63.0	50	1	AU106663	AU106663 AU106663
42	12.6	63.0	50	1	AU106664	AU106664 AU106664
43	12.6	63.0	50	1	AU106668	AU106668 AU106668
44	12.6	63.0	50	1	AU106670	AU106670 AU106670
45	12.6	63.0	50	1	AU106674	AU106674 AU106674

ALIGNMENTS

RESULT 1	BH215436	74 bp	DNA	linear	GSS 08-NOV-2001
LOCUS	BH215436				
DEFINITION	1006027A11.2SL.Y2 1006 - Rescuemu Grid G zea mays genomic, genomic survey sequence.				
ACCESSION	BH215436				
VERSION	BH215436.1	GI:16806094			
KEYWORDS	GSS.				
SOURCE	Zea mays				
ORGANISM	Zea mays				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.				
AUTHORS	1 (bases 1 to 74)				
TITLE	Maize genomic sequences found using engineered Rescuemu transposon				
JOURNAL	Unpublished (2001)				
COMMENT	Contact: Walbot V Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 725 8221 Email: walbot@stanford.edu				

Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1006027 row: 42
Class: transposon-tagged.
Location/Qualifiers

FEATURES

source

1..74
/organism="Zea mays"
/mol_type="genomic DNA"
/cuiovar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/cuiovar="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1006 - Rescuemu Grid G"
/note="Organ: leaf; Vector: Rescuemu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; Rescuemu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on Rescuemu, go to the web site 'www.zmbd.iastate.edu' and follow the links for

High quality sequence stop: 1.
Location/Qualifiers
1. 91

FEATURES
Source
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1373621"
/sex="female"
/tissue_type="ovary"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Ov2"
/note="Vector: PAMPI0; mRNA made from invasive ovarian tumor, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."

ORIGIN

Query Match 69.0%; Score 13.8; DB 1; Length 91;
Best Local Similarity 88.2%; Pred. No. 7.3e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 GCCGACGTGGAGCCAG 19
|||
30 GACGGCGTGGAGCCAG 46
|||

RESULT 5
CLUS20524/c 49 bp DNA linear GSS 02-APR-2004
LOCUS DAY7C01 Flanking Sequence Tag of Oryza sativa T-DNA insertion lines
DEFINITION Oryza sativa (japonica cultivar-group) genomic, genomic survey
sequence.
CLUS20524 49 bp DNA linear GSS 02-APR-2004
LOCUS CLUS20524.1 GI:46147324
GSS.

REFERENCE
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 49)
Sallaud, C., Gay, C., Larmande, P., Bes, M., Piffanel, P., Piegou, B.,
Droc, G., Regad, F., Bourgeois, E., Meynard, D., Perrin, C.,
Ghesquiere, A., Delenry, M., Glaszmann, J. C. and Guiderdoni, E.
High throughput T-DNA insertion mutagenesis in rice: A first step
towards in silico reverse genetics
Plant J. (2004) In press
Contact: Guiderdoni
IMR PTA Biotrop program

JOURNAL
COMMENT
CIRAD
TA 40/03 ave Agropolis 34398 Montpellier cedex 5 FRANCE
Tel: 33467615629
Fax: 33467615605
Email: emmanuel.guiderdon@cirad.fr
Class: T-DNA tagged.
Location/Qualifiers

FEATURES
Source
1. 49
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone_lib="Flanking Sequence Tag of Oryza sativa T-DNA
insertion lines"
/note="PCR was performed on DNA of primary transformants
of Oryza sativa plants. The DNA fragment(s) resulting of
PCR were directly sequenced from the left border to
determine the genomic sequence flanking the insertion.
T-DNA derived sequences were removed. Information to order
the corresponding mutant line and a link to a database
providing a graphical display is available from June 2004
at <http://genoplante-info.infobiogen.fr/oryzasatline/>.
This sequence has been generated in the framework of the

French plant genomics program Genoplante
(<http://www.genoplante.org> and
<http://genoplante-info.infobiogen.fr>).

ORIGIN

Query Match 68.0%; Score 13.6; DB 10; Length 49;
Best Local Similarity 80.0%; Pred. No. 9.2e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GTGCCGACGTGGAGCCAG 20
|||
40 GGGCCACAGTGGAGCCAG 21
|||

RESULT 6
CG627915 75 bp mRNA linear GSS 02-OCT-2003
LOCUS OST338592 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST338592,
DEFINITION mRNA sequence.
CG627915
VERSION CG627915.1 GI:37451764
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Mus.
1 (bases 1 to 75)
Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
Piggott, J., Beltrando, R., Buxton, E.C., Edwards, J., Finch, R.A.,
Fridde, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jasing, C.,
Key, B.W., Jr., Klipp, P., Kohlhauf, B., Ma, Z., -Q., Markesich, D.,
Payne, R., Potter, D.G., Qian, N., Shaw, U., Schrick, J., Shi, Z., -Z.,
Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,
Zhu, Q., Person, C. and Sands, A.T.
Mki kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
14610273
Contact: Zambrowicz BP
Omnibank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.
Location/Qualifiers

FEATURES
Source
1. 75
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST338592"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"

ORIGIN

Query Match 68.0%; Score 13.6; DB 10; Length 75;
Best Local Similarity 80.0%; Pred. No. 9.1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GTGCCGACGTGGAGCCAG 20
|||
42 GTGCCACAGGAGCCAG 61
|||

RESULT 7
AA930982 91 bp mRNA linear EST 23-APR-1998
LOCUS VY79505 r1 Stragene mouse macrophage (H937306) Mus musculus cDNA
DEFINITION clone IMAGE:1312449 5' similar to gb:52839 60S RIBOSOMAL PROTEIN
L17 (HUMAN);, mRNA sequence.

ACCESSION AA930982
 VERSION AA930982.1 GI:3079415
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS 1 (bases 1 to 91)
 Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gessel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
 The WashU-HMI Mouse EST Project
 Unpublished (1996)
 CONTACT: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
 MGI:682745
 Seq primer: -28m13 rev1 ET from Amersham
 High quality sequence stop: 20.

FEATURES
 source
 1..91
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="IMAGE:131249"
 /issue_type="macrophage"
 /dev_stage="WEHI-3 cell line"
 /lab_host="SOLR (kanamycin resistant)"
 /clone_lib="Stratagene mouse macrophage (#937306)"
 /note="Organ: blood; Vector: pBluescript SK-; Site: 1; EcorI; Site: 2; XhoI; Cloned unidirectionally. Primer: Oligo dT. WEHI-3 cell line. Average insert size: 1.5 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGCAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3' "

ORIGIN
 Query Match 68.0%; Score 13.6; DB 1; Length 91;
 Best Local Similarity 80.0%; Pred. No. 9.1e+04;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTGCCGACGTGGGACCCAGA 20
 |||||
 DB 21 GTGCCAGACTTGTGCCCCAGA 40

RESULT 8
 AZ776503 60 bp DNA linear GSS 16-FEB-2001
 LOCUS 2M0010J11F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 DEFINITION clone UGCG2M0010J11 F, genomic survey sequence.
 ACCESSION AZ776503
 VERSION AZ776503.1 GI:12904143
 KEYWORDS GSS.
 ORGANISM Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS 1 (bases 1 to 60)
 Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhuser, A. and Wright, D. Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL Plasmid inserts
 COMMENT Unpublished (2000)
 CONTACT: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0010 row: U column: 11
 Seq primer: CGTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 60.

FEATURES
 source
 1..60
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCG2M0010J11"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCGIM library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (9114732114 [gb] AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
 Query Match 67.0%; Score 13.4; DB 9; Length 60;
 Best Local Similarity 93.3%; Pred. No. 1.1e+05;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGCCGACGTGGGACC 16
 |||||
 DB 39 TGCCCTACGTGGGACC 25

RESULT 9
 CL520524 49 bp DNA linear GSS 02-APR-2004
 LOCUS DA11C01 Flanking Sequence Tag of Oryza sativa T-DNA insertion lines
 DEFINITION Oryza sativa (japonica cultivar-group) genomic, genomic survey
 sequence.
 ACCESSION CL520524
 VERSION CL520524.1 GI:46147324
 KEYWORDS GSS.
 ORGANISM Oryza sativa (japonica cultivar-group)
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhacridae; Oryzaceae; Oryza.

REFERENCE
 AUTHORS 1 (bases 1 to 49)
 Sallaud, C., Gay, C., Larnande, P., Bes, M., Piffanel, P., Piegou, B., Droc, G., Regad, F., Bourgeois, E., Meynard, D., Perin, C., Ghesquiere, A., Delseny, M., Glaszmann, J. C. and Guiderdoni, E.

TITLE High throughput T-DNA insertion mutagenesis in rice: A first step towards in silico reverse genetics
JOURNAL Plant J. (2004) In press
COMMENT Contact: Guiderdoni UMR PIA Biotech program CIRAD
 TA 40/03 ave Agropolis 34398 Montpellier cedex 5 FRANCE
 Tel: 33467615629
 Fax: 33467615605
 Email: emmanuel.guiderdoni@cirad.fr
FEATURES Classes: TDNA tagged.
source Location/Qualifiers
 1..49
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="Genomic DNA"
 /cultivar="Nipponbare"
 /db_xref="taxon:33947"
 /clone_lib="Flanking Sequence Tag of Oryza sativa T-DNA insertion lines"
 /note="PCR was performed on DNA of primary transformants of Oryza sativa plants. The DNA fragment(s) resulting of PCR were directly sequenced from the left border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display is available from June 2004 at <http://genoplante-info.infobiogen.fr/orysatagline/>. This sequence has been generated in the framework of the French plant genomics program Genoplante (<http://www.genoplante.org> and <http://genoplante-info.infobiogen.fr>."

ORIGIN
 Query Match 66.0%; Score 13.2; DB 10; Length 49;
 Best Local Similarity 83.3%; Pred. No.1.4e+05;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 1 GTCCGACGTGGACCCA 18
 | ||| ||||| |||||
 25 GGGCCACGTCGGCCCCA 42
 ||||| ||||| |||||

RESULT 10
LOCUS AU103727c
DEFINITION AU103727 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP06017, mRNA sequence.
ACCESSION AU103727
VERSION AU103727.1 GI:13553248
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 50)
 Suzuki,Y., Taira,H., Teunoda,T., Mizushima-Sugano,J., Seese,J.,
 Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
 Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
 Diverse transcriptional initiation revealed by fine, large-scale
 mapping of mRNA start sites
 EMBO Rep. 2 (5), 388-393 (2001)
 11375929
 Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokane-dai, Minato-ku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp
 Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
 Sugano,S. Construction and characterization of a full
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
 149-156 (1997).
 Location/Qualifiers

FEATURES
source Location/Qualifiers
 1..49
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="Genomic DNA"
 /cultivar="Nipponbare"
 /db_xref="taxon:33947"
 /clone_lib="Flanking Sequence Tag of Oryza sativa T-DNA insertion lines"
 /note="PCR was performed on DNA of primary transformants of Oryza sativa plants. The DNA fragment(s) resulting of PCR were directly sequenced from the left border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display is available from June 2004 at <http://genoplante-info.infobiogen.fr/orysatagline/>. This sequence has been generated in the framework of the French plant genomics program Genoplante (<http://www.genoplante.org> and <http://genoplante-info.infobiogen.fr>."

ORIGIN
 Query Match 66.0%; Score 13.2; DB 10; Length 49;
 Best Local Similarity 83.3%; Pred. No.1.4e+05;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 1 GTCCGACGTGGACCCA 18
 | ||| ||||| |||||
 25 GGGCCACGTCGGCCCCA 42
 ||||| ||||| |||||

RESULT 10
LOCUS AU103727c
DEFINITION AU103727 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP06017, mRNA sequence.
ACCESSION AU103727
VERSION AU103727.1 GI:13553248
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 50)
 Suzuki,Y., Taira,H., Teunoda,T., Mizushima-Sugano,J., Seese,J.,
 Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
 Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
 Diverse transcriptional initiation revealed by fine, large-scale
 mapping of mRNA start sites
 EMBO Rep. 2 (5), 388-393 (2001)
 11375929
 Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokane-dai, Minato-ku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp
 Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
 Sugano,S. Construction and characterization of a full
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
 149-156 (1997).
 Location/Qualifiers

FEATURES
source Location/Qualifiers
 1..49
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="Genomic DNA"
 /cultivar="Nipponbare"
 /db_xref="taxon:33947"
 /clone_lib="Flanking Sequence Tag of Oryza sativa T-DNA insertion lines"
 /note="PCR was performed on DNA of primary transformants of Oryza sativa plants. The DNA fragment(s) resulting of PCR were directly sequenced from the left border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display is available from June 2004 at <http://genoplante-info.infobiogen.fr/orysatagline/>. This sequence has been generated in the framework of the French plant genomics program Genoplante (<http://www.genoplante.org> and <http://genoplante-info.infobiogen.fr>."

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source
1. .50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEP06017"
/clone_lib="Sugano Homo sapiens cDNA library"

Query Match 66.0%; Score 13.2; DB 1; Length 50;
Best Local Similarity 83.3%; Pred. No. 1.4e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 3 GCCGACGCGGACCCAGA 20
||| ||||| ||||| |||||
Db 30 GCCAACGTCGACCTCAGA 13

RESULT 11
AZ438521/c
LOCUS AZ438521 51 bp DNA linear GSS 03-OCT-2000
DEFINITION IM0228112R Mouse 10kb plasmid U0GC1M library Mus musculus genomic
clone U0GC1M0228112 R, genomic survey sequence.
ACCESSION AZ438521
VERSION AZ438521.1 GI:10562534
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 51)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenan,B., Pedersen,T.,
Rellly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel.: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0228 row: I column: 12
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 51.
Location/Qualifiers
1. 51
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U0GC1M0228112"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid U0GC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative

```

of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 66.0%; Score 13.2; DB 9; Length 51;
Best Local Similarity 83.3%; Pred. No. 1.4e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 TGCCGACGTGGAGCCAG 19
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Db 31 TGCCGACGTGGAGCCAG 14

RESULT 12
CG503103
LOCUS
DEFINITION OST9376 Mus musculus 129SV/Ev Mus musculus cDNA clone OST9376,
mRNA sequence.
ACCESSION CG503103
VERSION CG503103.1 GI:37278741
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
Piggott, J., Baltranderio, H., Buxton, E.C., Edwards, J., Finch, R.A.,
Fridde, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jang, C.,
Key, B.W., Jr., Kipp, P., Kohlhauf, B., Ma, Z.-Q., Markesich, D.,
Payne, R., Porter, D.G., Qian, J., Shaw, J., Schrick, J., Shi, Z.-Z.,
Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,
Zhu, Q., Peterson, C. and Sands, A.T.
Wnk1 Kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
14610273
Contact: Zambrowicz BP
OmiBank

JOURNAL
PUBMED
COMMENT Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature, 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.
Location/Qualifiers
1..67
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129SV/Ev"
/db_xref="taxon:10090"
/clone="OST9376"
/cell_type="embryonic stem cell"
/clone_1ib="Mus musculus 129SV/Ev"

ORIGIN
source

Query Match 66.0%; Score 13.2; DB 10; Length 67;
Best Local Similarity 83.3%; Pred. No. 1.4e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 GTCCGACGTGGAGCCCA 18
|||||
Db 29 GTCCGACGTGGAGCCCA 46

RESULT 13
CC326401/c

LOCUS CC326401 68 bp mRNA linear GSS 16-MAY-2003
DEFINITION XN749 BayGenomics Gene Trap library pGT2Lxf Mus musculus cDNA, mRNA
sequence.
ACCESSION CC326401
VERSION CC326401.1 GI:30795572
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Murinae; Mus.
1 (bases 1 to 68)
http://baygenomics.ucsf.edu/
http://published (2001)
Contact: BayGenomics

Bay Area Functional Genomics Consortium (BayGenomics)
Email: info@baygenomics.ucsf.edu
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from BayGenomics. Annotation
information available from
http://baygenomics.ucsf.edu/cgi-bin/Baysearch.py?OPTION=EXACTTYPE=CELL_LINERKEY=XN749
Class: Gene Trap.
Location/Qualifiers
1..68
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 Ola"
/db_xref="taxon:10090"
/sex="Male"
/cell_type="Embryonic stem cell"
/clone_1ib="BayGenomics Gene Trap Library pGT2Lxf"
/note="Vector: pGT2Lxf"

FEATURES
source

ORIGIN
Query Match 66.0%; Score 13.2; DB 9; Length 68;
Best Local Similarity 83.3%; Pred. No. 1.4e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 TGCCGACGTGGAGCCAG 19
|||||
Db 64 TGCCGACGTGGAGCCAG 47

RESULT 14
BX287246 75 bp DNA linear GSS 02-APR-2004
LOCUS BX287246
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-398F02-017892,
genomic survey sequence.
ACCESSION BX287246
VERSION BX287246.1 GI:2886242
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta, eudicotyledons, core eudicotyledons;
rosids; eurosid II; Brassicales; Brassicaceae; Arabidopsids.
1
Li, Y., Rosso, M.G., Strizhov, N., Viehoever, P. and Weishaar, B.
GABI-Kat Simplesearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
Bioinformatics 19 (11), 1441-1442 (2003)
12874060

REFERENCE
AUTHORS Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and
Weishaar, B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)
14756321
JOURNAL
PUBMED

REFERENCE
AUTHORS 3
Strizhov,N., Li,Y., Rosso,M.G., Viehovever,P., Dekker,K.A. and
Weishaar,B.
TITLE High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines
JOURNAL Biotechniques 35 (6), 1164-1168 (2003)
PUBMED 14682050
REFERENCE 4 (bases 1 to 75)
AUTHORS Rosso,M.G., Strizhov,N., Li,Y. and Weishaar,B.
TITLE Direct Submission
JOURNAL Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer
Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence has been recovered from the left border of the T-DNA.
It indicates an insertion within the locus defined by BAC clone
c186. Details on the protocols used for generation of the sequence
are described in References 1-3. The sequences are generated at the
MPI for Plant Breeding Research in the context of the GABI-Kat
project. GABI-Kat is part of the German Plant Genomics program
designated 'GABI'. Information on line availability can be found
at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.
Location/Qualifiers
1..75
/organism="Arabidopsis thaliana"
/mol_type="Genomic DNA"
/db_xref="taxon:3702"
/clone="GK-398P02-017892"
/clone_id="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector PAC161 (Genbank accession number: AJ537514). The
lines contain one or more T-DNA insertions. The DNA
fragment(s) resulting from the PCR were directly sequenced
to determine the genomic sequence flanking the insertion.
T-DNA derived sequences were removed."

ORIGIN
Query Match 66.0%; Score 13.2; DB 10; Length 75;
Best Local Similarity 83.3%; Pred.No.1.4e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 1 GTCCGACGTGGACCCA 18
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Db 20 GTGGCACTGGGCCCA 37

RESULT 15
CL903354/c 79 bp mRNA linear GSS 01-SEP-2004
LOCUS RR2600 BayGenomics Gene Trap Library pGT2Lxf Mus musculus cDNA,
DEFINITION mRNA sequence.
ACCESSION CL903354
VERSION CL903354.1 GI:51832700
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 79)
BayGenomics.
<http://baygenomics.ucsf.edu/>
Unpublished (2001)
Contact: BayGenomics
Bay Area Functional Genomics Consortium (BayGenomics)
Email: info@baygenomics.ucsf.edu
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from BayGenomics. Annotation
information available from
http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=CELL_LINE&KEY=RR2600
Class: Gene Trap.

FEATURES
source Location/Qualifiers
1..79
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/mol_type="mRNA"
/strain="129 Ola"
/db_xref="taxon:10090"
/sex="Male"
/cell_type="Embryonic stem cell"
/clone_id="BayGenomics Gene Trap Library pGT2Lxf"
/note="Vector: pGT2Lxf"

ORIGIN
Query Match 66.0%; Score 13.2; DB 10; Length 79;
Best Local Similarity 83.3%; Pred.No.1.4e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 2 TGCCGACGTGGACCCAG 19
||| ||||| |||||
Db 43 TGCTGGCGTGGGATCCAG 26

Search completed: December 24, 2005, 18:28:41
Job time : 1574 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 18:29:07 : Search time 135.3 Seconds
(without alignments)
76.712 Million cell updates/sec

Title: US-09-296-264-9
Perfect score: 20
Sequence: 1 tgaggtcgcggtggaatgc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4168288 seqs, 259477437 residues

Total number of hits satisfying chosen parameters: 1608458

Minimum DB seq length: 20
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA New:
1: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
10: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15.2	76.0	25	US-11-121-849-398180	Sequence 398180,
2	13.8	69.0	25	US-11-121-849-319018	Sequence 319018,
3	13.8	69.0	25	US-11-121-849-444612	Sequence 444612,
4	13.8	69.0	25	US-11-121-849-446110	Sequence 446110,
5	13.2	66.0	25	US-11-121-849-219600	Sequence 219600,
6	13.2	66.0	25	US-11-121-849-361208	Sequence 361208,
7	13.2	66.0	25	US-11-121-849-382504	Sequence 382504,
8	13.2	66.0	25	US-11-121-849-430379	Sequence 430379,
9	13.2	66.0	25	US-11-121-849-541084	Sequence 541084,
10	12.8	64.0	25	US-11-121-849-44457	Sequence 44457,
11	12.8	64.0	25	US-11-121-849-462472	Sequence 462472,
12	12.8	64.0	25	US-11-121-849-509636	Sequence 509636,
13	12.8	64.0	25	US-11-121-849-509636	Sequence 509636,
14	12.6	63.0	21	US-10-770-726-31094	Sequence 60, Appl
15	12.6	63.0	21	US-10-770-726-31095	Sequence 31094, A
16	12.6	63.0	25	US-11-121-849-71670	Sequence 31095, A
17	12.6	63.0	25	US-11-121-849-71671	Sequence 71670, A
18	12.6	63.0	25	US-11-121-849-71672	Sequence 71671, A
19	12.6	63.0	25	US-11-121-849-71673	Sequence 71672, A
20	12.6	63.0	25	US-11-121-849-72121	Sequence 71673, A
21	12.6	63.0	25	US-11-121-849-197732	Sequence 72121, A
22	12.6	63.0	25	US-11-121-849-275097	Sequence 197732, A
23	12.6	63.0	25	US-11-121-849-281195	Sequence 275097, A
					Sequence 281195,

c 24	12.6	63.0	25	US-11-121-849-472861	Sequence 472861,
c 25	12.6	63.0	25	US-11-121-849-670747	Sequence 670747,
c 26	12.6	63.0	32	US-10-939-294A-17649	Sequence 17649, A
c 27	12.6	63.0	32	US-10-939-294A-19547	Sequence 19547, A
c 28	12.6	63.0	36	US-10-893-584-181	Sequence 181, App
c 29	12.6	62.0	25	US-11-121-849-178887	Sequence 178887,
c 30	12.4	62.0	25	US-11-121-849-454693	Sequence 454693,
c 31	12.4	62.0	25	US-11-121-849-454694	Sequence 454694,
c 32	12.4	62.0	25	US-11-121-849-626774	Sequence 626774,
c 33	12.4	62.0	32	US-10-939-294A-15650	Sequence 15650, A
c 34	12.4	62.0	36	US-10-845-413-415	Sequence 415, App
c 35	12.4	62.0	36	US-10-845-413-415	Sequence 415, App
c 36	12.2	61.0	21	US-10-770-726-23690	Sequence 23690, A
c 37	12.2	61.0	21	US-11-069-908-1485	Sequence 1485, App
c 38	12.2	61.0	21	US-11-069-908-3851	Sequence 3851, App
c 39	12.2	61.0	25	US-11-121-849-15659	Sequence 15659, A
c 40	12.2	61.0	25	US-11-121-849-21171	Sequence 21171, A
c 41	12.2	61.0	25	US-11-121-849-221805	Sequence 221805,
c 42	12.2	61.0	25	US-11-121-849-221806	Sequence 221806,
c 43	12.2	61.0	25	US-11-121-849-221973	Sequence 221973,
c 44	12.2	61.0	25	US-11-121-849-229969	Sequence 229969,
c 45	12.2	61.0	25	US-11-121-849-374133	Sequence 374133,

ALIGNMENTS

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RESULT 1
US-11-121-849-398180
; Sequence 398180, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 398180
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-398180

Query Match      76.0% Score 15.2; DB 7; Length 25;
Best Local Similarity 85.0%; Pred. No. 3.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 TGAGGTGCGGTGGAATGC 20
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Db  3 TGAGGTGCGGTGGAATGC 22

RESULT 2
US-11-121-849-319018
; Sequence 319018, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 319018

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; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-319018

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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGGTGCGGCTGGAAGT 18
DB 1 GAGCTGCGGCTGGAATT 17

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US-11-121-849-444612
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; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 444612
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-444612

Query Match
Best Local Similarity 69.0%; Score 13.8; DB 7; Length 25;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGGTGCGGCTGGAAGT 18
DB 9 GAGCTGCGGCTGGAAGT 25

RESULT 4
US-11-121-849-446110
; Sequence 446110, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 446110
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-446110

Query Match
Best Local Similarity 69.0%; Score 13.8; DB 7; Length 25;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGGTGCGGCTGGAAGT 18
DB 9 GAGCTGCGGCTGGAAGT 25

RESULT 5
US-11-121-849-219600/c
; Sequence 219600, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 219600
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-219600

Query Match
Best Local Similarity 66.0%; Score 13.2; DB 7; Length 25;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAGGTGCTGGTGGAGT 18
DB 21 TGAGGTCTGGTGGAGT 4

RESULT 6
US-11-121-849-361208
; Sequence 361208, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 361208
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-361208

Query Match
Best Local Similarity 66.0%; Score 13.2; DB 7; Length 25;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGAGGTGCTGGTGGAGT 18
DB 4 TGAGTGTCTGGTGGAGT 21

RESULT 7
US-11-121-849-382504
; Sequence 382504, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
```


PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 382504
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-382504

Query Match 66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 2.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TGAGTGGCGGTGGAAGT 18
Db 8 TGAGTTCGGGTAGAAAT 25

RESULT 8
US-11-121-849-430379/C

Sequence 430379, Application US/11121849
Publication No. US20050272080A1

GENERAL INFORMATION:

APPLICANT: John Palma

TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S

TITLE OF INVENTION: Microarrays

FILE REFERENCE: 3684.1

CURRENT APPLICATION NUMBER: US/11/121.849

CURRENT FILING DATE: 2005-05-03

PRIOR APPLICATION NUMBER: 60/567,949

PRIOR FILING DATE: 2004-05-03

NUMBER OF SEQ ID NOS: 673904

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 430379

LENGTH: 25

TYPE: DNA

ORGANISM: Homo sapien

US-11-121-849-430379

Query Match 66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 2.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TGAGTGGCGGTGGAAGT 18
Db 24 TGAGTTCGGGTAGAAAT 7

RESULT 9
US-11-121-849-541084/C

Sequence 541084, Application US/11121849
Publication No. US20050272080A1

GENERAL INFORMATION:

APPLICANT: John Palma

TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S

TITLE OF INVENTION: Microarrays

FILE REFERENCE: 3684.1

CURRENT APPLICATION NUMBER: US/11/121.849

CURRENT FILING DATE: 2005-05-03

PRIOR APPLICATION NUMBER: 60/567,949

PRIOR FILING DATE: 2004-05-03

NUMBER OF SEQ ID NOS: 673904

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 541084

LENGTH: 25

TYPE: DNA

ORGANISM: Homo sapien

US-11-121-849-541084

Query Match 66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 2.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GAGTGGCGGTGGAAGT 19
Db 25 GAGTTCGGGTAGAAAT 8

RESULT 10
US-11-121-849-44457/C

Sequence 44457, Application US/11121849
Publication No. US20050272080A1

GENERAL INFORMATION:

APPLICANT: John Palma

TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded

TITLE OF INVENTION: Microarrays

FILE REFERENCE: 3684.1

CURRENT APPLICATION NUMBER: US/11/121.849

CURRENT FILING DATE: 2005-05-03

PRIOR APPLICATION NUMBER: 60/567,949

PRIOR FILING DATE: 2004-05-03

NUMBER OF SEQ ID NOS: 673904

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 44457

LENGTH: 25

TYPE: DNA

ORGANISM: Homo sapien

US-11-121-849-44457

Query Match 64.0%; Score 12.8; DB 7; Length 25;
Best Local Similarity 87.5%; Pred. No. 3.8e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AGGTGGCGGTGGAAGT 18
Db 17 AAGTCTCGTGAAGT 2

RESULT 11
US-11-121-849-462472

Sequence 462472, Application US/11121849
Publication No. US20050272080A1

GENERAL INFORMATION:

APPLICANT: John Palma

TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded

TITLE OF INVENTION: Microarrays

FILE REFERENCE: 3684.1

CURRENT APPLICATION NUMBER: US/11/121.849

CURRENT FILING DATE: 2005-05-03

PRIOR APPLICATION NUMBER: 60/567,949

PRIOR FILING DATE: 2004-05-03

NUMBER OF SEQ ID NOS: 673904

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 462472

LENGTH: 25

TYPE: DNA

ORGANISM: Homo sapien

US-11-121-849-462472

Query Match 64.0%; Score 12.8; DB 7; Length 25;
Best Local Similarity 87.5%; Pred. No. 3.8e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGAGTGGCGGTGGA 16
Db 5 TGAAGTCTGCTGGA 20

RESULT 12
US-11-121-849-509636

Sequence 509636, Application US/11121849
Publication No. US20050272080A1

GENERAL INFORMATION:

APPLICANT: John Palma

TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded

TITLE OF INVENTION: Microarrays

```
FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 509636
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-509636

Query Match          64.0%; Score 12.8; DB 7; Length 25;
Best Local Similarity 87.5%; Pred. No. 3.8e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4 GGTGGCGGTGGAAGTG 19
        ||||| |||||
Db      2 GGTGGCGGAGAGGTG 17

RESULT 13
US-11-123-115-60
; Sequence 60, Application US/11123115
; Publication No. US2005026657A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Tzu-Chih
; TITLE OF INVENTION: PROCESS FOR PRODUCING POLY-UNSATURATED FATTY ACIDS BY OLEAGINOUS
; FILE REFERENCE: 4867-0102PUS2
; CURRENT APPLICATION NUMBER: US/11/123,115
; CURRENT FILING DATE: 2005-05-06
; PRIOR APPLICATION NUMBER: US 60/568,692
; PRIOR FILING DATE: 2004-05-07
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 60
; LENGTH: 59
; TYPE: DNA
; ORGANISM: Mortierella alpine
; FEATURE:
; NAME/KEY: primer
; LOCATION: (1)..(59)
; OTHER INFORMATION: reverse primer of D12-desaturase gene
US-11-123-115-60

Query Match          64.0%; Score 12.8; DB 7; Length 59;
Best Local Similarity 87.5%; Pred. No. 3.8e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5 GTGGCGGTGGAAGTGC 20
        ||||| |||||
Db      36 GTACGTGTGGAAGTGC 51

RESULT 14
US-10-770-726-31094
; Sequence 31094, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 31094
; LENGTH: 21
```

```
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-770-726-31094

Query Match          63.0%; Score 12.6; DB 6; Length 21;
Best Local Similarity 78.9%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 TGAGTGGCGGTGGAAGTG 19
        ||||| |||||
Db      3 TGAGGTGCACTGGACATG 21

RESULT 15
US-10-770-726-31095
; Sequence 31095, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 31095
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi
US-10-770-726-31095

Query Match          63.0%; Score 12.6; DB 6; Length 21;
Best Local Similarity 57.9%; Pred. No. 4.6e+03;
Matches 11; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      1 TGAGTGGCGGTGGAAGTG 19
        ||||| |||||
Db      1 TGAGGUGCAGCUGGACAU 19

Search completed: December 25, 2005, 04:37:03
Job time : 135.3 secs
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; CURRENT APPLICATION NUMBER: US/09/888,413
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 09/337,325
; PRIOR FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 09/218,166
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 09/109,076
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/068,291
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 162
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-888-413-162

Query Match 71.0%; Score 14.2; DB 3; Length 60;
Best Local Similarity 84.2%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTCCGACGTGGAGCCCA 19
|||||
Db 48 GTGCTACTGTGCACCTCAG 30

RESULT 3
US-08-976-703-10/c
; Sequence 10, Application US/08976703
; Patent No. 5945288
; GENERAL INFORMATION:
; APPLICANT: CHANG, ZHIYU
; APPLICANT: MORGAN, RICHARD D.
; TITLE OF INVENTION: METHOD FOR CLONING AND
; TITLE OF INVENTION: PRODUCING THE PmeI RESTRICTION ENDONUCLEASE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: New England Biolabs, Inc.
; STREET: 32 Tozer Road
; CITY: Beverly
; STATE: MA
; COUNTRY: US
; ZIP: 01915
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976,703
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Gregory D
; REGISTRATION NUMBER: 30901
; REFERENCE/DOCKET NUMBER: NEB-132
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 978-927-5054
; TELEFAX: 978-927-1705
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: Genomic DNA
US-08-976-703-10

Query Match 69.0%; Score 13.8; DB 2; Length 28;
Best Local Similarity 88.2%; Pred. No. 2.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGCCGACGTGGAGCCCA 18
|||||
Db 19 TGCCGACGTGGATCCA 3

RESULT 4
US-09-396-196G-14669/c
; Sequence 14669, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14669
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-14669

Query Match 68.0%; Score 13.6; DB 3; Length 25;
Best Local Similarity 80.0%; Pred. No. 2.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GTCCGACGTGGAGCCCA 20
|||||
Db 24 GAGCCGACATGAGACCCAGA 5

RESULT 5
US-09-396-196G-14668/c
; Sequence 14668, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14668
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-14668

Query Match 66.0%; Score 13.2; DB 3; Length 25;
Best Local Similarity 83.3%; Pred. No. 4.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GCCGACGTGGAGCCCA 20
|||||

Db 24 GCCGACATGAGACCCAGA 7

RESULT 6
US-09-396-196G-26712/c
Sequence 26712, Application US/09396196G

Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 26712
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-09-396-196G-26712

Query Match 66.0%; Score 13.2; DB 3; Length 25;
Best Local Similarity 83.3%; Pred. No. 4.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TGCCGACGTGGAGCCAG 19
20 TGCGCATGTAGAGCCAG 3

RESULT 7
US-09-237-712-41

Sequence 41, Application US/09237712
Patent No. 6180391
GENERAL INFORMATION:
APPLICANT: BROWN, WILLIAM C.
TITLE OF INVENTION: HIGHLY EFFICIENT CONTROLLED EXPRESSION OF EXOGENOUS
FILE REFERENCE: A-518
CURRENT APPLICATION NUMBER: US/09/237,712
CURRENT FILING DATE: 1999-01-26
EARLIER APPLICATION NUMBER: 60/072,794
EARLIER FILING DATE: 1998-01-28
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 41
LENGTH: 33
TYPE: DNA
ORGANISM: oligonucleotide
US-09-237-712-41

Query Match 66.0%; Score 13.2; DB 3; Length 33;
Best Local Similarity 83.3%; Pred. No. 4.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TGCCGACGTGGAGCCAG 19
12 TGCTTACTGTGGTCTCTAG 29

RESULT 8
US-09-237-712-42/c
Sequence 42, Application US/09237712
Patent No. 6180391
GENERAL INFORMATION:
APPLICANT: BROWN, WILLIAM C.
TITLE OF INVENTION: HIGHLY EFFICIENT CONTROLLED EXPRESSION OF EXOGENOUS
GENES IN E. COLI

FILE REFERENCE: A-518
CURRENT APPLICATION NUMBER: US/09/237,712
CURRENT FILING DATE: 1999-01-26
EARLIER APPLICATION NUMBER: 60/072,794
EARLIER FILING DATE: 1998-01-28
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 42
LENGTH: 33
TYPE: DNA
ORGANISM: oligonucleotide
US-09-237-712-42

Query Match 66.0%; Score 13.2; DB 3; Length 33;
Best Local Similarity 83.3%; Pred. No. 4.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TGCCGACGTGGAGCCAG 19
26 TGCTTACTGTGGTCTCTAG 9

RESULT 9
US-08-829-525-34/c
Sequence 34, Application US/0829525
Patent No. 6084083

GENERAL INFORMATION:
APPLICANT: Levinson, Douglas A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:

ADDRESSER: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036/2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/829,525
FILING DATE: 28-MAR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/609,583
FILING DATE: 01-MAR-1996
APPLICATION NUMBER: US 08/487,748
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/398,633
FILING DATE: 03-MAR-1995

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-081
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8664
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:
LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-829-525-34

Query Match 66.0%; Score 13.2; DB 3; Length 44;
Best Local Similarity 83.3%; Pred. No. 4.3e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTGCCGACTGGACCCA 18
||| ||| ||| ||| ||| |||
Db 33 GTGCAGACTGGATCCA 16

RESULT 10

US-08-609-583A-34/C
; Sequence 34, Application US/08609583A
; Patent No. 6204371

; GENERAL INFORMATION:

; APPLICANT: Levinson, Douglas A.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

; TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS

; NUMBER OF SEQUENCES: 37

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036/2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/609,583A

; FILING DATE: 01-MAR-1996

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/487,748

; FILING DATE: 07-JUN-1995

; APPLICATION NUMBER: US 08/398,633

; FILING DATE: 03-MAR-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Coruzzi, Laura A.

; REGISTRATION NUMBER: 30,742

; REFERENCE/DOCKET NUMBER: 7853-048

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-790-9090

; TELEFAX: 212-869-8864

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 34:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 44 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; US-08-609-583A-34

Query Match 66.0%; Score 13.2; DB 3; Length 44;

Best Local Similarity 83.3%; Pred. No. 4.3e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTGCCGACTGGACCCA 18
||| ||| ||| ||| ||| |||
Db 33 GTGCAGACTGGATCCA 16

RESULT 11

US-08-937-399-34/C

; Sequence 34, Application US/08937399

; Patent No. 6288218

; GENERAL INFORMATION:

; APPLICANT: Levinson, Douglas A.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

; TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS

; NUMBER OF SEQUENCES: 37

; CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036/2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/937,399

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/609,583

FILING DATE: 01-MAR-1996

APPLICATION NUMBER: US 08/487,748

FILING DATE: 07-JUN-1995

APPLICATION NUMBER: US 08/398,633

FILING DATE: 03-MAR-1995

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7853-048

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-790-9090

TELEFAX: 212-869-8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:

LENGTH: 44 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-08-937-399-34

Query Match 66.0%; Score 13.2; DB 3; Length 44;

Best Local Similarity 83.3%; Pred. No. 4.3e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTGCCGACTGGACCCA 18
||| ||| ||| ||| ||| |||
Db 33 GTGCAGACTGGATCCA 16

RESULT 12

US-09-560-639-27/C

; Sequence 27, Application US/09560639

; Patent No. 6323334

; GENERAL INFORMATION:

; APPLICANT: Kingsbury, G.

; APPLICANT: Leiby, K.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND

; TREATMENT OF IMMUNE DISORDERS

; FILE REFERENCE: 7853-158

; CURRENT APPLICATION NUMBER: US/09/560,639

; CURRENT FILING DATE: 2000-04-28

; EARLIER APPLICATION NUMBER: 60/155,862

; EARLIER FILING DATE: 1999-09-24

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 27

LENGTH: 44

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: 3' oligonucleotide

US-09-560-639-27

Query Match 66.0%; Score 13.2; DB 3; Length 44;

Best Local Similarity 83.3%; Pred. No. 4.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTGCCGACGTGGGACCCA 18
Db 33 GTGCAGACTTGGGATCCA 16

RESULT 13

US-09-310-367-34/c
; Sequence 34, Application US/09110367
; Patent No. 6414117
; GENERAL INFORMATION:
; APPLICANT: Levinson, Douglas A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/310,367
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,525
; FILING DATE: 28-MAR-1997
; APPLICATION NUMBER: US 08/609,583
; FILING DATE: 01-MAR-1996
; APPLICATION NUMBER: US 08/487,748
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/398,633
; FILING DATE: 03-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-081
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 44 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-310-367-34

Query Match 66.0%; Score 13.2; DB 3; Length 44;
Best Local Similarity 83.3%; Pred. No. 4.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTGCCGACGTGGGACCCA 18
Db 33 GTGCAGACTTGGGATCCA 16

RESULT 14
US-09-032-337-34/c
; Sequence 34, Application US/09032337
; Patent No. 6455685
; GENERAL INFORMATION:

APPLICANT: Levinson, Douglas A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,337
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/609,583
FILING DATE: 01-MAR-1996
APPLICATION NUMBER: US 08/487,748
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/398,633
FILING DATE: 03-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-016
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-032-337-34

Query Match 66.0%; Score 13.2; DB 3; Length 44;
Best Local Similarity 83.3%; Pred. No. 4.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTGCCGACGTGGGACCCA 18
Db 33 GTGCAGACTTGGGATCCA 16

RESULT 15
US-09-464-231-34/c
; Sequence 34, Application US/09464231
; Patent No. 6562343
; GENERAL INFORMATION:
; APPLICANT: Levinson, Douglas A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS

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; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/464,231
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,583
; FILING DATE: 01-MAR-1996
; APPLICATION NUMBER: US 08/487,748
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/398,633
; FILING DATE: 03-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-048
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 44 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-464-231-34

Query Match 66.0%; Score 13.2; DB 3; Length 44;
Best Local Similarity 83.3%; Pred. No. 4.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTGCGAGCGTGGAGCCCA 18
Db 33 GTGCAACTTGGGATCCA 16
```

Search completed: December 24, 2005, 18:36:30
Job time : 49.1 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 14:06:30 ; Search time 337.6 Seconds
(without alignments)
489.892 Million cell updates/sec

Title: US-09-296-264-10

Perfect score: 20

Sequence: 1 gtgcgcacgtgaccacaga 20

Scoring table: IDENTITY_NUC

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 9887334

Minimum DB seq length: 20

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
6: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3	US-09-296-264-10
2	15.4	77.0	25	10	US-11-036-317-797309
3	15.2	76.0	25	5	US-10-098-263B-90358
4	14.8	74.0	25	8	US-10-719-900-32172
5	14.8	74.0	25	8	US-10-098-263B-125937
6	14.2	71.0	25	5	US-10-098-263B-125939
7	14.2	71.0	25	8	US-10-719-900-149619
8	14.2	71.0	25	8	US-10-719-900-460924
9	14.2	71.0	25	8	US-10-719-900-908051
10	14.2	71.0	25	10	US-11-036-317-797309
11	14.2	71.0	25	10	US-09-888-413-162
12	14.2	71.0	25	8	US-10-865-853-162
13	13.8	69.0	25	5	US-10-098-263B-82739
14	13.8	69.0	25	5	US-10-098-263B-126401
15	13.8	69.0	25	10	US-11-036-317-797308
16	13.8	69.0	25	10	US-11-036-317-797308
17	13.8	69.0	25	7	US-10-681-818-256
18	13.8	69.0	25	7	US-10-681-818-256
19	13.8	69.0	25	3	US-09-908-975-2227
20	13.6	68.0	25	5	US-10-098-263B-90357
21	13.6	68.0	25	7	US-10-719-956-29463
22	13.6	68.0	25	7	US-10-719-956-648937
23	13.6	68.0	25	7	US-10-719-956-648938

24	13.6	68.0	25	7	US-10-719-956-649365	Sequence 649365,
25	13.6	68.0	25	7	US-10-719-956-649366	Sequence 649366,
26	13.6	68.0	25	7	US-10-719-956-649367	Sequence 649367,
27	13.6	68.0	25	8	US-10-719-900-702543	Sequence 702543,
28	13.6	68.0	25	8	US-10-719-900-856352	Sequence 856352,
29	13.6	68.0	25	8	US-10-719-900-943473	Sequence 943473,
30	13.6	68.0	25	8	US-10-719-900-981074	Sequence 981074,
31	13.6	68.0	25	9	US-10-809-189-14669	Sequence 14669, A
32	13.6	68.0	25	9	US-10-956-157-271970	Sequence 271970,
33	13.6	68.0	25	9	US-10-956-157-294897	Sequence 294897,
34	13.6	68.0	25	10	US-11-036-317-728659	Sequence 728659,
35	13.6	68.0	25	10	US-11-036-317-842622	Sequence 842622,
36	13.6	68.0	65	3	US-09-908-975-2565	Sequence 2565, Ap
37	13.6	68.0	65	3	US-09-908-975-2565	Sequence 2565, Ap
38	13.4	67.0	25	5	US-10-098-263B-35524	Sequence 35524, A
39	13.4	67.0	25	8	US-10-719-900-156716	Sequence 156716,
40	13.4	67.0	25	10	US-11-036-317-467428	Sequence 467428,
41	13.4	67.0	25	10	US-11-036-317-797017	Sequence 797017,
42	13.2	66.0	25	5	US-10-098-263B-25231	Sequence 25231, A
43	13.2	66.0	25	5	US-10-098-263B-109368	Sequence 109368,
44	13.2	66.0	25	7	US-10-719-956-181453	Sequence 181453,
45	13.2	66.0	25	7	US-10-719-956-181454	Sequence 181454,

ALIGNMENTS

```

RESULT 1
US-09-296-264-10
; Sequence 10, Application US/09296264
; Publication No. US20030083274A1
; GENERAL INFORMATION:
; APPLICANT: WRIGHT, Jim A.
; APPLICANT: YOUNG, Aiping H.
; TITLE OF INVENTION: NEUROPEPTIDE ANTISENSE OLIGONUCLEOTIDE SEQUENCES AND
; TITLE OF INVENTION: METHODS OF USING SAME TO MODULATE CELL GROWTH
; FILE REFERENCE: 032396-043
; CURRENT APPLICATION NUMBER: US/09/296,264
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 60/082,791
; EARLIER FILING DATE: 1998-04-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-09-296-264-10

Query Match      100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 GTGCCGACGTGGACCCAGA 20
Db      1 GTGCCGACGTGGACCCAGA 20

RESULT 2
US-11-036-317-797309
; Sequence 797309, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174

```

```
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 797309
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-797309
```

```
Query Match          77.0%; Score 15.4; DB 10; Length 25;
Best Local Similarity 94.1%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      4 CCGACGTGGAGCCCA 20
         |||||||
DB      4 CCCACGTGGAGCCCA 20
```

```
RESULT 3
US-10-098-263B-90358/c
; Sequence 90358, Application US/10098263B
; Publication No. US20030104410A1
```

```
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
```

```
TITLE OF INVENTION: Human Microarray
```

```
FILE REFERENCE: 3118.1
```

```
CURRENT APPLICATION NUMBER: US/10/098,263B
```

```
CURRENT FILING DATE: 2003-01-08
```

```
PRIOR APPLICATION NUMBER: 60/276,759
```

```
PRIOR FILING DATE: 2001-03-16
```

```
NUMBER OF SEQ ID NOS: 131066
```

```
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
```

```
SEQ ID NO 90358
```

```
LENGTH: 25
```

```
TYPE: DNA
```

```
ORGANISM: Homo sapien
```

```
US-10-098-263B-90358
```

```
Query Match          76.0%; Score 15.2; DB 5; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 GTGCCGACGTGGAGCCCA 20
         |||||||
DB      23 GTGCCGACGTGGAGCCCA 4
```

```
RESULT 4
US-10-719-900-32172
; Sequence 32172, Application US/10719900
; Publication No. US20050026164A1
```

```
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
```

```
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
```

```
FILE REFERENCE: 3528.1
```

```
CURRENT APPLICATION NUMBER: US/10/719,900
```

```
CURRENT FILING DATE: 2003-11-20
```

```
PRIOR APPLICATION NUMBER: 60/427,808
```

```
PRIOR FILING DATE: 2002-11-20
```

```
NUMBER OF SEQ ID NOS: 982914
```

```
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
```

```
SEQ ID NO 32172
```

```
LENGTH: 25
```

```
TYPE: DNA
```

```
ORGANISM: Mus musculus
```

```
US-10-719-900-32172
```

```
Query Match          74.0%; Score 14.8; DB 8; Length 25;
Best Local Similarity 88.9%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      3 GCCGACGTGGAGCCCA 20
         |||||||
DB      6 GCCGAGTAGAGCCCA 23
```

```
RESULT 5
US-10-719-900-799047
; Sequence 799047, Application US/10719900
; Publication No. US20050026164A1
```

```
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
```

```
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
```

```
FILE REFERENCE: 3528.1
```

```
CURRENT APPLICATION NUMBER: US/10/719,900
```

```
CURRENT FILING DATE: 2003-11-20
```

```
PRIOR APPLICATION NUMBER: 60/427,808
```

```
PRIOR FILING DATE: 2002-11-20
```

```
NUMBER OF SEQ ID NOS: 982914
```

```
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
```

```
SEQ ID NO 799047
```

```
LENGTH: 25
```

```
TYPE: DNA
```

```
ORGANISM: Mus musculus
```

```
US-10-719-900-799047
```

```
Query Match          74.0%; Score 14.8; DB 8; Length 25;
Best Local Similarity 88.9%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1 GTGCCGACGTGGAGCCCA 18
         |||||||
DB      7 GTGCTACTTGGAGCCCA 24
```

```
RESULT 6
US-10-098-263B-125939/c
; Sequence 125939, Application US/10098263B
; Publication No. US20030104410A1
```

```
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
```

```
TITLE OF INVENTION: Human Microarray
```

```
FILE REFERENCE: 3118.1
```

```
CURRENT APPLICATION NUMBER: US/10/098,263B
```

```
CURRENT FILING DATE: 2003-01-08
```

```
PRIOR APPLICATION NUMBER: 60/276,759
```

```
PRIOR FILING DATE: 2001-03-16
```

```
NUMBER OF SEQ ID NOS: 131066
```

```
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
```

```
SEQ ID NO 125939
```

```
LENGTH: 25
```

```
TYPE: DNA
```

```
ORGANISM: Homo sapien
```

```
US-10-098-263B-125939
```

```
Query Match          71.0%; Score 14.2; DB 5; Length 25;
Best Local Similarity 84.2%; Pred. No. 4.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      2 TGCCGACGTGGAGCCCA 20
         |||||||
DB      25 TGACGACGTAGAGCCCA 7
```

```
RESULT 7
US-10-719-900-149619/c
; Sequence 149619, Application US/10719900
; Publication No. US20050026164A1
```

```
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
```

```
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
```

```
FILE REFERENCE: 3528.1
```

```
CURRENT APPLICATION NUMBER: US/10/719,900
```

```
CURRENT FILING DATE: 2003-11-20
```

```
PRIOR APPLICATION NUMBER: 60/427,808
```

```
PRIOR FILING DATE: 2002-11-20
```

```
NUMBER OF SEQ ID NOS: 982914
```

```
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
```

SEQ ID NO 149619
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-10-719-900-149619

Query Match 71.0%; Score 14.2; DB 8; Length 25;
Best Local Similarity 84.2%; Pred. No. 4.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTCCGACGTGGAGCCAG 19
DB 22 GTGCTGATGTGGATCCAG 4

RESULT 8
US-10-719-900-460924/c
Sequence 460924, Application US/10719900
Publication No. US20050026164A1
GENERAL INFORMATION:

APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
PRIOR FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 460924
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-10-719-900-460924

Query Match 71.0%; Score 14.2; DB 8; Length 25;
Best Local Similarity 84.2%; Pred. No. 4.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTCCGACGTGGAGCCAG 19
DB 21 GAGCCGATGTGGAGCCAG 3

RESULT 9
US-10-719-900-908051
Sequence 908051, Application US/10719900
Publication No. US20050026164A1
GENERAL INFORMATION:

APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
PRIOR FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 908051
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-10-719-900-908051

Query Match 71.0%; Score 14.2; DB 8; Length 25;
Best Local Similarity 84.2%; Pred. No. 4.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGCCGACGTGGAGCCAG 20
DB 1 TGTGACTTGGAGCCAG 19

RESULT 10
US-11-036-317-153174/c
Sequence 153174, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:

APPLICANT: Williams, Alan
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
PRIOR FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 153174
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-153174

Query Match 71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 4.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGCCGACGTGGAGCCAG 20
DB 20 TACCGACGTGAGACCTGA 2

RESULT 11
US-09-888-413-162/c
Sequence 162, Application US/09888413
Publication No. US20030096232A1
GENERAL INFORMATION:

APPLICANT: KRIS, RICHARD M.
TITLE OF INVENTION: HIGH THROUGHPUT ASSAY SYSTEM
FILE REFERENCE: NEOGEN-1 P4
CURRENT APPLICATION NUMBER: US/09/888,413
PRIOR FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: 09/337,325
PRIOR FILING DATE: 1999-06-21
PRIOR APPLICATION NUMBER: 09/218,166
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 09/109,076
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/068,291
PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 165
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 162
LENGTH: 60
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-888-413-162

Query Match 71.0%; Score 14.2; DB 3; Length 60;
Best Local Similarity 84.2%; Pred. No. 3.5e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTCCGACGTGGAGCCAG 19
DB 48 GTGCTTACGTGGACCTCA 30

RESULT 12
US-10-865-853-162/c
Sequence 162, Application US/10865853
Publication No. US20050026193A1

```
/ GENERAL INFORMATION:
/ APPLICANT: KRIS, RICHARD M.
/ APPLICANT: FELDER, STEPHEN
/ TITLE OF INVENTION: HIGH THROUGHPUT ASSAY SYSTEM
/ FILE REFERENCE: NEOGEN-1 P4
/ CURRENT APPLICATION NUMBER: US/10/865,853
/ CURRENT FILING DATE: 2004-06-14
/ PRIOR APPLICATION NUMBER: US/09/888,413
/ PRIOR FILING DATE: 2001-06-26
/ PRIOR APPLICATION NUMBER: 09/337,325
/ PRIOR FILING DATE: 1999-06-21
/ PRIOR APPLICATION NUMBER: 09/218,166
/ PRIOR FILING DATE: 1998-12-22
/ PRIOR APPLICATION NUMBER: 09/109,076
/ PRIOR FILING DATE: 1998-07-02
/ PRIOR APPLICATION NUMBER: 60/068,291
/ PRIOR FILING DATE: 1997-12-19
/ NUMBER OF SEQ ID NOS: 165
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 162
/ LENGTH: 60
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: linker oligonucleotide
US-10-865-853-162
```

```
Query Match      71.0%; Score 14.2; DB 8; Length 60;
Best Local Similarity 84.2%; Pred. No. 3.5e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      1 GTGCCGAGCTGGGACCCAG 19
Db      48 GTGCCCTACGTGGCAGCTCAG 30
```

```
RESULT 13
US-10-098-263B-82739
/ Sequence 82739, Application US/10098263B
/ Publication No. US20030104410A1
/ GENERAL INFORMATION:
/ APPLICANT: Miltman, Michael
/ TITLE OF INVENTION: Human Microarray
/ FILE REFERENCE: 3118.1
/ CURRENT APPLICATION NUMBER: US/10/098,263B
/ CURRENT FILING DATE: 2003-01-08
/ PRIOR APPLICATION NUMBER: 60/276,759
/ PRIOR FILING DATE: 2001-03-16
/ NUMBER OF SEQ ID NOS: 131066
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 82739
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-10-098-263B-82739
```

```
Query Match      69.0%; Score 13.8; DB 5; Length 25;
Best Local Similarity 88.2%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      4 CCGACGTGGGACCCAGA 20
Db      7 CCGACCTGGGACCCAGA 23
```

```
RESULT 14
US-10-098-263B-126401
/ Sequence 126401, Application US/10098263B
/ Publication No. US20030104410A1
/ GENERAL INFORMATION:
/ APPLICANT: Miltman, Michael
/ TITLE OF INVENTION: Human Microarray
```

```
/ FILE REFERENCE: 3118.1
/ CURRENT APPLICATION NUMBER: US/10/098,263B
/ CURRENT FILING DATE: 2003-01-08
/ PRIOR APPLICATION NUMBER: 60/276,759
/ PRIOR FILING DATE: 2001-03-16
/ NUMBER OF SEQ ID NOS: 131066
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 126401
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-10-098-263B-126401
```

```
Query Match      69.0%; Score 13.8; DB 5; Length 25;
Best Local Similarity 88.2%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      4 CCGACGTGGGACCCAGA 20
Db      4 CCGACGTGGGACCCAGA 20
```

```
RESULT 15
US-11-036-317-664199
/ Sequence 664199, Application US/11036317
/ Publication No. US20050214823A1
/ GENERAL INFORMATION:
/ APPLICANT: Blume, John
/ APPLICANT: Williams, Alan
/ TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
/ FILE REFERENCE: 3654.1
/ CURRENT APPLICATION NUMBER: US/11/036,317
/ CURRENT FILING DATE: 2005-01-13
/ PRIOR APPLICATION NUMBER: US 60/536,639
/ PRIOR FILING DATE: 2004-01-13
/ NUMBER OF SEQ ID NOS: 991174
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 664199
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Mus musculus
US-11-036-317-664199
```

```
Query Match      69.0%; Score 13.8; DB 10; Length 25;
Best Local Similarity 88.2%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      2 TGCCGAGCTGGGACCCCA 18
Db      6 TGCTGCCCTGGGACCCCA 22
```

```
Search completed: December 25, 2005, 04:14:24
Job time : 337.6 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 18:29:07 ; Search time 135.3 Seconds
(without alignments)
76.712 Million cell updates/sec

Title: US-09-296-264-10

Perfect score: 20
Sequence: 1 gtgcgcagctgagaccaga 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4168288 seqs, 259477437 residues

Total number of hits satisfying chosen parameters: 1608458

Minimum DB seq length: 20
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA_New:

1: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	17.6	88.0	21	US-10-831-997-2443	Sequence 2443, Ap
C 2	14.4	72.0	25	US-11-121-849-262718	Sequence 262718, A
C 3	13.8	69.0	25	US-11-121-849-464323	Sequence 464323, A
C 4	13.8	69.0	25	US-11-121-849-543962	Sequence 543962, A
C 5	13.6	68.0	25	US-11-121-849-25423	Sequence 25423, A
C 6	13.6	68.0	25	US-11-121-849-58450	Sequence 58450, A
C 7	13.6	68.0	25	US-11-121-849-295520	Sequence 295520, A
C 8	13.4	67.0	25	US-11-121-849-437066	Sequence 437066, A
C 9	13.2	66.0	25	US-11-121-849-642465	Sequence 642465, A
C 10	12.8	64.0	25	US-11-121-849-214760	Sequence 214760, A
C 11	12.8	64.0	25	US-11-121-849-228144	Sequence 228144, A
C 12	12.6	63.0	25	US-11-121-849-7040	Sequence 7040, Ap
C 13	12.6	63.0	25	US-11-121-849-40743	Sequence 40743, A
C 14	12.6	63.0	25	US-11-121-849-245344	Sequence 245344, A
C 15	12.6	63.0	25	US-11-121-849-245345	Sequence 245345, A
C 16	12.6	63.0	25	US-11-121-849-536316	Sequence 536316, A
C 17	12.6	63.0	25	US-11-121-849-577016	Sequence 577016, A
C 18	12.6	63.0	25	US-11-121-849-609410	Sequence 609410, A
C 19	12.6	63.0	25	US-11-121-849-623806	Sequence 623806, A
C 20	12.6	63.0	25	US-11-121-849-657376	Sequence 657376, A
C 21	12.4	62.0	20	US-10-949-720-209	Sequence 209, App
C 22	12.4	62.0	20	US-11-006-031-71	Sequence 71, App1
C 23	12.4	62.0	25	US-11-121-849-38318	Sequence 38318, A

ALIGNMENTS

C 24	12.4	62.0	25	US-11-121-849-98520	Sequence 98520, A
C 25	12.4	62.0	25	US-11-121-849-449264	Sequence 449264, A
C 26	12.4	62.0	25	US-11-121-849-543564	Sequence 543564, A
C 27	12.4	62.0	25	US-11-121-849-636232	Sequence 636232, A
C 28	12.4	62.0	30	US-10-857-780-1665	Sequence 1665, Ap
C 29	12.2	61.0	25	US-11-121-849-25334	Sequence 25334, A
C 30	12.2	61.0	25	US-11-121-849-43541	Sequence 43541, A
C 31	12.2	61.0	25	US-11-121-849-507286	Sequence 507286, A
C 32	12.2	61.0	25	US-11-121-849-211263	Sequence 211263, A
C 33	12.2	61.0	25	US-11-121-849-231409	Sequence 231409, A
C 34	12.2	61.0	25	US-11-121-849-332670	Sequence 332670, A
C 35	12.2	61.0	25	US-11-121-849-239731	Sequence 239731, A
C 36	12.2	61.0	25	US-11-121-849-299167	Sequence 299167, A
C 37	12.2	61.0	25	US-11-121-849-388073	Sequence 388073, A
C 38	12.2	61.0	25	US-11-121-849-471473	Sequence 471473, A
C 39	12.2	61.0	25	US-11-121-849-471822	Sequence 471822, A
C 40	12.2	61.0	25	US-11-121-849-517468	Sequence 517468, A
C 41	12.2	61.0	32	US-10-939-2944-15292	Sequence 15292, A
C 42	12	60.0	25	US-11-121-849-13433	Sequence 13433, A
C 43	12	60.0	25	US-11-121-849-13434	Sequence 13434, A
C 44	12	60.0	25	US-11-121-849-33500	Sequence 33500, A
C 45	12	60.0	25	US-11-121-849-80232	Sequence 80232, A

```

RESULT 1
US-10-831-997-2443/c
; Sequence 2443, Application US/10831997
; Publication No. US20050244834A1
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Boik, Stacey
; APPLICANT: Daley, George Q.
; APPLICANT: McCarthy, Jeanette J.
; TITLE OR INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
; FILE REFERENCE: 2825.1027-001
; CURRENT APPLICATION NUMBER: US/10/831,997
; PRIOR FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: US/09/657,472
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/153,357
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 60/220,947
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: US 60/225,724
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 2551
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2443
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-831-997-2443

Query Match      88.0%; Score 17.6; DB 6; Length 21;
Best Local Similarity 94.4%; Pred. No. 23;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy      1 GTGCCGACGTGGACCCA 18
Db      18 GTGCCGAGTGGACCCA 1

RESULT 2
US-11-121-849-262718/c
; Sequence 262718, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma

```

```

; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 262718
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-262718

Query Match
Best Local Similarity 93.8%; Score 14.4; DB 7; Length 25;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGCCGACGTGGGACC 16
DB 19 GTGCCGACCTGGGACC 4

RESULT 3
US-11-121-849-464323/c
; Sequence 464323, Application US/11/121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 464323
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-464323

Query Match
Best Local Similarity 69.0%; Score 13.8; DB 7; Length 25;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GCCGACGTGGGACCAG 19
DB 17 GCCGAGTGGTCCAG 1

RESULT 4
US-11-121-849-543962/c
; Sequence 543962, Application US/11/121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 543962
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien

US-11-121-849-543962

Query Match
Best Local Similarity 69.0%; Score 13.8; DB 7; Length 25;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GCCGACGTGGGACCAG 19
DB 17 GCCGAGTGGTCCAG 1

RESULT 5
US-11-121-849-25423
; Sequence 25423, Application US/11/121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 25423
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-25423

Query Match
Best Local Similarity 68.0%; Score 13.6; DB 7; Length 25;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTGCCGACGTGGGACCAGA 20
DB 4 GTGCCGTGTGGGCCACAGA 23

RESULT 6
US-11-121-849-58450/c
; Sequence 58450, Application US/11/121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 58450
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-58450

Query Match
Best Local Similarity 68.0%; Score 13.6; DB 7; Length 25;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTGCCGACGTGGGACCAGA 20
DB 22 GTGCCAAGTGGGCCACAGA 3

RESULT 7
US-11-121-849-295520
```

```
; Sequence 295520, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 295520
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-295520

Query Match          68.0%; Score 13.6; DB 7; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Cy 1 GTCCGACGTGGAGCCAG 20
    |||||
Db 2 GTCCGACATGTGACACAGA 21

RESULT 8
US-11-121-849-437066
; Sequence 437066, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 437066
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-437066

Query Match          67.0%; Score 13.4; DB 7; Length 25;
Best Local Similarity 93.3%; Pred. No. 1.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 2 TGCCGACGTGGAGCC 16
    |||||
Db 1 TGCCGACGTGGAGCC 15

RESULT 9
US-11-121-849-642465
; Sequence 642465, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
```

```
; SEQ ID NO 642465
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-642465

Query Match          66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy 2 TGCCGACGTGGAGCCAG 19
    |||||
Db 6 TCCCTACATGTGGAGCCAG 23

RESULT 10
US-11-121-849-214760
; Sequence 214760, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 214760
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-214760

Query Match          64.0%; Score 12.8; DB 7; Length 25;
Best Local Similarity 87.5%; Pred. No. 3.2e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 2 TGCCGACGTGGAGCC 17
    |||||
Db 2 TGCCGCGGTGGAGCC 17

RESULT 11
US-11-121-849-228144
; Sequence 228144, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 228144
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-228144

Query Match          64.0%; Score 12.8; DB 7; Length 25;
Best Local Similarity 87.5%; Pred. No. 3.2e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 4 CCGACGTGGAGCCAG 19
    |||||
Db 10 CCGACATGGAGCCCTG 25
```

```
RESULT 12
US-11-121-849-7040
; Sequence 7040, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 7040
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-7040

Query Match
Best Local Similarity 63.0%; Score 12.6; DB 7; Length 25;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTGCCGACGTGGAGCCAG 19
Db 6 GTGCCTAAGTGAGATCCAG 24

RESULT 13
US-11-121-849-40743
; Sequence 40743, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 40743
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-40743

Query Match
Best Local Similarity 63.0%; Score 12.6; DB 7; Length 25;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 TGGCCAGCTGGAGCCAGA 20
Db 7 TGGCACCGTGAGACACAGA 25

RESULT 14
US-11-121-849-245344
; Sequence 245344, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT FILING DATE: 2005-05-03
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```
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 245344
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-245344

Query Match
Best Local Similarity 63.0%; Score 12.6; DB 7; Length 25;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTGCCGACGTGGAGCCAG 19
Db 5 GAGCTGGCGTTGGAGCCAG 23

RESULT 15
US-11-121-849-245345
; Sequence 245345, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 245345
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-245345

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Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTGCCGACGTGGAGCCAG 19
Db 1 GAGCTGGCGTTGGAGCCAG 19
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Search completed: December 25, 2005, 04:37:04
Job time : 136.3 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 10:28:41 ; Search time 582 Seconds
(without alignments)
1953.383 Million cell updates/sec

Title: US-09-296-264-11

Perfect score: 20
Sequence: 1 gacccccagggcactcatg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 1858228

Minimum DB seq length: 20
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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11: gb_ey:*
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13: gb_vl:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	BD211668	BD211668 Antisense
2	17.6	88.0	21	AX153915	AX153915 Sequence
3	16	80.0	20	BD211677	BD211677 Antisense
4	15.2	76.0	44	108796	108796 Sequence 18
5	15.2	76.0	51	CQ001874	CQ001874 Sequence
6	15.2	76.0	60	CQ537667	CQ537667 Sequence
7	14.4	72.0	39	AR302389	AR302389 Sequence
8	14.2	71.0	51	CQ001873	CQ001873 Sequence
9	14.2	71.0	51	CQ001875	CQ001875 Sequence
10	14.2	71.0	60	CQ562289	CQ562289 Sequence
11	13.8	69.0	51	CQ001876	CQ001876 Sequence
12	13.8	69.0	100	CQ667191	CQ667191 Sequence
13	13.6	68.0	51	CQ002646	CQ002646 Sequence
14	13.6	68.0	59	AR073712	AR073712 Sequence
15	13.6	68.0	60	CQ542906	CQ542906 Sequence
16	13.6	68.0	61	AX085810	AX085810 Sequence
17	13.6	68.0	93	E29108	E29108 Expression
18	13.4	67.0	47	AR288463	AR288463 Sequence

19	13.4	67.0	78	6	BD177575	BD177575 Anti-1gE
20	13.4	67.0	78	6	AR652888	AR652888 Sequence
21	13.4	67.0	78	6	AX404028	AX404028 Sequence
22	13.2	66.0	24	6	AR104159	AR104159 Sequence
23	13.2	66.0	39	6	CQ888497	CQ888497 Sequence
24	13.2	66.0	50	6	CQ002645	CQ002645 Sequence
25	13.2	66.0	51	6	AX117457	AX117457 Sequence
26	13.2	66.0	51	6	AX158478	AX158478 Sequence
27	13.2	66.0	51	8	AB013762	AB013762 Macaca as
28	13.2	66.0	51	8	AB013763	AB013763 Macaca as
29	13.2	66.0	51	8	AB013764	AB013764 Macaca fa
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32	13.2	66.0	75	6	AR128284	AR128284 Sequence
33	13	65.0	50	6	CQ005220	CQ005220 Sequence
34	12.8	64.0	20	6	CQ774755	CQ774755 Sequence
35	12.8	64.0	20	6	AR582069	AR582069 Sequence
36	12.8	64.0	25	6	AR525293	AR525293 Sequence
37	12.8	64.0	25	6	AX937336	AX937336 Sequence
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39	12.8	64.0	66	6	E03396	E03396 DNA encodin
40	12.8	64.0	69	6	I66412	I66412 Sequence 10
41	12.8	64.0	71	6	CS136211	CS136211 Sequence
42	12.8	64.0	71	6	AX955894	AX955894 Sequence
43	12.8	64.0	87	6	AX135351	AX135351 Sequence
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ALIGNMENTS

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LOCUS BD211668 20 bp DNA linear PAT 17-JUN-2003
DEFINITION Antisense oligonucleotide sequence of neuropilin and method of using the same for controlling cell proliferation.

ACCESSION BD211668.1 GI:33021438
VERSION BD211668
KEYWORDS JP 2002512793-A/11.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 20)

AUTHORS Wright,J.A., Young,A.H. and Lee,Y.S.

TITLE Antisense oligonucleotide sequence of neuropilin and method of using the same for controlling cell proliferation

JOURNAL Patent: JP 2002512793-A 11 08-MAY-2002;

COMMENT GENENSENSE TECHNOLOGIES INC
OS Homo sapiens (human)
PN JP 2002512793-A/11
PD 08-MAY-2002
PF 23-APR-1998 JP 2000545999

PR 23-APR-1998 US 60/082791
PT JIM A WRIGHT, AIPING H YOUNG, YOON S LEE
PC C12N15/09,A61K31/711,A61K48/00,A61P35/00,C12N15/00 CC
Antisense oligonucleotide sequence of neuropilin and method of

CC same for controlling cell proliferation
FH key Location/Qualifiers
FT source 1..20
FT Location/Qualifiers

FEATURES
source 1..20
Location/Qualifiers
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Db 1 GACCCCGAGGCATCATGG 20

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AX153915/c
LOCUS AX153915 21 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 13 from Patent WO0138576.
ACCESSION AX153915
VERSION AX153915.1 GI:14535529
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE 1
AUTHORS Cargill, M., Ireland, J.S. and Lander, E.S.
TITLE Human single nucleotide polymorphisms
JOURNAL Patent: WO 0138576-A 13 31-MAY-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
FEATURES Location/Qualifiers
source 1..21
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Db 21 CCCCCAGGGCACTCATGG 4

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BD211677
LOCUS BD211677 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Antisense oligonucleotide sequence of neuropilin and method of
using the same for controlling cell proliferation.
ACCESSION BD211677
VERSION BD211677.1 GI:33021447
KEYWORDS JP 2002512793-A/20.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 20)
REFERENCE Wright, J.A., Young, A.H. and Lee, Y.S.
AUTHORS Antisense oligonucleotide sequence of neuropilin and method of
TITLE using the same for controlling cell proliferation
JOURNAL Patent: JP 2002512793-A 20 08-MAY-2002;
GENESENSE TECHNOLOGIES INC
COMMENT OS Homo sapiens (human)
PN JP 2002512793-A/20
PD 08-MAY-2002
PR 23-APR-1999 JP 2000545999
PI CJM A WRIGHT, AIPING H YOUNG, YOON S LEE
PC C12N15/09, A61K31/711, A61K48/00, A61P35/00, C12N15/00 CC
Antisense oligonucleotide sequence of neuropilin and method of
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CC same for controlling cell proliferation
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FEATURES Location/Qualifiers

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Db 1 CCCCAGGCATCATGG 16

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LOCUS I08796 44 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 18 from Patent WO 8804690.
ACCESSION I08796
VERSION I08796.1 GI:588501
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 44)
AUTHORS Bollen, A.J., Gheysen, D., Jacobs, P., Pierard, L. and Collen, D.J.
JOURNAL Patent: WO 8804690-A 18 30-JUN-1988;
FEATURES Location/Qualifiers
source 1..44
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Db 42 GACCCCGAGGCATCATGG 23

RESULT 5
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LOCUS CQ001874 51 bp DNA linear PAT 16-JAN-2004
DEFINITION Sequence 514 from Patent WO0147944.
ACCESSION CQ001874
VERSION CQ001874.1 GI:4108506
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1
REFERENCE Shinkens, R.A. and Leach, M.
AUTHORS Nucleic acids containing single nucleotide polymorphisms and
TITLE methods of use thereof
JOURNAL Patent: WO 0147944-A 514 05-JUL-2001;
Curegen Corporation (US)
COMMENT OS Homo sapiens (human)
PN JP 2002512793-A/20
PD 08-MAY-2002
PR 23-APR-1999 JP 2000545999
PI CJM A WRIGHT, AIPING H YOUNG, YOON S LEE
PC C12N15/09, A61K31/711, A61K48/00, A61P35/00, C12N15/00 CC
Antisense oligonucleotide sequence of neuropilin and method of
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Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GACCCCGAGGCACTCATGG 20
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DB 26 GAGCCTCAGGCGACTCATGG 45

RESULT 6
LOCUS COS37667/c 60 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 7302 from Patent WO0210449.
ACCESSION COS37667
VERSION COS37667.1 GI:41503931
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
AUTHORS Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
TITLE Oligonucleotide library for detecting rna transcripts and splice
variants that populate a transcritpome
JOURNAL Patent: WO 0210449-A 7302 07-FEB-2002;
CompuGen Inc. (US)
FEATURES
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QY 1 GACCCCGAGGCGACTCATGG 20
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DB 46 GAGCCTCAGGCGACTCATGG 27

RESULT 7
LOCUS AR302389/c 39 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 16 from patent US 6541224.
ACCESSION AR302389
VERSION AR302389.1 GI:31690644
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 39)
AUTHORS Yu,G.-L., Ni,J., Gentz,R.L. and Dillon,P.J.
TITLE Tumor necrosis factor delta polypeptides
JOURNAL Patent: US 6541224-A 16 01-APR-2003;
Human Genome Sciences, Inc.; Rockville, MD
FEATURES
source location/Qualifiers
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DB 32 CCCAGGCGACTCATGG 17

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LOCUS CQ001873 51 bp DNA linear PAT 16-JAN-2004
DEFINITION Sequence 513 from Patent WO0147944.

ACCESSION CQ001873
VERSION CQ001873.1 GI:41008505
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0147944-A 513 05-JUL-2001;
Curagen Corporation (US)
FEATURES
source location/Qualifiers
1..51
/organism="Homo sapiens"
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/note="Accession number cg43918942"

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DB 30 AGCCTCAGGCGACTCATGG 48

RESULT 9
LOCUS CQ001875 51 bp DNA linear PAT 16-JAN-2004
DEFINITION Sequence 515 from Patent WO0147944.
ACCESSION CQ001875
VERSION CQ001875.1 GI:41008507
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0147944-A 515 05-JUL-2001;
Curagen Corporation (US)
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Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 6 AGCCTCAGGCGACTCATGG 24

RESULT 10
LOCUS CQ562289/c 60 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 31924 from Patent WO0210449.
ACCESSION CQ562289
VERSION CQ562289.1 GI:41528716
KEYWORDS

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
REFERENCE 1
JOURNAL Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
Oligonucleotide library for detecting rna transcripts and splice
variants that populate a transcriptome
Patent: WO 0210449-A 31924 07-FEB-2002;
COMPUGEN Inc. (US)
FEATURES Location/Qualifiers
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RESULT 11
LOCUS CQ001876 51 bp DNA linear PAT 16-JAN-2004
DEFINITION Sequence 516 from Patent WO0147944.
ACCESSION CQ001876
VERSION CQ001876.1 GI:41008508
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
REFERENCE 1
JOURNAL Shinkets,R.A. and Leach,M.
Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
Patent: WO 0147944-A 516 05-JUL-2001;
CURAGEN Corporation (US)
FEATURES Location/Qualifiers
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RESULT 12
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DEFINITION Sequence 12117 from Patent WO02070737.
ACCESSION CQ667191
VERSION CQ667191.1 GI:42152617
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE 1
AUTHORS Liew,C.C., Marshall,W.E. and Zhang,H.
TITLE Compositions and methods relating to osteoarthritis
JOURNAL Patent: WO 02070737-A 12117 12-SEP-2002;
Chondrogene Inc. (CA)
FEATURES Location/Qualifiers
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RESULT 13
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DEFINITION Sequence 1286 from Patent WO0147944.
ACCESSION CQ002646
VERSION CQ002646.1 GI:41009278
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
REFERENCE 1
JOURNAL Shinkets,R.A. and Leach,M.
Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
Patent: WO 0147944-A 1286 05-JUL-2001;
CURAGEN Corporation (US)
FEATURES Location/Qualifiers
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DB 41 GTCTCCAGGCGACATCATG 22
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RESULT 14
LOCUS AR073712 59 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 5 from patent US 5952190.
ACCESSION AR073712
VERSION AR073712.1 GI:10000472
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 59)
AUTHORS Joenje,H. and Jo Ten Hoe,J.R.
TITLE CDNA for farnoni anemia complementation group A
JOURNAL Patent: US 5952190-A 5 14-SEP-1999;
FEATURES Location/Qualifiers
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LOCUS CQ542906 60 bp DNA linear PAT 30-JAN-2004
DEFINITION Sequence 12541 from Patent WO0210449.
ACCESSION CQ542906
VERSION CQ542906.1 GI:41509170
KEYWORDS

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE 1
AUTHORS Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
TITLE Oligonucleotide library for detecting rna transcripts and splice
JOURNAL variants that populate a transcriptome
Patent: WO 0210449-A 12541 07-FEB-2002;
Compugen Inc. (US)

FEATURES
source location/Qualifiers
1..60
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 68.0%; Score 13.6; DB 6; Length 60;
Best Local Similarity 80.0%; Pred. No. 1.1e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GACCCCGAGGCACTCATGG 20
Db 29 GACCTCCAGGSCATCAAGG 10

Search completed: December 24, 2005, 14:06:18
Job time : 585 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 01:41:40 ; Search time 171.4 Seconds
(without alignments)
777.677 Million cell updates/sec

Title: US-09-296-264-11

Perfect score: 20
Sequence: 1 gacccccagggcactcatg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 3390896

Minimum DB seq length: 20
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

N Geneseq_21:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000b:*
- 4: geneseqn2001a:*
- 5: geneseqn2001b:*
- 6: geneseqn2002a:*
- 7: geneseqn2002b:*
- 8: geneseqn2003a:*
- 9: geneseqn2003b:*
- 10: geneseqn2003c:*
- 11: geneseqn2003d:*
- 12: geneseqn2004a:*
- 13: geneseqn2004b:*
- 14: geneseqn2005a:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3	AAZ31441
2	18.4	92.0	20	4	ADA74693
3	16.4	82.0	21	4	AAH62112
4	16	80.0	20	3	AAZ31450
5	16	80.0	20	9	ADA74702
6	15.2	76.0	39	12	ADP04390
7	15.2	76.0	51	4	AAI27306
8	15.2	76.0	60	6	ABN34554
9	14.4	72.0	20	12	ADN97884
10	14.4	72.0	20	12	ADN40820
11	14.4	72.0	25	13	ADU06785
12	14.4	72.0	39	6	ABK88692
13	14.4	72.0	39	6	ABK13410
14	14.4	72.0	39	10	ADP72622
15	14.4	72.0	74	13	ADU06792
16	14.2	71.0	51	4	AAI27305
17	14.2	71.0	51	4	AAI27307
18	14.2	71.0	60	6	ABN59176
19	14	70.0	20	12	ADN97873

20	14	70.0	20	12	ADN40809	Adn40809 Human for
21	13.8	69.0	51	4	AAI27308	AAI27308 Human SNP
22	13.8	69.0	80	12	ADN95272	Adm95272 Rat antic
23	13.6	68.0	25	9	ACI97315	Act97315 Human mlc
24	13.6	68.0	25	9	ACK08854	Act08854 Human mlc
25	13.6	68.0	41	11	ADM11706	Adm11706 Amplifica
26	13.6	68.0	41	11	ADM11708	Adm11708 Amplifica
27	13.6	68.0	51	4	AAI28078	AAI28078 Human SNP
28	13.6	68.0	59	2	AAV18190	AAV18190 Primer fo
29	13.6	68.0	60	6	ABN39793	Abn39793 Human spl
30	13.6	68.0	61	4	AAI75272	AAI75272 Human ppa
31	13.6	68.0	93	2	AAZ27697	AAZ27697 Intron fir
32	13.4	67.0	20	14	ADY54617	Ady54617 Mouse Myb
33	13.4	67.0	30	14	ADX8798	Adx8798 PCR prime
34	13.4	67.0	36	10	ABZ80496	Abz80496 I98 cytoC
35	13.4	67.0	40	10	ACA55295	Acas55295 Baculovir
36	13.4	67.0	40	10	ACA55254	Acas55254 Human IGE
37	13.4	67.0	40	10	ACA55251	Acas55251 Human IGE
38	13.2	66.0	24	2	AAK90284	Aax90284 Macrophag
39	13.2	66.0	25	10	ABZ84504	Abz84504 Toxicolog
40	13.2	66.0	31	2	AAK07235	Aax07235 PCR prime
41	13.2	66.0	38	3	AAK82076	Aac82076 p53 PCR p
42	13.2	66.0	39	13	ADT07017	Adt07017 Rabbit pa
43	13.2	66.0	40	10	ADP15475	Adp15475 Human alb
44	13.2	66.0	40	10	ADH21445	Adh21445 Human TR6
45	13.2	66.0	43	10	ADP15481	Adp15481 Human alb

ALIGNMENTS

RESULT 1
AAZ31441
ID AAZ31441 standard; DNA; 20 BP.
AC AAZ31441;
XX
XX
DT 07-FEB-2000 (first entry)
XX
DE Human neuropilin mRNA specific antisense oligo GTT3611.
XX
KW Neuropilin; human; growth; metastasis; tumor; neovascularisation; cancer;
KW papilloma; diabetic retinopathy; antisense; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX W0955855-A2.
XX
XX PD 04-NOV-1999.
XX
XX PF 23-APR-1999; 99WO-CA000324.
XX
XX PR 23-APR-1998; 98US-0082791P.
XX
XX (GENE-) GENESENSE TECHNOLOGIES INC.
XX
XX Wright JA, Young AH, Lee YS;
XX
XX WPI; 2000-023357/02.
XX
XX Antisense oligonucleotides that inhibit neuropilin expression, useful for
XX treating cancer.
XX
XX PS Claim 4; Page 16; 57pp; English.
XX
XX Sequences AAZ31431-460 represent antisense oligonucleotides which inhibit
XX human neuropilin expression. The antisense oligonucleotides can be used
XX to inhibit the growth of a mammalian tumor and inhibit
XX neovascularisation. The oligonucleotides may be used to treat various
XX forms of cancers or tumors, such as sarcomas, melanomas, adenomas,
XX carcinomas of solid tissue, hypoxic tumors, squamous cell carcinomas of
XX the mouth, throat, larynx and lung, genitourinary cancers such as

CC cervical and bladder cancer, hematopoietic cancers, colon cancer, breast
 CC cancer, pancreatic cancer, renal cancer, brain cancer, skin cancer, liver
 CC cancer, head and neck cancers, and nervous system cancers, as well as
 CC benign lesions such as papillomas. The methods may be used to treat
 CC neovascularisation disorders such as diabetic retinopathy, and
 CC retinopathy of prematurity and age related macular degeneration
 XX
 SQ Sequence 20 BP; 4 A; 8 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 20;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GACCCCGAGGCACTCATGG 20
 |||||
 Db 1 GACCCCGAGGCACTCATGG 20

RESULT 2
 ADA74693

ID ADA74693 standard; DNA; 20 BP.

AC ADA74693;

DT 20-NOV-2003 (first entry)

XX GT13611 antisense oligonucleotide targeted to human neuropilin mRNA.

XX neurophilin; VEGF165R; vascular endothelial growth factor receptor;

XX cyclostatic; growth; tumour metastasis; angiogenesis; gene therapy;

XX GT13611; antisense; human; ss.

XX Homo sapiens.

XX US2003083274-A1.

XX 01-MAY-2003.

XX 22-APR-1999; 99US-00296264.

XX 23-APR-1998; 98US-0082791P.

XX (WRIG/) WRIGHT J A.

XX (YOUN/) YOUNG A H.

XX (LEBY/) LEE Y S.

XX Wright JA, Young AH, Lee YS;

XX WPI; 2003-576622/54.

XX New antisense oligonucleotide that inhibits neuropilin expression, useful

XX for inhibiting growth of mammalian tumor or inhibiting metastasis of a

XX mammalian tumor.

XX Claim 1; Page 5; 27PD; English.

XX The invention relates to a novel antisense oligonucleotide that inhibits

XX the expression of neuropilin, also known as VEGF165R (vascular

XX endothelial growth factor receptor). The oligonucleotide of the invention

XX demonstrates cytostatic activity and may be useful for inhibiting the

XX growth or metastasis of a mammalian tumour and to inhibit angiogenesis in

XX mammals. Furthermore, the oligonucleotide may be utilised during gene

XX therapy. The current sequence is that of the GT13611 antisense

CC oligonucleotide of the invention which is targeted to human neuropilin

CC mRNA.

XX
 SQ Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 92.0%; Score 18.4; DB 9; Length 20;
 Best Local Similarity 95.0%; Pred. No. 79;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GACCCCGAGGCACTCATGG 20

Db 1 GACCCCGAGGCACTCATGG 20
 |||||

RESULT 3
 AAH62112/C

ID AAH62112 standard; DNA; 21 BP.

XX AAH62112;

XX 09-SEP-2004 (revised)

XX 12-SEP-2001 (first entry)

XX Neuropilin 1 (NRP1) polymorphism containing DNA fragment #13.

XX Single nucleotide polymorphism; SNP; human; cancer; inflammation;

XX heart disease; paternity testing; forensic science; ds.

XX Homo sapiens.

XX Unidentified.

XX Key

XX variation

XX location/Qualifiers

XX /*tag= a

XX /standard_name= "single nucleotide polymorphism"

XX MO200138576-A2.

XX 31-MAY-2001.

XX 17-NOV-2000; 2000WO-US031639.

XX 24-NOV-1999; 99US-016734P.

XX (WHEH) WHITEHEAD INST BIOMEDICAL RES.

XX Cargill M, Ireland JS, Lander ES;

XX WPI; 2001-367705/38.

XX New nucleic acid segments of the human genome, particularly from genes

XX including polymorphic sites, for phenotype correlation, forensics,

XX paternity testing, medicine and genetic analysis.

XX Claim 1; Page 29; 80PD; English.

XX DNA sequences AAH62100 - AAH62688 represent segments of human genes which

XX contain single nucleotide polymorphisms (SNPs). A method is included in

XX the invention for analysing a nucleic acid sample, which consists of

XX determining the base occupying any one of the polymorphic sites given in

XX the SNP containing sequences. The nucleotide sequences can be used in the

XX diagnosis or monitoring of diseases, such as cancer, inflammation, heart

XX diseases, diseases of the cardiovascular system, and infection by

XX microorganisms. The oligonucleotides are also useful in the manufacture

XX of a pharmaceutical. SNP containing oligonucleotides are useful in

XX applications such as phenotype correlation, forensics, paternity testing,

XX medicine and genetic analysis

CC Revised record issued on 09-SEP-2004 : Correction to Feature Table Key

CC
 SQ Sequence 21 BP; 3 A; 6 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 82.0%; Score 16.4; DB 4; Length 21;
 Best Local Similarity 94.4%; Pred. No. 6.6e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 3 CCCCCGAGGCACTCATGG 20
 |||||
 Db 21 CCCCCGAGGCGCTCATGG 4

RESULT 4

AAZ31450
ID AAZ31450 standard; DNA; 20 BP.
XX
AC AAZ31450;
XX
DT 07-FEB-2000 (first entry)
XX
DE Human neuropilin mRNA specific antisense oligo GT13621.
XX
KM Neuropilin; human; growth; metastasis; tumor; neovascularisation; cancer;
XX papilloma; diabetic retinopathy; antisense; ss.
OS Synthetic.
OS Homo sapiens.
PN W09955855-A2.
XX
PD 04-NOV-1999.
XX
PF 23-APR-1999; 99MO-CA000324.
XX
PR 23-APR-1998; 98US-0082791P.
XX
PA (GENE-) GENENSENSE TECHNOLOGIES INC.
XX
PI Wright JA, Young AH, Lee YS;
XX WPI; 2000-023357/02.
DR
PT Antisense oligonucleotides that inhibit neuropilin expression, useful for
XX treating cancer.
XX
PS Claim 4; Page 16; 57bp; English.
XX
CC Sequences AAZ31431-460 represent antisense oligonucleotides which inhibit
CC human neuropilin expression. The antisense oligonucleotides can be used
CC to inhibit the growth or metastasis of a mammalian tumor and inhibit
CC neovascularisation. The oligonucleotides may be used to treat various
CC forms of cancers or tumors, such as sarcomas, melanomas, adenomas, of
CC carcinomas of solid tissue, hypoxic tumors, squamous cell carcinomas of
CC the mouth, throat, larynx and lung, genitourinary cancers such as
CC cervical and bladder cancer, hematopoietic cancers, colon cancer, breast
CC cancer, pancreatic cancer, renal cancer, brain cancer, skin cancer, liver
CC cancer, head and neck cancers, and nervous system cancers, as well as
CC benign lesions such as papillomas. The methods may be used to treat
CC neovascularisation disorders such as diabetic retinopathy, and
CC retinopathy of prematurity and age related macular degeneration
CC
XX
SQ Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
XX
Query Match 80.0%; Score 16; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 5 CCCAGGGGCACTCATGG 20
DB 1 CCCAGGGGCACTCATGG 16
XX
RESULT 5
ADA74702
ID ADA74702 standard; DNA; 20 BP.
XX
AC ADA74702;
XX
DT 20-NOV-2003 (first entry)
XX
DE GT13621 antisense oligonucleotide targeted to human neuropilin mRNA.
XX
KM neuropilin; VEGF165R; vascular endothelial growth factor receptor;
XX cytostatic; growth; tumour metastasis; angiogenesis; gene therapy;
XX GT13621; antisense; human; ss.

OS Homo sapiens.
XX
PN US2003083274-A1.
XX
PD 01-MAY-2003.
XX
PF 22-APR-1999; 99US-00296264.
XX
PR 23-APR-1998; 98US-0082791P.
XX
PA (WRIGHT) WRIGHT J A.
XX (YOUNG) YOUNG A H.
XX (LEEY) LEE Y S.
PI Wright JA, Young AH, Lee YS;
XX WPI; 2003-576622/54.
DR
XX
PF New antisense oligonucleotide that inhibits neuropilin expression, useful
XX for inhibiting growth of mammalian tumor or inhibiting metastasis of a
XX mammalian tumor.
XX
PS Claim 1; Page 5; 27bp; English.
XX
CC The invention relates to a novel antisense oligonucleotide that inhibits
CC the expression of neuropilin, also known as VEGF165R (vascular
CC endothelial growth factor receptor). The oligonucleotide of the invention
CC demonstrates cytostatic activity and may be useful for inhibiting the
CC growth or metastasis of a mammalian tumor and to inhibit angiogenesis in
CC mammals. Furthermore, the oligonucleotide may be utilized during gene
CC therapy. The current sequence is that of the GT13621 antisense
CC oligonucleotide of the invention which is targeted to human neuropilin
CC mRNA.
XX
SQ Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
XX
Query Match 80.0%; Score 16; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 5 CCCAGGGGCACTCATGG 20
DB 1 CCCAGGGGCACTCATGG 16
XX
RESULT 6
ADP04390/C
ID ADP04390 standard; DNA; 39 BP.
XX
AC ADP04390;
XX
DT 12-AUG-2004 (first entry)
XX
DE PCR primer 1 used to amplify human SRC-1 (PPARdelta coactivator) cDNA.
XX
KM transcriptional regulation;
XX peroxisome proliferator activated receptor delta; PPARdelta;
XX retinoid X receptor; RXR; cytostatic; antiarteriosclerotic; antiipaeamic;
XX osteopathic; osteoporosis; colon cancer; arteriosclerosis; PCR; primer;
XX ss; human; coactivator; SRC-1.
OS Homo sapiens.
XX
PN JP2004141120-A.
XX
PD 20-MAY-2004.
XX
PF 28-OCT-2002; 2002JP-00312619.
XX
PR 28-OCT-2002; 2002JP-00312619.
XX
PA (FUJI) FUJISAWA PHARM CO LTD.
XX

DR WPI: 2004-382695/36.
XX Measuring influence of test compound on transcriptional-regulation
PT activity of peroxisome proliferator activated receptor (PPAR delta), and
PT comprises contacting test compound with cell expressing PPAR delta, and
PT measuring signal.
PS Example 1; SEQ ID NO 9; 30pp; Japanese.
XX
CC The invention relates to a novel method of measuring the influence of a
CC test compound on the transcriptional-regulatory activity of peroxisome
CC proliferator activated receptor delta (PPARdelta). The method comprises
CC contacting the test compound with a cell expressing PPARdelta or a
CC protein functionally equivalent to PPARdelta, retinoid X receptor (RXR)
CC or a protein functionally equivalent to RXR and a protein which acts as a
CC co-activator of PPARdelta. Subsequently, the signal generated by the cell
CC is measured. The method of the invention has cytosstatic,
CC antiatherosclerotic, antiinpaemic and osteopathic applications and may
CC be useful for evaluating the influence of a test compound on the
CC transcriptional-regulatory activity of PPARdelta and for screening a
CC compound which controls the transcriptional-regulatory activity of
CC PPARdelta. The PPARdelta regulator may be useful for treating diseases
CC including osteoporosis, colon cancer and arteriosclerosis. The current
CC sequence is that of the PCR primer 1 of the invention which was used to
CC amplify human SRC-1 (PPARdelta coactivator) cDNA.
XX
SQ Sequence 39 BP; 8 A; 10 C; 11 G; 10 T; 0 U; 0 Other:
Query Match 76.0%; Score 15.2; DB 12; Length 39;
Best Local Similarity 85.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GACCCCGAGGCGCATCATGG 20
DB 32 GTCCCGAGGCGCATCATGG 13
RESULT 7
AAL27306
ID AAL27306 standard; DNA; 51 BP.
XX
AC AAL27306;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human SNP oligonucleotide #514.
XX
XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX
OS Homo sapiens.
XX
PN WO200147944-A2.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US035498.
XX
PR 28-DEC-1999; 99US-0173419P.
XX
PR 27-DEC-2000; 2000US-00173419.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkete RA, Leach M;
XX
DR WPI: 2001-465210/50.
XX

PT Polymorphic nucleic acids encoding e.g. amyloses, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
PT autoimmune diseases and infections.
PS Claim 1; Page 1536; 4143pp; English.
XX
XX The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amyloses, amyloid proteins, angiotensin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-
CC protein coupled receptors and thioesterases. The present sequence is one
CC such oligonucleotide. The oligonucleotides and the peptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of the proteins listed above.
CC Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, cancer
CC systemic lupus erythematosis and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukaemia), diseases of the nervous system and an infection of pathogenic
CC organisms
XX
SQ Sequence 51 BP; 10 A; 18 C; 11 G; 12 T; 0 U; 0 Other:
Query Match 76.0%; Score 15.2; DB 4; Length 51;
Best Local Similarity 85.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GACCCCGAGGCGCATCATGG 20
DB 26 GAGCCTCAGGCGCATCATGG 45
RESULT 8
ABN34554/C
ID ABN34554 standard; DNA; 60 BP.
XX
AC ABN34554;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human spliced transcript detection oligonucleotide SEQ ID NO: 7302.
XX
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
XX Homo sapiens.
XX
OS WO200210449-A2.
XX
PN WO200210449-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WO-IB001903.
XX
PR 28-JUL-2000; 2000US-0221607P.
XX
PR 02-MAY-2001; 2001US-0287724P.
XX
PA (COMP-) COMPUGEN INC.
XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
DR WPI: 2002-257383/30.
XX
XX New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of a
PT genome, useful for detecting tissue-, pathology-, and developmental-
PT specific genes.
PS Example 1; SEQ ID NO 7302; 47pp; English.
XX
XX The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-

CC)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises several
CC oligonucleotides, each capable of hybridising selectively to a set of
CC messenger RNAs transcribed from a given transcription unit of the genome,
CC which encodes one or more messenger RNA splice variants. The
CC oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterising the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a particular
CC biological or pathological state, and so allowing the detection of tissue
CC - and pathology-specific genes such as those genes only expressed in
CC specific tissue under a specific pathological condition; to detect
CC developmental specific genes; and to detect RNA transcripts and splice
CC variants of a transcriptome of a patient suffering from a particular
CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
CC rats, humans and mice, which are used in the exemplification of the
CC present invention. N.B. The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 60 BP; 17 A; 14 C; 19 G; 10 T; 0 U; 0 Other;

Query Match 76.0%; Score 15.2; DB 6; Length 60;
Best Local Similarity 85.0%; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 GACCCGAGGCACTCATG 20
Db 46 GAGCCTCAGGCACTCATG 27

RESULT 9
ADN97884
ID ADN97884 standard; DNA; 20 BP.
XX
AC ADN97884;
XX
DT 01-JUL-2004 (first entry)
XX
DE Monkey foxhead box O1A sequence inhibitory oligo #3.
XX
KM ss; cytosaratic; antidiabetic; foxhead box O1A inhibitor;
KM forkhead box O1A; hyperproliferative disorder; cancer; rhabdomyosarcoma;
KM diabetes; H-ras gene; antisense; gene expression; primer.
XX
OS Synthetic.
XX
PN WO2004031350-A2.
XX
PD 15-APR-2004.
XX
PF 25-SEP-2003; 2003WO-US030352.
XX
PR 26-SEP-2002; 2002US-00260203.
XX
PA (AMGE-) AMGEN INC.
PA (ISIS-) ISIS PHARM INC.
PI Dobie KM, Bhanot S, Veniant-Elisson M, Lindberg RA, Shutter JR;
XX
DR WPI; 2004-330164/30.
XX
PT New compounds, particularly antisense oligonucleotides, targeted to a
PT nucleic acid molecule encoding forkhead box O1A, useful for treating
PT cancer, or type 2 diabetes.
XX
PS Example 25; SEQ ID NO 174; 146bp; English.
XX
CC The invention relates to a compound 8-80 nucleobases in length targeted
CC to a nucleic acid molecule encoding forkhead box O1A, where the compound
CC is at least 70% complementary to a nucleic acid molecule encoding

CC forkhead box O1A and modulates expression of forkhead box O1A by at least
CC 10%. The compound is useful for treating an animal having a disease or
CC condition associated with forkhead box O1A, e.g. a hyperproliferative
CC disorder (cancer, preferably rhabdomyosarcoma), or type 2 diabetes. This
CC sequence corresponds to an oligonucleotide targeted to the monkey foxhead
CC box O1A genes in order to inhibit gene expression.

XX SQ Sequence 20 BP; 3 A; 9 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 72.0%; Score 14.4; DB 12; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 3 CCCCCAGGCACTCAT 18
Db 1 CCGCCAGGCACTCAT 16

RESULT 10
ADN40820
ID ADN40820 standard; DNA; 20 BP.
XX
AC ADN40820;
XX
DT 12-AUG-2004 (first entry)
XX
DE Monkey forkhead box O1A DNA antisense oligonucleotide #3.
XX
KM Monkey; forkhead box O1A; ss; antisense oligonucleotide;
KM phosphorothioate linkage; 2'-O-methoxyethyl sugar moiety;
KM 5-methylcytosine; hyperproliferative disorder; cancer; rhabdomyosarcoma;
KM type 2 diabetes; cytosaratic; antidiabetic.
XX
OS Primates.
XX
PN US2004097459-A1.
XX
PD 20-MAY-2004.
XX
PF 25-SEP-2003; 2003US-00671074.
XX
PR 26-SEP-2002; 2002US-00260203.
XX
PA (DOBI/) DOBIE K W.
PA (BHAN/) BHANOT S.
PA (VENI/) VENIANT-ELISSON M.
PA (LIND/) LINDBERG R A.
PA (SHUT/) SHUTTER J R.
PI Dobie KM, Bhanot S, Veniant-Elisson M, Lindberg RA, Shutter JR;
XX
DR WPI; 2004-389194/36.
XX
PT New compounds, particularly antisense oligonucleotides, targeted to a
PT nucleic acid molecule encoding forkhead box O1A, useful for treating
PT cancer, or type 2 diabetes.
XX
PS Example 25; SEQ ID NO 174; 80bp; English.
XX
CC The invention relates to a compound targeted to a nucleic acid molecule
CC encoding the human forkhead box O1A polypeptide. The compound is an
CC antisense oligonucleotide that specifically hybridises with the nucleic
CC acid and inhibits expression of the polypeptide. The antisense
CC oligonucleotide comprises at least one modified internucleoside linkage
CC i.e. a phosphorothioate linkage, at least one modified sugar moiety,
CC preferably a 2'-O-methoxyethyl sugar moiety, or at least one modified
CC nucleobase comprising a 5-methylcytosine. The antisense compounds are
CC useful for modulating the expression of the human forkhead box O1A
CC polypeptide and in preparation of a composition for treating
CC hyperproliferative disorders, e.g. cancer, preferably rhabdomyosarcoma,
CC and type 2 diabetes. This sequence represents an antisense
CC oligonucleotide targeted to DNA encoding the monkey forkhead O1A
CC polypeptide of the invention.

XX Sequence 20 BP; 3 A; 9 C; 5 G; 3 T; 0 U; 0 Other;
SQ Query Match 72.0%; Score 14.4; DB 12; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CCCCCGAGGCACTCAT 18
1 CCGCCAGGCACTCAT 16
Db

RESULT 11
ID ADU06785 standard; DNA; 25 BP.
XX ADU06785;
AC ADU06785;
XX
DT 27-JAN-2005 (first entry)
XX
DE Mouse GPR4 cDNA probe.
XX
KW ss; antiinflammatory; GPR4 signal transduction inhibitor;
KW neutrophil inflammation disease; signal transduction; GPR4; probe.
XX
OS Mus musculus.
XX
PN WO2004093912-A1.
XX
PD 04-NOV-2004.
XX
PF 23-APR-2004; 2004WO-JP005930.
XX
PR 23-APR-2003; 2003JP-00118432.
PR 26-FEB-2004; 2004JP-00052191.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Saki M, Nonaka H, Miyaji H, Takahashi C, Manabe H, Hiura N;
PI Miki I, Abe Y, Sasaki K, Kobatake C, Ichikawa S, Goto A, Suda T;
XX
DR WPI; 2004-795424/78.
XX
PT Agent comprises nitrogen-containing tricyclic compound, as active
PT ingredient capable of inhibiting signal transduction function of protein,
PT useful for treating or preventing neutrophil inflammation disease.
XX
PS Example 6; SEQ ID NO 19; 293bp; Japanese.
XX
XX The invention relates to a preventive and/or therapeutic agent (P1) of
CC neutrophil inflammation disease, comprises nitrogen-containing tricyclic
CC compound, as an active ingredient that is capable of inhibiting signal
CC transduction function of a protein. (P1) comprises a fully defined
CC sequence of 362 (S1) amino acids as given in the specification, an
CC antibody that recognizes (S1) or two fully defined sequence having 365
CC (S2) amino acids as given in the specification, in which one or more
CC amino acids are deleted, substituted or added, an oligonucleotide (ON)
CC complementary to 15-60 continuous bases of a fully defined sequence of
CC 2932 (S3), 1098 (S4) or 1098 (S5) nucleotides as given in the
CC specification or its derivative or an oligonucleotide sequence that
CC hybridizes with (S3)-(S5) under stringent conditions, an antibody (P2)
CC that specifically recognizes (S1) or (S2), or nitrogen-containing
CC tricyclic compound of formula (I) or (II) or its quaternary ammonium
CC salt, as an active ingredient that is capable of inhibiting signal
CC transduction function of a protein. (P1) is useful for preventing and/or
CC treating neutrophil inflammation disease. (P2) is useful for producing
CC (P1). (P1) enables to inhibit GPR4 signal transduction. This sequence
CC corresponds to a probe for the cDNA encoding the mouse GPR4 signal
CC transduction protein of the invention. The sequence corresponds to
CC nucleotides 577-601 of the mouse GPR4 cDNA.
XX
XX Sequence 25 BP; 2 A; 10 C; 5 G; 8 T; 0 U; 0 Other;
SQ

Query Match 72.0%; Score 14.4; DB 13; Length 25;
Best Local Similarity 93.8%; Pred. No. 5.6e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CCCCCGAGGCACTCATG 19
6 CCCCCTGGGCACTCATG 21
Db

RESULT 12
ID ABK86892/C
XX ABK86892 standard; DNA; 39 BP.
XX
AC ABK86892;
XX
DT 07-OCT-2002 (first entry)
XX
DE Human transmembrane activator and CAML-interactor (TACI), PCR primer #2.
XX
KW Human; tumour necrosis factor; TNF delta; pulmonary system disorder;
KW immunoglobulin production; B-cell proliferation; immune system disorder;
KW autoimmune disease; cancer; lymphoproliferative disorder; pain;
KW microbial infection; parasitic infection; bone disease; atherosclerosis;
KW cardiovascular disorder; neurodegenerative disease; wound healing;
KW graft versus host disease; haematopoietic cell disorder; nephritis;
KW transmembrane activator and CAML-interactor; TACI; TNF epsilon; PCR;
KW primer; ss.
XX
XX Homo sapiens.
XX
PN US2002064829-A1.
XX
PD 30-MAY-2002.
XX
PF 14-JUN-2001; 2001US-00879919.
XX
PR 14-MAR-1996; 96US-0016812P.
PR 12-MAR-1997; 97US-00815783.
PR 15-JUN-2000; 2000US-0211537P.
PR 23-OCT-2000; 2000US-0241952P.
PR 13-DEC-2000; 2000US-0254875P.
PR 16-MAR-2001; 2001US-0276248P.
PR 23-MAR-2001; 2001US-0277978P.
PR 25-MAY-2001; 2001US-0293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Yu G, Ni J, Gentz RL, Dillon PJ;
XX
DR WPI; 2002-556722/59.
XX
PT Novel human multimeric tumor necrosis factor delta or epsilon protein
PT useful for treating disease or disorder of immune system such as
PT autoimmune disease, immunodeficiency, or cancer of immune system.
XX
PS Example 29; Page 115; 143bp; English.
XX
XX The present invention relates to the isolation of human tumour necrosis
CC factor (TNF) delta and TNF epsilon proteins, and the polynucleotide
CC sequences encoding them. The proteins are useful for modulating
CC immunoglobulin production or for modulating proliferation of B-cells. The
CC sequences of the invention are useful for treating diseases or disorders
CC of the immune system. Such disorders include autoimmune diseases (e.g.
CC systemic lupus erythematosus (SLE), acquired immunodeficiency syndrome
CC (AIDS)), cancers of the immune system (e.g. chronic lymphocytic leukaemia
CC (CLL), multiple myeloma, non-Hodgkin's lymphoma or Hodgkin's disease),
CC immunoproliferative disorders, microbial infections (e.g. viral,
CC bacterial), parasitic infections, nephritis, bone disease (e.g.
CC osteoporosis), atherosclerosis, pain, cardiovascular disorders (e.g.
CC myocardial infarction, stroke), neurodegenerative diseases (e.g.
CC Alzheimer's disease, Parkinson's disease), graft versus host disease,
CC wound healing, haematopoietic cell disorders (e.g. anaemia), inflammatory
CC disorders (e.g. asthma), diseases or disorders associated with various

PA (GENT/) GENTZ R.
XX
PI Yu G, Ni J, Gentz R;
XX
DR WPI: 2003-898107/82.
XX
PT New human tumor necrosis factor (TNF) delta and epsilon, useful for
PT diagnosing, preventing or treating dysfunctions or diseases associated
PT with aberrant activity of TNF delta or epsilon, e.g. septic shock,
PT inflammation or cancer.
XX
PS Example 30; SEQ ID NO 16; 155bp; English.
XX
CC The invention relates to human tumor necrosis factor (TNF) polypeptides
CC and the polynucleotides encoding them. The sequences of the invention are
CC useful in research, biological, clinical and therapeutic purposes. In
CC particular, these are used in diagnosing, preventing, treating or
CC ameliorating dysfunctions or diseases associated with aberrant endogenous
CC activity of TNF delta or epsilon, such as septic shock, inflammation,
CC cancer, cerebral malaria, activation of HIV virus, bone resorption,
CC rheumatoid arthritis, cachexia, Grave's disease, diabetes, hepatitis,
CC asthma, cardiovascular disorders, infections, allergies, Alzheimer's
CC disease, Parkinson's disease and nephritis. The sequences may also be
CC used for chromosome identification or genetic mapping. This sequence
CC represents a human TNF-related PCR primer of the invention.
SQ Sequence 39 BP; 8 A; 11 C; 13 G; 7 T; 0 U; 0 Other;
XX
Query Match 72.0%; Score 14.4; DB 10; Length 39;
Best Local Similarity 93.8%; Pred. No. 5.7e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 CCCAGGGCAGCTCATGG 20
DB 32 CCCAGGGCAGCTCATGG 17
RESULT 15
ADU06792
ID ADU06792 standard; DNA; 74 BP.
XX
AC ADU06792;
XX
DT 27-JAN-2005 (first entry)
XX
DE Mouse GPR4 cDNA sequencing fragment.
XX
KW ss; antiinflammatory; GPR4 signal transduction inhibitor;
KW neutrophil inflammation disease; signal transduction; GPR4.
XX
OS Mus musculus.
XX
FN WO2004093912-A1.
XX
PD 04-NOV-2004.
XX
PF 23-APR-2004; 2004WO-JP005930.
XX
PR 23-APR-2003; 2003JP-00118432.
XX
PR 26-FEB-2004; 2004JP-00052191.
XX
PA (KYOM) KYOMA HAKKO KOGYO KK.
XX
PI Saki M, Nonaka H, Miyaji H, Takahashi C, Manabe H, Hiura N;
PI Miki I, Abe Y, Sasaki K, Kobatake C, Ichikawa S, Goto A, Suda T;
XX
DR WPI: 2004-795424/78.
XX
PT Agent comprises nitrogen-containing tricyclic compound, as active
PT ingredient capable of inhibiting signal transduction function of protein,
PT useful for treating or preventing neutrophil inflammation disease.
XX
PS Example 6; SEQ ID NO 26; 293bp; Japanese.

XX The invention relates to a preventive and/or therapeutic agent (P1) of
CC neutrophil inflammation disease, comprises nitrogen-containing tricyclic
CC compound, as an active ingredient that is capable of inhibiting signal
CC transduction function of a protein. (P1) comprises a fully defined
CC sequence of 362 (S1) amino acids as given in the specification, an
CC antibody that recognizes (S1) or two fully defined sequence having 365
CC (S2) amino acids as given in the specification, in which one or more
CC amino acids are deleted, substituted or added, an oligonucleotide (ON)
CC complementary to 15-60 continuous bases of a fully defined sequence of
CC 2932 (S3), 1098 (S4) or 1098 (S5) nucleotides as given in the
CC specification or its derivative or an oligonucleotide sequence that
CC hybridizes with (S3)-(S5) under stringent conditions, an antibody (P2)
CC that specifically recognizes (S1) or (S2), or nitrogen-containing
CC tricyclic compound of formula (I) or (II) or its quaternary ammonium
CC salt, as an active ingredient that is capable of inhibiting signal
CC transduction function of a protein. (P1) is useful for preventing and/or
CC treating neutrophil inflammation disease. (P2) is useful for producing
CC (P1). (P1) enables to inhibit GPR4 signal transduction. This sequence
CC corresponds to a sequenced fragment of the cDNA encoding the mouse GPR4
CC signal transduction protein DNA of the invention.

SQ Sequence 74 BP; 8 A; 23 C; 19 G; 24 T; 0 U; 0 Other;

Query Match 72.0%; Score 14.4; DB 13; Length 74;
Best Local Similarity 93.8%; Pred. No. 5.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCCAGGGCAGCTCATG 19
DB 34 CCCCTGGGCGACTCATG 49

Search completed: December 24, 2005, 12:29:06
UoD time : 173.4 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 10:37:31 ; Search time 1572 Seconds
(without alignments)
595.256 Million cell updates/sec

Title: US-09-296-264-11

Perfect score: 20
Sequence: 1 gaccccccagggcactcatcg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 768474

Minimum DB seq length: 20
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_eest1:*
2: gb_eest2:*
3: gb_eest3:*
4: gb_hc:*
5: gb_eest4:*
6: gb_eest5:*
7: gb_eest6:*
8: gb_eest7:*
9: gb_gest1:*
10: gb_gest2:*
11: gb_gest3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	15.8	79.0	76	8	DR767343 ILLUMIGEN
C 2	15.8	79.0	81	7	CO581042 ILLUMIGEN
C 3	15.2	76.0	70	8	DN390652 LIB3896-0
C 4	14.8	74.0	24	9	AZ428700 LM0212116
C 5	14.4	72.0	96	7	CF982929 ma195910.
C 6	14.2	71.0	76	1	A1304064 ui63907.y
C 7	14.2	71.0	94	7	CO720109 ta138e07.
C 8	14.2	71.0	68	9	CC514177 CH240.358
C 9	13.8	69.0	64	7	CV306707 t33h11.b
C 10	13.8	69.0	64	7	CV306708 t33h11.g
C 11	13.8	69.0	79	7	CV308171 t35b03.b
C 12	13.8	69.0	79	7	CV308172 t35b03.b
C 13	13.8	69.0	100	1	AL595750 AL595750
C 14	13.8	69.0	100	5	CA035542 4001479.B
C 15	13.6	68.0	50	1	AU105199 AU105199
C 16	13.6	68.0	50	1	AU105204 AU105204
C 17	13.6	68.0	50	1	AU105204 AU105204
C 18	13.6	68.0	50	1	AU105205 AU105205
C 19	13.6	68.0	50	1	AU105206 AU105206
C 20	13.6	68.0	50	1	AU105207 AU105207
C 21	13.6	68.0	57	1	AU259073 AU259073
C 22	13.6	68.0	70	1	A1829164 wk76a07.x

23	13.6	68.0	90	10	BX547351
24	13.6	68.0	95	10	CG784638
25	13.4	67.0	59	1	AL800251
26	13.4	67.0	89	10	CM208596
C 27	13.4	67.0	92	11	CR234318
C 28	13.2	66.0	57	10	BX947560
C 29	13.2	66.0	66	1	AV771725
C 30	13.2	66.0	75	11	CR061068
31	13.2	66.0	76	10	CG549951
32	13.2	66.0	88	1	AM028956
33	13.2	66.0	89	4	AK203504
34	13.2	66.0	92	1	AA525968
C 35	13.2	66.0	97	1	A1756476
C 36	13.2	66.0	100	6	CD962144
37	12.8	64.0	46	6	CA968315
38	12.8	64.0	52	1	A1310821
C 39	12.8	64.0	52	8	W90057
C 40	12.8	64.0	57	9	B01045
41	12.8	64.0	57	9	B06891
C 42	12.8	64.0	58	9	AZ767622
C 43	12.8	64.0	69	6	CB221517
C 44	12.8	64.0	78	1	AA958370
45	12.8	64.0	78	10	CL215248

ALIGNMENTS

RESULT 1
LOCUS DR767343/c
DEFINITION ILLUMIGEN MOQ 59763 Katze.MMOV Macaca mulatta cDNA clone
IBIUM:37993 5' similar to Bases 1 to 76 highly similar to human
TRAI (Hs.192374), mRNA sequence.

ACCESSION DR767343
VERSION DR767343
KEYWORDS
SOURCE

ORGANISM Macaca mulatta (rhesus monkey)
Macaca mulatta

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecoidea; Cercopithecinae; Macaca.

1 (bases 1 to 76)
Magnes,C.L., Pellin,P.C., Thomas,M.J., Korth,M.J., Agy,M.B.,
Proff,S.C., Fitzgibbon,M., Scherer,C.A., Miner,D.G., Katze,M.G. and
Iadonato,S.P.

Analysis of the Macaca mulatta transcriptome and the sequence
divergence between Macaca and human
Genome Biol. 6 (7), R60 (2005)

CONTACT: C. Magnes
Contact: C. Magnes
Illumigen Biosciences Inc.

2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408

Email: cmagnes@illumigen.com
Sequenced on 2005.03.23. 76 Q20 bases. Library Preparation: Prof.
Michael Katze lab at University of Washington DNA Sequencing:
Illumigen Biosciences Inc. For further information, see
http://www.macaque.org

PCR Primers
FORWARD: CCTCTACTAAGGACAA
BACKWARD: CACTATAGGCGAATGGTA
Insert Length: 76 Std Error: 0.00
Plate: C1000649 row: E column: 06
Seq primer: CCTCTACTAAGGACAA

POLYA=NO location/Qualifiers

FEATURES
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1..76
/organism="Macaca mulatta"
/mol_type="mRNA"
/strain="Indian"
/db_xref="taxon:9544"

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/clone="IBIUM:37993"
/sex="female"
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/clone_lib="Katze_MM0V"
/notes="Organ: ovary; Vector: pDONR 222; Site_1: Barg I;
Site_2: Barg I; Created from Cloneminer cDNA Library
Construction kit (catalog #18249-029)"
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ORIGIN

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Query Match      79.0%; Score 15.8; DB 8; Length 76;
Best Local Similarity 89.5%; Pred. No. 1.1e+04;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 2 ACCCCAGGGCCTCATGG 20
|||||

Db 40 ACCCAGGGGCCCTCATGG 22

RESULT 2
COS81042/c 81 bp mRNA linear EST 20-JUL-2004
DEFINITION ILLUMIGEN MQC_47838 Katze_MM1L Macaca mulatta cDNA clone
IBIUM:19831 5' similar to Bases 5 to 81 highly similar to human
TRAI (Hs.192374), mRNA sequence.
ACCESSION COS81042
VERSION COS81042.1 GI:50412312
KEYWORDS EST.
SOURCE Macaca mulatta (rhesus monkey)
ORGANISM Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecoidea; Cercopithecinae; Macaca.
1 (bases 1 to 81)
Magnees,C.L., Fellin,P.C., Thomas,M.J., Korth,M.J., Agy,M.B.,
Prohl,S.C., Flitzgibbon,M., Scherer,C.A., Miner,D.G., Katze,W.G. and
Iadonato,S.P.
TITLE Analysis of the Macaca mulatta transcriptome and the sequence
divergence between Macaca and human
Genome Biol. 6 (7), R60 (2005)
15998449
COMMENT Contact: C. Magnees
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagnees@illumigen.com
Sequenced on 2004.06.30. 81 Q20 bases. Library Preparation: Prof.
Michael Katze lab at University of Washington DNA Sequencing:
Illumigen Biosciences Inc. For further information, see
http://www.macaque.org

PCR Primers
FORWARD: CCTCTACTAAGGGAACAATA
BACKWARD: CACTATAGGCGCAATTGGTA
Insert Length: 81 Std Error: 0.00
Plate: CL000436 row: B column: 06
Seq primer: CCTCTACTAAGGGAACAATA
POLYA-No.

FEATURES

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Location/Qualifiers
1..81
/organism="Macaca mulatta"
/mol_type="mRNA"
/strain="indian"
/db_xref="taxon:9544"
/clone="IBIUM:19831"
/sex="male"
/dev stage="adult"
/lab host="Electromax DH10B"
/clone_lib="Katze_MM1L"
/notes="Organ: ileum; Vector: pDONR 222; Site_1: Barg I;
Site_2: Barg I; Created from Cloneminer cDNA Library
Construction kit (catalog #18249-029)"
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ORIGIN

```
Query Match      79.0%; Score 15.8; DB 7; Length 81;
Best Local Similarity 89.5%; Pred. No. 1.1e+04;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Qy 2 ACCCCAGGGCCTCATGG 20
|||||

Db 45 ACCCAGGGGCCCTCATGG 27

RESULT 3

DN390652/c 70 bp mRNA linear EST 07-MAR-2005
LOCUS DN390652
DEFINITION LIB3896-026-Q6-K1-B6 LIB3896 Canis familiaris cDNA clone
LINB893833, mRNA sequence.

ACCESSION DN390652
VERSION DN390652.1 GI:60571873
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;

REFERENCE 1 (bases 1 to 70)
Staten,N.R.
TITLE Direct Submission (Staten,N.R.)
JOURNAL Unpublished (2005)
COMMENT Contact: Nick Staten
Tel: 636 247 6855
Email: nicholas.r.staten@fizer.com.

FEATURES

```
Location/Qualifiers
1..70
/organism="Canis familiaris"
/mol_type="mRNA"
/strain="beagle"
/db_xref="taxon:9615"
/clone="LINB893833"
/tissue_type="skeletal muscle"
/lab host="DH10B"
/clone_lib="LIB3896"
/notes="Vector: pSPORT1; Site_1: SalI; Site_2: NotI;
skeletal muscle"
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ORIGIN

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Query Match      76.0%; Score 15.2; DB 8; Length 70;
Best Local Similarity 85.0%; Pred. No. 2.1e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Qy 1 GACCCAGGGCCTCATGG 20
|||||

Db 27 GACCCAGGGGCCCTCATGG 8

RESULT 4

AZ428700/c 24 bp DNA linear GSS 03-OCT-2000
LOCUS IM0212L16F Mouse 10kb plasmid UUC1M library Mus musculus genomic
DEFINITION clone UUC1M0212L16 F, genomic survey sequence.

ACCESSION AZ428700
VERSION AZ428700.1 GI:10552713
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 24)
Islam,H., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Isiam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2002)
Contact: McCarrey/

Unpublished (2002)
Contact: McCarrey/Eddy NIEHS Mouse
NIEHS Mouse
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
Library constructed and donated by J. McCarrey, Ph.D. (Southwest
Foundation for Biomedical Research, Dept. of Genetics) - exclamation
done by E.M. Eddy, Ph.D. (National Institutes of Health, National
Institute of Environmental Health Sciences).
Seq primer: Primer name ambiguous.
Location/Qualifiers

```

/organism="Mus musculus"
/mol_type="mRNA"
/strain="CD-1"
/db_xref="taxon:10090"
/clone="IMAGE:7033692"
/sex="male"
/tissue_type="Type A spermatogonia, pooled from multiple mice"
/dev_stage="8 day"
/lab_host="DH10B (phage-resistant)"
/clone_lib="McCarrey Eddy type A spermatogonia"
/notes="Organ: testis; Vector: pBlueScript SK+ (Stratagene); Site 1: XhoI; Site 2: EcoRI; cDNA oligo dt-primed [5'-(GA)10-ACTAGCTCGAGTTTATTTT-3'] and directionally cloned using 5' linkers 5'-ATTGCGACGAG-3' and 5'-CTCGGCGG-3'. Size selection of >400bp material gives average insert size ranging from 1-2 kb. Library was mass excised (from lambda-Phi21ap-XR) and resulting single-stranded phagemids were prepared and transformed into DH10B. Library contains 96.5% recombinants. References: J. Androl. 20:635-639 and Gene 25:263-269. Library constructed and donated by J. McCarrey, Ph.D. (Southwest Foundation for Biomedical Research, Dept. of Genetics); excision done by E.M. Eddy, Ph.D. (National Institutes of Health, National Institute of Environmental Health Sciences). Original lambda-based library is available through ATCC, catalog #63416."

```

Query Match	92.0%;	Score 14.4;	DB 7;	Length 96;
Best Local Similarity	73.8%;	Pred. No. 5.2e+04;		
Matches	15;	Conservative	0;	Mismatches 1;
			Indels	0;
			Gaps	0;
5	CCGAGGGCACTCATGG	20		
28	CCGAGGGCACTCATGG	13		

u163g07.y1 Sugano mouse liver mla Mus musculus cDNA clone
IMAGE:1887132.5' similar to gb:M6961 ALPHA-2-HS-GLYCOPROTEIN
PRECURSOR (HUMAN) ; mRNA sequence.

AI304064
AI304064.1 GI:3987814

Mus musculus (house mouse)
Mus musculus
Euharpyota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciuromorphi, Muridae, Murinae, Mus.

1 (bases 1 to 76)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Geisels, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, R., Moore, B., Theising, B., Wyle, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

TITLE	JOURNAL	COMMENT
The MASHU-HHMI Mouse EST Project	Unpublished (1996)	Contact: Marra M/Mouse EST Project

FEATURES

Source

ORIGIN

Query Match	71.0%	Score 14.2	DB 1	Length 76
Best Local Similarity	84.2%	Pred. No. 6.3e+04		
Matches 16	Conservative	0	Mismatches 3	Indels 0
			Gaps	0

Db 31 ACCCCGAGGATGTCATGG 13

RESULT 7			
CO720109/c			
LOCUS	CO720109	94 bp	mRNA
DEFINITION	ta338e07.y1 HyeCh JMY T1 Hydractinia echinata cDNA 5' similar to	linear	EST 27-JUL-2001

FEATURES
source

Source

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Library was constructed by Marcus Frohme and Urr Frank Library
materials provided by Marcus Frohme, German Cancer Research
Center (DKFZ) Heidelberg, Urr Frank, University of Heidelberg
Library re-arrived by Jorge Sozaard (DKFZ) DNA sequencing by:
Washington University Genome Sequencing Center for information
obtaining a clone please contact: Hans Bode (hbode@wustl.edu)
Seq primer: -40RP from Gibco
High quality sequence scop: 94.

ORIGIN

[illegible]

LOCUS DEFINITION	68 bp DNA linear	GSS 17-JUN-2002
CC514177		
CH240_35BP24, TARBAC13P2	CHORI-240 Bos taurus genomic clone	
CH240_35BP24, genomic survey sequence.		

availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.choi.org/bacpac/ordering_information.html). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBMC) by CSIRO Livestock Industries, Australia and the
British Columbia Genome Sciences Centre, Canada.

Plate: 358 row: P column: 24
Seq primer: SP6
Class: BAC ends.

FEATURES

source

Location/Qualifiers

1..68

/organism="Bos taurus"

/mol_type="genomic DNA"

/strain="bred: Hereford"

/db_xref="taxon:9913"

/clone="CH240_358P24"

/sex="Male"

/cell_type="Blood"

/clone_id="CHORI-240"

/note="Vector: pTARBAC1.3; Site 1: Mbol; Site 2: Mbol;

Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC

library (Male) produced by Pieter de Jong"

ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 68;
Best Local Similarity 100.0%; Pred. No. 7.7e+04; Mismatches 0; Indels 0; Gaps 0;

Matches 14; Conservative 0;

QY 1 GACCCCGAGGCAC 14
PUBMED
45 GACCCCGAGGCAC 58

Db

RESULT 9
CV306707/c

LOCUS t133h11.b7 Mouse 5' RACE clones Mus musculus cDNA 5', mRNA
DEFINITION sequence.

CV306707

VERSION CV306707.1 GI:52624040

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

CONTACT: Balija VS

McCombie Laboratory

Cold Spring Harbor Laboratory

500 Sunnyside Blvd, Woodbury, NY 11797, USA

Fax: 516 422 4109

Email: balija@cshl.org

Location/Qualifiers

1..64

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone_id="Mouse 5' RACE clones"

/note="Vector: PCR-TOPO2.1; Cloned 5' RACE fragments

amplified from 5' RACE cDNA generated from 15 pooled mouse

tissues and stages: 7, 11, 15, & 17-day total embryo,

whole brain, eye, kidney, liver, lung, prostate,

submaxillary gland, smooth muscle, spleen, testes and

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Query Match 69.0%; Score 13.8; DB 7; Length 64;
Best Local Similarity 88.2%; Pred. No. 9.5e+04; Mismatches 2; Indels 0; Gaps 0;

Matches 15; Conservative 0;

QY 4 CCCGAGGCACTCATGG 20
PUBMED
41 CACCAAGGCGCCCTCATGG 25

Db

RESULT 10

CV306708

LOCUS t133h11.g7 Mouse 5' RACE clones Mus musculus cDNA 5', mRNA

DEFINITION sequence.

CV306708

VERSION CV306708.1 GI:52624041

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

CONTACT: Balija VS

McCombie Laboratory

Cold Spring Harbor Laboratory

500 Sunnyside Blvd, Woodbury, NY 11797, USA

Fax: 516 422 4109

Email: balija@cshl.org

Location/Qualifiers

1..64

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone_id="Mouse 5' RACE clones"

/note="Vector: PCR-TOPO2.1; Cloned 5' RACE fragments

amplified from 5' RACE cDNA generated from 15 pooled mouse

tissues and stages: 7, 11, 15, & 17-day total embryo,

whole brain, eye, kidney, liver, lung, prostate,

submaxillary gland, smooth muscle, spleen, testes and

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uterus."

Palmer L.E., Hammon G., Zhang M.Q. and McCombe W.R.
The mouse genome: Experimental examination of gene predictions and
transcriptional start sites
Genome Res. 14 (12), 2424-2429 (2004)
15574821
Contact: Balija VS

FEATURES	Location/Qualifiers
source	1. .79

ORIGIN

Query March	69.0%;	Score 13.8;	DB 7;	Length 79;
Best Local Similarity	88.2%;	Pred. No. 9.7e+04;		
Matches 15;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0

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QY      4 CCCCAGGGCACTCATGG  20
          |||||
Db     39 CACCAGGGCCCTCATGG  55

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RESULT 12				
CV308172/c				
LOCUS	CV308172	79 bp	mRNA	linear
DEFINITION	tj50b03.g7 Mouse 5' RACE clones Mus musculus cDNA 5', mRNA			EST 23-SEP-2004

AUTHORS Dike, S., Balija, V.S., Nascimento, L.U., Xuan, Z., Ou, J., Zutavern, T.,

TITLE The mouse genome: Experimental examination of gene predictions and transcriptional start sites
JOURNAL Genome Res. 14 (12), 2424-2429 (2004)

FEATURES	Location/Qualifiers
source	1. .79

Query Match	69.0%;	Score 13.8;	DB 7;	Length 79;
Best Local Similarity	88.2%;	Pred. No. 9.7e+04;		
Matches 15; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

Qy	4	CCCCAGGGCACTCATGG	20
Db	41	CACCAGGGCCCTCATGG	25

RESULT 13	LOCUS	DEFINITION	100 bp	mRNA	linear	EST 19-JUL-2004
AL595750	AL595750	XGC-gastrula	Xenopus	tropicalis	cDNA clone	TGase004g01 5'
		mRNA sequence.				

REFERENCE 1 (bases 1 to 100)
AUTHORS Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
TITLE Sanger xenopus tropicalis EST project 2001 (11_2003)
JOURNAL Unpublished (2003)
COMMENT Contact: Croning MDR

FEATURES

ORIGIN

Query Match	69.0%	Score 13.8;	DB 1;	Length 100;
Best Local Similarity	88.2%	Pred. No. 9.9e+04;		
Matches 15; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0

QY	1	GACCCCGAGGCACTCA	17
Db	41	GGCCCCGGGGCACTCA	57

RESULT 14	CA035542	LOCUS	DEFINITION
CA035542	100 bp	mRNA	linear
4001479	BARC 5BOV Bos taurus CDNA clone 5BOV_78G22 3'	mRNA	EST 24-OCT-2001
sequence.			

ORIGIN

KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus

REFERENCE
AUTHORS Sonstegard, T., Capuco, A.V., White, J., Van Tassel, C.P., and Queckebush, J.
1 (bases 1 to 100)
Sonstegard, T., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D. and Queckebush, J.
Analysis of bovine mammary gland EST and functional annotation of the Bos taurus gene index
Mamm. Genome 13 (7), 373-379 (2002)
12140684

JOURNAL
PUBMED Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tads@psu.barc.usda.gov

COMMENT Single pass sequencing. Bases called and trimmed with phred 0.000925 using options -trim_alt '-trim_fasta. Vector identified by cross match using options -mismatch 12 -minscore 12
Plate: 78 row: G column: 22
Seq primer: CCFAGTCAGACGCTGTAAACG
High quality sequence stop: 100.
Location/Qualifiers
1..100
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/clone="5BOV 78G22"
/issue_type="pooled"
/lab_host="DH10B"
/clone_lib="BARC 5BOV"
/note="Vector: PCMV SPORT6; Site 1: NotI; Site 2: SalI; Library made from pooled mRNA isolated from mammary tissues at eight physiological, developmental, and disease states."

ORIGIN
Query Match 69.0%; Score 13.8; DB 5; Length 100;
Best Local Similarity 88.2%; Pred. No. 9.9e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CCCGAGGCGACTCATGG 20
|||
61 CCCGAGGCGACACTTGG 77

RESULT 15
AUI05199/c 50 bp mRNA linear EST 28-JAN-2004
LOCUS AUI05199 Sugano Homo sapiens CDNA library Homo sapiens CDNA clone
DEFINITION HRC00642, mRNA sequence.
ACCESSION AUI05199
VERSION AUI05199.1 GI:13554720
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 50)
REFERENCE Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isegai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
11375929
JOURNAL
PUBMED Contact: Yutaka Suzuki
COMMENT Department of Virology

Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched CDNA library. Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HRC00642"
/clone_lib="Sugano Homo sapiens CDNA library"

ORIGIN
Query Match 68.0%; Score 13.6; DB 1; Length 50;
Best Local Similarity 80.0%; Pred. No. 1.1e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GACCCCGAGGCGACTCATGG 20
|||
DB 35 GGCTCCGAGGCGCTCCCATGG 16

Search completed: December 24, 2005, 18:28:44
Job time : 1575 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 11:34:25 ; Search time 48.1 Seconds
(without alignments)
739.111 Million cell updates/sec

Title: US-09-296-264-11

Perfect score: 20
Sequence: 1 Gaccccgagcgactcatg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1134872

Minimum DB seq length: 20
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*
1: /cgn2_6/ptodata/1/ina/1 COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5 COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6 COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6 COMB.seq:*
5: /cgn2_6/ptodata/1/ina/6 COMB.seq:*
6: /cgn2_6/ptodata/1/ina/6 COMB.seq:*
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8: /cgn2_6/ptodata/1/ina/6 COMB.seq:*
9: /cgn2_6/ptodata/1/ina/6 COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.4	72.0	39	3	US-09-879-919-16
2	13.6	68.0	25	3	US-09-396-196G-65755
3	13.6	68.0	59	2	US-08-726-012B-5
4	13.4	67.0	25	3	US-09-396-196G-31948
5	13.4	67.0	25	3	US-09-396-196G-31959
6	13.4	67.0	47	3	US-09-423-978-198
7	13.4	67.0	78	3	US-09-938-700-25
8	13.2	66.0	24	3	US-09-005-165-8
9	13.2	66.0	75	3	US-09-060-756-146
10	13.2	66.0	75	3	US-09-670-314-146
11	13.2	66.0	80	3	US-09-282-996-9
12	13.2	66.0	82	3	US-09-282-996-8
13	12.8	64.0	20	3	US-10-031-636-1
14	12.8	64.0	25	3	US-09-305-856B-93
15	12.8	64.0	25	3	US-09-396-196G-56240
16	12.8	64.0	66	3	US-07-728-220C-14
17	12.8	64.0	69	2	US-08-352-179-10
18	12.6	63.0	21	3	US-09-657-472-1188
19	12.6	63.0	25	3	US-09-396-196G-8693
20	12.6	63.0	25	3	US-09-396-196G-8694
21	12.6	63.0	25	3	US-09-396-196G-31248
22	12.6	63.0	25	3	US-09-396-196G-31248
23	12.6	63.0	25	3	US-09-396-196G-86582
24	12.6	63.0	25	3	US-09-396-196G-104877

25	12.6	63.0	25	3	US-09-396-196G-108466	Sequence 108466,
26	12.6	63.0	25	3	US-09-396-196G-108483	Sequence 108483,
27	12.6	63.0	25	3	US-09-396-196G-110802	Sequence 110802,
28	12.6	63.0	25	3	US-09-396-196G-116344	Sequence 116344,
29	12.6	63.0	28	3	US-08-617-874-4	Sequence 4, Appl1
30	12.6	63.0	28	3	US-08-617-874-6	Sequence 6, Appl1
31	12.6	63.0	29	3	US-09-194-285-4	Sequence 4, Appl1
32	12.6	63.0	30	2	US-08-670-175-7	Sequence 7, Appl1
33	12.6	63.0	40	2	US-08-596-187B-39	Sequence 39, Appl1
34	12.6	63.0	40	3	US-09-067-615-39	Sequence 39, Appl1
35	12.6	63.0	40	6	PCT-US95-09816A-39	Sequence 39, Appl1
36	12.6	63.0	45	2	US-08-596-387B-104	Sequence 104, App
37	12.6	63.0	45	3	US-09-067-615-104	Sequence 104, App
38	12.6	63.0	45	6	PCT-US95-09816A-104	Sequence 104, App
39	12.6	63.0	99	3	US-09-513-999C-26781	Sequence 26781, A
40	12.4	62.0	24	2	US-08-288-508C-10	Sequence 10, Appl1
41	12.4	62.0	24	3	US-08-289-222B-20	Sequence 20, Appl1
42	12.4	62.0	24	3	US-09-054-526B-20	Sequence 20, Appl1
43	12.4	62.0	24	3	US-09-386-450D-10	Sequence 10, Appl1
44	12.4	62.0	25	3	US-09-396-196G-54334	Sequence 54334, A
45	12.4	62.0	25	3	US-09-396-196G-54335	Sequence 54335, A

ALIGNMENTS

RESULT 1
US-09-879-919-16/c
; Sequence 16, Application US/09879919
; Patent No. 6541224
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang, et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
; FILE REFERENCE: P7253P1
; CURRENT APPLICATION NUMBER: US/09/879, 919
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/293, 499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277, 978
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/276, 248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/254, 875
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/241, 952
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/211, 537
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 08/815, 783
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: 60/016, 812
; PRIOR FILING DATE: 1996-03-14
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-879-919-16

Query Match 72.0%; Score 14.4; DB 3; Length 39;
Best Local Similarity 93.8%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCGAGGCGACTCATGG 20
DB 32 CCGAGGCGACTCATGG 17

RESULT 2
US-09-396-196G-65755
; Sequence 65755, Application US/09396196G
; Patent No. 6821724

```

; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65755
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
; US-09-396-196G-65755

Query Match          68.0%; Score 13.6; DB 3; Length 25;
Best Local Similarity 80.0%; Pred. No. 4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 GACCCCGAGGCACTCATG 20
    ||||| |||||
Db 2 GACCCCATCGCAGCATCG 21

RESULT 3
US-08-726-012B-5
; Sequence 5, Application US/08726012B
; Patent No. 5952190
; GENERAL INFORMATION:
; APPLICANT: Hans Joenje, et al
; TITLE OF INVENTION: CDNA FOR FANCONI ANEMIA COMPLEMENTATION GROUP A
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh & Whinston, LLP
; STREET: One World Trade Center, Suite 1600, 121 S.W. Salmon Street
; CITY: Portland
; STATE: OR
; COUNTRY: USA
; ZIP: 97204-2988
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3.5-inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: WordPerfect 5.1+, ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/726,012B
; FILING DATE: 10/04/96
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Richard J. Polley
; REGISTRATION NUMBER: 28,107
; REFERENCE/DOCKET NUMBER: 3812-45520/RUP/DUE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 59
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-726-012B-5

Query Match          68.0%; Score 13.6; DB 2; Length 59;
Best Local Similarity 80.0%; Pred. No. 4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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```

Oy 1 GACCCCGAGGCACTCATG 20
    ||||| |||||
Db 27 GACCCCATCGCAGCATCG 46

RESULT 4
US-09-396-196G-31948/C
; Sequence 31948, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31948
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-396-196G-31948

Query Match          67.0%; Score 13.4; DB 3; Length 25;
Best Local Similarity 93.3%; Pred. No. 4.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 5 CCCAGGCACTCATG 19
    ||||| |||||
Db 22 CCTGGGCACTCATG 8

RESULT 5
US-09-396-196G-31959/C
; Sequence 31959, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31959
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-396-196G-31959

Query Match          67.0%; Score 13.4; DB 3; Length 25;
Best Local Similarity 93.3%; Pred. No. 4.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 5 CCCAGGCACTCATG 19
    ||||| |||||
Db 19 CCTGGGCACTCATG 5

RESULT 6
US-09-422-978-198
; Sequence 198, Application US/09422978
```



```
Patent No. 6537751
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CPI
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: US 60/082,614
EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 198
LENGTH: 47
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 24
OTHER INFORMATION: 99-13489-396 : polymorphic base C or T
US-09-422-978-198

Query Match      67.0%; Score 13.4; DB 3; Length 47;
Best Local Similarity 82.4%; Pred. No. 4.9e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy      2 ACCCCAGGCGCACTCAT 18
Db      8 ACAGCCAGGCGCACTCAT 24

RESULT 7
US-09-938-700-25
Sequence 25, Application US/09938700
GENERAL INFORMATION:
APPLICANT: Morsey, et al.
TITLE OF INVENTION: Anti-1GE Vaccines
FILE REFERENCE: PCI0761A
CURRENT APPLICATION NUMBER: US/09/938,700
CURRENT FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 25
LENGTH: 78
TYPE: DNA
ORGANISM: DOG CH3/CH4 NUCLEOTIDE SEQUENCE
US-09-938-700-25

Query Match      67.0%; Score 13.4; DB 3; Length 78;
Best Local Similarity 93.3%; Pred. No. 5e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      5 CCCAGGCGCACTCATG 19
Db      25 CCCAGGCGCCTCATG 39

RESULT 8
US-09-005-165-8/c
Sequence 8, Application US/09005165
GENERAL INFORMATION:
APPLICANT: ROMANO, JOSEPH
APPLICANT: SHURTLEIFF, ROXANNE
APPLICANT: PAL, RANAJIT
TITLE OF INVENTION: ISOTHERMAL TRANSCRIPTION BASED
TITLE OF INVENTION: AMPLIFICATION ASSAY FOR THE DETECTION AND QUANTITATION OF
TITLE OF INVENTION: MACROPHAGE DERIVED CHEMOKINE RNA
```

```
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: AKZO NOBEL PATNT DEPARTMENT
STREET: 1300 PICCARD DRIVE, SUITE 206
CITY: ROCKVILLE
STATE: MARYLAND
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,165
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: KLESNER, SHARON N.
REGISTRATION NUMBER: 36,335
REFERENCE/DOCKET NUMBER: MDC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-948-7400
TELEFAX: 301-948-9751
INFORMATION FOR SRO ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-005-165-8

Query Match      66.0%; Score 13.2; DB 3; Length 24;
Best Local Similarity 83.3%; Pred. No. 6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy      3 CCCCCAGGCGCACTCATG 20
Db      23 CAGCCAGGCGCACTCTGGG 6

RESULT 9
US-09-060-756-146
Sequence 146, Application US/09060756
GENERAL INFORMATION:
APPLICANT: Cole, Stewart
APPLICANT: Buchrieser-Brosch, Roland
APPLICANT: Gordon, Stephen
APPLICANT: Billaault, Alain
TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
FILE REFERENCE: 3495-0169
CURRENT APPLICATION NUMBER: US/09/060,756
CURRENT FILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 743
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 146
LENGTH: 75
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
US-09-060-756-146

Query Match      66.0%; Score 13.2; DB 3; Length 75;
Best Local Similarity 83.3%; Pred. No. 6.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy      2 ACCCCAGGCGCACTCATG 19
Db      30 ACCCCAGGCGCACTCATG 47
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```
RESULT 10
US-09-670-314-146
; Sequence 146, Application US/09670314
; Patent No. 6492506
; GENERAL INFORMATION:
; APPLICANT: Buchrieser-Brosch, Roland
; APPLICANT: Cole, Stewart
; APPLICANT: Gordon, Stephen
; APPLICANT: Billault, Alain
; TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
; TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
; TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
; FILE REFERENCE: 3495-0169
; CURRENT APPLICATION NUMBER: US/09/670,314
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/060,756
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 146
; LENGTH: 75
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-670-314-146

Query Match          66.0%; Score 13.2; DB 3; Length 75;
Best Local Similarity 83.3%; Pred. No. 6.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2  ACCCCGAGGCACTCATG 19
      ||||| ||||| |||||
DB      30  ACCCCGAGGCACTCATG 47

RESULT 11
US-09-282-996-9/c
; Sequence 9, Application US/09282996
; Patent No. 6143502
; GENERAL INFORMATION:
; APPLICANT: Grentzmann, Guido
; APPLICANT: Gesteland, Raymond F.
; APPLICANT: Atkins, John F.
; TITLE OF INVENTION: Dual-Luciferase Reporter System
; FILE REFERENCE: T5864.NP
; CURRENT APPLICATION NUMBER: US/09/282,996
; CURRENT FILING DATE: 1999-03-31
; EARLIER APPLICATION NUMBER:
; EARLIER FILING DATE:
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: WordPerfect 8.0
; SEQ ID NO 9
; LENGTH: 80
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide Luc12
US-09-282-996-9

Query Match          66.0%; Score 13.2; DB 3; Length 80;
Best Local Similarity 83.3%; Pred. No. 6.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      3  CCCCCGAGGCACTCATG 20
      ||||| ||||| |||||
DB      50  CCCCCGAGGCACTCATG 33

RESULT 12
US-09-282-996-8
; Sequence 8, Application US/09282996
; Patent No. 6143502
; GENERAL INFORMATION:
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; APPLICANT: Grentzmann, Guido
; APPLICANT: Gesteland, Raymond F.
; APPLICANT: Atkins, John F.
; TITLE OF INVENTION: Dual-Luciferase Reporter System
; FILE REFERENCE: T5864.NP
; CURRENT APPLICATION NUMBER: US/09/282,996
; CURRENT FILING DATE: 1999-03-31
; EARLIER APPLICATION NUMBER:
; EARLIER FILING DATE:
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: WordPerfect 8.0
; SEQ ID NO 8
; LENGTH: 82
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide Luc1
US-09-282-996-8

Query Match          66.0%; Score 13.2; DB 3; Length 82;
Best Local Similarity 77.8%; Pred. No. 6.1e+03;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      3  CCCCCGAGGCACTCATG 20
      ||||| ||||| |||||
DB      35  CCCCCGAGGCACTCATG 52

RESULT 13
US-10-031-636-1
; Sequence 1, Application US/10031636
; Patent No. 6794140
; GENERAL INFORMATION:
; APPLICANT: Cyclope Genome Sciences Limited
; APPLICANT: Goldsborough, Andrew S.
; TITLE OF INVENTION: ISOLATION OF NUCLEIC ACID
; FILE REFERENCE: US2.GOLDSBOROUGH
; CURRENT APPLICATION NUMBER: US/10/031,636
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: UK 9910154.5
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: UK 9910157.8
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: UK 9910156.0
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: UK 9910158.6
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Brome Mosaic Virus (BMV)
; FEATURE:
; NAME/KEY: primer bind
; LOCATION: (1)..(20)
US-10-031-636-1

Query Match          64.0%; Score 12.8; DB 3; Length 20;
Best Local Similarity 87.5%; Pred. No. 9.2e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  GACCCGAGGCACTC 16
      ||||| ||||| |||||
DB      1  GACCCGAGGCACTC 16

RESULT 14
US-09-305-856B-93
; Sequence 93, Application US/09305856B
; Patent No. 6479236
; GENERAL INFORMATION:
; APPLICANT: Penny, Laura
```

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; APPLICANT: Galvin, Margaret
; TITLE OF INVENTION: Genotyping the Human
; FILE REFERENCE: UDP-Glucuronosyltransferase 1 (UGT1) Gene
; CURRENT APPLICATION NUMBER: US/09/305,856B
; CURRENT FILING DATE: 1999-05-05
; PRIOR APPLICATION NUMBER: 60/084,807
; PRIOR FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 93
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-305-856B-93

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Query Match          64.0%; Score 12.8; DB 3; Length 25;
Best Local Similarity 87.5%; Pred. No. 9.2e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY      4 CCCCAGGCGACTCATG 19
          |||||  |||||
Db      3 CCCCAGGCCAATCATG 18

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RESULT 15
US-09-396-196G-56240/C
; Sequence 56240, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittleman
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56240
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-56240

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Query Match          64.0%; Score 12.8; DB 3; Length 25;
Best Local Similarity 87.5%; Pred. No. 9.2e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY      1 GACCCCGAGGCGACTC 16
          |||||  |||||
Db      20 GACTCCGAGGCGCTCTC 5

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Search completed: December 24, 2005, 18:36:30
 Job time : 48.1 secs

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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 14:06:30 ; Search time 337.6 Seconds
(without alignments)
489.892 Million cell updates/sec

Title: US-09-296-264-11

Perfect score: 20

Sequence: 1 gaccccgagcgcactcgtg 20

Scoring table: IDENTITY_NUC

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 9887334

Minimum DB seq length: 20
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA Main:

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10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3	US-09-296-264-11
2	16.8	84.0	25	9	US-10-956-157-229257
3	16	80.0	20	3	US-09-296-264-20
4	15.8	79.0	25	7	US-10-719-956-416913
5	15.8	79.0	25	7	US-10-719-956-580760
6	15.8	79.0	25	10	US-11-036-317-131184
7	15.8	79.0	25	10	US-11-036-317-755963
8	15.8	79.0	25	10	US-11-036-317-836367
9	15.4	77.0	25	10	US-11-036-317-33549
10	15.4	77.0	25	10	US-11-036-317-61202
11	15.2	76.0	60	3	US-09-908-975-7302
12	14.8	74.0	25	10	US-11-036-317-57475
13	14.4	72.0	20	7	US-10-671-074-1174
14	14.4	72.0	25	10	US-11-036-317-88768
15	14.4	72.0	39	3	US-09-879-919-16
16	14.4	72.0	39	6	US-10-268-951-16
17	14.2	71.0	25	7	US-10-719-956-94275
18	14.2	71.0	25	7	US-10-719-956-350836
19	14.2	71.0	25	7	US-10-719-956-416914
20	14.2	71.0	25	7	US-10-719-956-580759
21	14.2	71.0	25	8	US-10-719-900-373673
22	14.2	71.0	25	8	US-10-719-900-394801
23	14.2	71.0	25	9	US-10-956-157-183204

24	14.2	71.0	25	10	US-11-036-317-49011	Sequence 49011, A
25	14.2	71.0	25	10	US-11-036-317-262309	Sequence 262309, A
26	14.2	71.0	25	10	US-11-036-317-364550	Sequence 364550, A
27	14.2	71.0	25	10	US-11-036-317-516353	Sequence 516353, A
28	14.2	71.0	25	10	US-11-036-317-755962	Sequence 755962, A
29	14.2	71.0	25	10	US-11-036-317-836366	Sequence 836366, A
30	14.2	71.0	60	3	US-09-908-975-11924	Sequence 31924, A
31	14.2	71.0	80	9	US-10-971-736-56	Sequence 56, App
32	14	70.0	20	7	US-10-671-074-163	Sequence 163, App
33	14	70.0	25	7	US-10-719-956-239339	Sequence 239339, A
34	14	70.0	25	8	US-10-719-900-258242	Sequence 258242, A
35	14	70.0	25	10	US-11-060-756-194883	Sequence 194883, A
36	14	70.0	25	10	US-11-060-756-194884	Sequence 194884, A
37	13.8	69.0	25	7	US-10-719-956-80800	Sequence 80800, A
38	13.8	69.0	25	7	US-10-719-956-203307	Sequence 203307, A
39	13.8	69.0	25	8	US-10-719-900-460659	Sequence 460659, A
40	13.8	69.0	25	8	US-10-719-900-479930	Sequence 479930, A
41	13.8	69.0	25	10	US-11-036-317-339780	Sequence 339780, A
42	13.8	69.0	25	10	US-11-036-317-385058	Sequence 385058, A
43	13.8	69.0	80	7	US-10-384-245-165	Sequence 165, App
44	13.8	69.0	100	7	US-10-242-535A-12117	Sequence 12117, A
45	13.8	69.0	100	7	US-10-085-783A-12117	Sequence 12117, A

ALIGNMENTS

```
RESULT 1
US-09-296-264-11
Sequence 11, Application US/09296264
GENERAL INFORMATION:
APPLICANT: WRIGHT, Jim A.
APPLICANT: YOUNG, Aiping H.
TITLE OF INVENTION: NEUROPELIN ANTISENSE OLIGONUCLEOTIDE SEQUENCES AND
TITLE OF INVENTION: METHODS OF USING SAME TO MODULATE CELL GROWTH
FILE REFERENCE: 023396-043
CURRENT APPLICATION NUMBER: US/09/296,264
CURRENT FILING DATE: 1999-04-22
EARLIER APPLICATION NUMBER: US 60/082,791
EARLIER FILING DATE: 1998-04-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 20
TYPE: DNA
ORGANISM: Human
US-09-296-264-11

Query Match      100.0%; Score 20; DB 3; Length 20;
Best local Similarity 100.0%; Pred. No. 8.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 GACCCCGAGCCTCATGG 20
Db      1 GACCCCGAGCCTCATGG 20

RESULT 2
US-10-956-157-229257
Sequence 229257, Application US/10956157
GENERAL INFORMATION:
APPLICANT: Wyeach
APPLICANT: Mounts, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOCARTRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: PatentIn version 3.2
```

; SEQ ID NO 229257
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-229257

Query Match 84.0%; Score 16.8; DB 9; Length 25;
Best Local Similarity 90.0%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GACCCCGAGGCACTCATG 20
|||||
Db 1 GACCCCGAGGCACTCATG 20

RESULT 3
; Sequence 20, Application US/09296264
; Publication No. US20030083274A1
; GENERAL INFORMATION:
; APPLICANT: WRIGHT, Jim A.
; APPLICANT: YOUNG, Aiping H.
; APPLICANT: LEE, Yoon S.
; TITLE OF INVENTION: NEUROFILIN ANTISENSE OLIGONUCLEOTIDE SEQUENCES AND
; FILE REFERENCE: 032396-043
; CURRENT FILING DATE: 1999-04-22
; EARLIER FILING DATE: 1998-04-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 20
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Human
US-09-296-264-20

Query Match 80.0%; Score 16; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCCAGGCACTCATG 20
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Db 1 CCCAGGCACTCATG 16

RESULT 4
; Sequence 416913, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT FILING DATE: 2003-11-20
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 416913
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-416913

Query Match 79.0%; Score 15.8; DB 7; Length 25;
Best Local Similarity 89.5%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GACCCCGAGGCACTCATG 19
|||||

Db 7 GACCTCCAGGCACTCATG 25

RESULT 5
; Sequence 580760, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT FILING DATE: 2003-11-20
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 580760
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-580760

Query Match 79.0%; Score 15.8; DB 7; Length 25;
Best Local Similarity 89.5%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GACCCCGAGGCACTCATG 19
|||||
Db 20 GACCCCGAGGCACTCATG 2

RESULT 6
; Sequence 131184, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT FILING DATE: 2005-01-13
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 131184
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-131184

Query Match 79.0%; Score 15.8; DB 10; Length 25;
Best Local Similarity 89.5%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GACCCCGAGGCACTCATG 19
|||||
Db 24 GACCTCCAGGCACTCATG 6

RESULT 7
; Sequence 755963, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT FILING DATE: 2005-01-13

PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 755963
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-755963

Query Match 79.0%; Score 15.8; DB 10; Length 25;
Best Local Similarity 89.5%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GACCCCGAGGCGACTCATG 19
DB 24 GACCTCGAGGCGACTCTTG 6

RESULT 8
US-11-036-317-836367/C

Sequence 836367, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 836367
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-836367

Query Match 79.0%; Score 15.8; DB 10; Length 25;
Best Local Similarity 89.5%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ACCCCGAGGCGACTCATG 20
DB 23 ACCCGAGGCGACTCATG 5

RESULT 9
US-11-036-317-33549

Sequence 33549, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 33549
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-33549

Query Match 77.0%; Score 15.4; DB 10; Length 25;
Best Local Similarity 94.1%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCCGAGGCGACTCATG 20
DB 9 CCCGAGGCGACTCATG 25

RESULT 10
US-11-036-317-61202

Sequence 61202, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 61202
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-61202

Query Match 77.0%; Score 15.4; DB 10; Length 25;
Best Local Similarity 94.1%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCCGAGGCGACTCATG 20
DB 4 CCCGAGGCGACTCATG 20

RESULT 11
US-09-908-975-7302/C

Sequence 7302, Application US/09908975
Publication No. US20030165843A1
GENERAL INFORMATION:
APPLICANT: SHOSHAN, Avi
APPLICANT: MASSEMAN, Alon
APPLICANT: MINTZ, Eli
APPLICANT: FAIGLER, Simchon
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
FILE REFERENCE: 36688-0005
CURRENT APPLICATION NUMBER: US/09/908,975
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/221,607
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 32337
SOFTWARE: PatentIn version 3.0
SEQ ID NO 7302
LENGTH: 60
TYPE: DNA
ORGANISM: Homo sapiens
US-09-908-975-7302

Query Match 76.0%; Score 15.2; DB 3; Length 60;
Best Local Similarity 85.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GACCCCGAGGCGACTCATG 20
DB 46 GACCTCGAGGCGACTCATG 27

RESULT 12

```
US-11-036-317-57475/c
; Sequence 57475, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; PRIOR FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; NUMBER OF SEQ ID NOS: 2004-01-13
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 57475
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-57475
```

```
Query Match          74.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 88.9%; Pred. No. 2.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2 ACCCCGAGGCACTCATG 19
Db 25 ACCCCGAGGCACTCATG 8
```

RESULT 13

```
US-10-671-074-174
; Sequence 174, Application US/10671074
; Publication No. US20040097459A1
; GENERAL INFORMATION:
; APPLICANT: Dodie, Kenneth W.
; APPLICANT: Bhanot, Sanjay
; APPLICANT: Veniant-Elison, Murielle
; APPLICANT: Lindberg, Richard A.
; APPLICANT: Shuter, John R.
; TITLE OF INVENTION: MODULATION OF FORKHEAD BOX O1A EXPRESSION
; FILE REFERENCE: AMGN001-101
; CURRENT APPLICATION NUMBER: US/10/671,074
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: US 10/260,203
; PRIOR FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 176
; SEQ ID NO 174
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-671-074-174
```

```
Query Match          72.0%; Score 14.4; DB 7; Length 20;
Best Local Similarity 93.8%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 3 CCCCGAGGCACTCAT 18
Db 1 CCCCGAGGCACTCAT 16
```

RESULT 14

```
US-11-036-317-88788/c
; Sequence 88788, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
```

```
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 88788
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-88788
```

```
Query Match          72.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%; Pred. No. 4.2e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 4 CCCCGAGGCACTCATG 19
Db 16 CTCGAGGCACTCATG 1
```

RESULT 15

```
US-09-879-919-16/c
; Sequence 16, Application US/09879919
; Patent No. US20020064829A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang, et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
; FILE REFERENCE: PEP53P1
; CURRENT APPLICATION NUMBER: US/09/879,919
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,978
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/254,875
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/241,952
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/211,537
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 08/815,783
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: 60/016,812
; PRIOR FILING DATE: 1996-03-14
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-879-919-16
```

```
Query Match          72.0%; Score 14.4; DB 3; Length 39;
Best Local Similarity 93.8%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 5 CCCAGGCACTCATGG 20
Db 32 CCCAGGCACTCATGG 17
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Search completed: December 25, 2005, 04:14:25
Job time : 338.6 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 18:29:07 ; Search time 135.3 Seconds
(without alignments)
76.712 Million cell updates/sec

Title: US-09-296-264-11

Perfect score: 20
Sequence: 1 gacccccagggcactcatg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4168288 seqs, 259477437 residues

Total number of hits satisfying chosen parameters: 1608458

Minimum DB seq length: 20
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA New:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14.2	71.0	25	US-11-121-849-322903	Sequence 322903,
2	13.6	68.0	25	US-11-121-849-215831	Sequence 215831,
3	13.6	68.0	25	US-11-121-849-242774	Sequence 242774,
4	13.4	67.0	25	US-11-121-849-453616	Sequence 453616,
5	13.4	67.0	30	US-10-857-780-231	Sequence 231, App
6	13.2	66.0	25	US-11-121-849-29381	Sequence 29381, A
7	13.2	66.0	25	US-11-121-849-242451	Sequence 242451,
8	13.2	66.0	25	US-11-121-849-257893	Sequence 257893,
9	13.2	66.0	25	US-11-121-849-257894	Sequence 257894,
10	13.2	66.0	25	US-11-121-849-281463	Sequence 281463,
11	13.2	66.0	25	US-11-121-849-322904	Sequence 322904,
12	13.2	66.0	25	US-11-121-849-339761	Sequence 339761,
13	13.2	66.0	25	US-11-121-849-529808	Sequence 529808,
14	13.2	66.0	25	US-11-121-849-579848	Sequence 579848,
15	13.2	66.0	20	US-10-802-796-146	Sequence 146, App
16	13.2	65.0	20	US-11-111-288-42	Sequence 42, App
17	13.2	65.0	25	US-11-121-849-13517	Sequence 13517, A
18	13.2	65.0	25	US-11-121-849-20003	Sequence 20003, A
19	13.2	65.0	25	US-11-121-849-134267	Sequence 134267,
20	13.2	65.0	25	US-11-121-849-322063	Sequence 322063,
21	13.2	65.0	25	US-11-121-849-389089	Sequence 389089,
22	13.2	65.0	25	US-11-121-849-486563	Sequence 486563,
23	12.8	64.0	20	US-11-057-808A-1	Sequence 1, Appli

24	12.8	64.0	25	US-11-121-849-4736	Sequence 4736, Ap
25	12.8	64.0	25	US-11-121-849-44648	Sequence 44648, A
26	12.8	64.0	25	US-11-121-849-81862	Sequence 81862, A
27	12.8	64.0	25	US-11-121-849-85032	Sequence 85032, A
28	12.8	64.0	25	US-11-121-849-102642	Sequence 102642,
29	12.8	64.0	25	US-11-121-849-451815	Sequence 451815,
30	12.8	64.0	32	US-10-939-294A-15871	Sequence 15871, A
31	12.8	64.0	32	US-10-939-294A-17408	Sequence 17408, A
32	12.8	64.0	32	US-10-939-294A-18881	Sequence 18881, A
33	12.6	63.0	21	US-10-831-997-1188	Sequence 11880, A
34	12.6	63.0	25	US-11-121-849-44860	Sequence 44860, A
35	12.6	63.0	25	US-11-121-849-110613	Sequence 110613,
36	12.6	63.0	25	US-11-121-849-127925	Sequence 127925,
37	12.6	63.0	25	US-11-121-849-282667	Sequence 282666,
38	12.6	63.0	25	US-11-121-849-346687	Sequence 346687,
39	12.6	63.0	25	US-11-121-849-429253	Sequence 429253,
40	12.6	63.0	25	US-11-121-849-604445	Sequence 604445,
41	12.6	63.0	25	US-11-121-849-653664	Sequence 653664,
42	12.6	63.0	26	US-11-069-908-2184	Sequence 2184, Ap
43	12.6	63.0	26	US-11-069-908-4550	Sequence 4550, Ap
44	12.6	63.0	30	US-10-850-359-957	Sequence 957, App
45	12.4	62.0	25	US-11-121-849-25269	Sequence 25269, A

ALIGNMENTS

```
RESULT 1
US-11-121-849-322903/c
; Sequence 322903, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 322903
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-322903

Query Match      71.0% Score 14.2; DB 7; Length 25;
Best Local Similarity 84.2% Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GACCCCGAGGCACTCATG 19
Db      20 GACGTCAGGCGACACATG 2

RESULT 2
US-11-121-849-215831
; Sequence 215831, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 215831
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/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-11-121-849-215831

Query Match 68.0%; Score 13.6; DB 7; Length 25;
Best Local Similarity 80.0%; Pred. No. 8.8e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GACCCCGAGGCACTCATG 20
DB 5 GAGTCCAGGCGATTTCAGG 24

RESULT 3
US-11-121-849-242774
/ Sequence 242774, Application US/11121849
/ Publication No. US20050272080A1
/ GENERAL INFORMATION:
/ APPLICANT: John Palma
/ TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
/ FILE REFERENCE: 3684.1
/ CURRENT APPLICATION NUMBER: US/11/121,849
/ CURRENT FILING DATE: 2005-05-03
/ PRIOR APPLICATION NUMBER: 60/567,949
/ PRIOR FILING DATE: 2004-05-03
/ NUMBER OF SEQ ID NOS: 673904
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 242774
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-11-121-849-242774

Query Match 68.0%; Score 13.6; DB 7; Length 25;
Best Local Similarity 80.0%; Pred. No. 8.8e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GACCCCGAGGCACTCATG 20
DB 4 GATCCCGCGGCTCTCATG 23

RESULT 4
US-11-121-849-453616/c
/ Sequence 453616, Application US/11121849
/ Publication No. US20050272080A1
/ GENERAL INFORMATION:
/ APPLICANT: John Palma
/ TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
/ FILE REFERENCE: 3684.1
/ CURRENT APPLICATION NUMBER: US/11/121,849
/ CURRENT FILING DATE: 2005-05-03
/ PRIOR APPLICATION NUMBER: 60/567,949
/ PRIOR FILING DATE: 2004-05-03
/ NUMBER OF SEQ ID NOS: 673904
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 453616
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-11-121-849-453616

Query Match 67.0%; Score 13.4; DB 7; Length 25;
Best Local Similarity 93.3%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ACCCCGAGGCACTC 16
DB 23 ACCCACAGGCGACTC 9

RESULT 5
US-10-857-780-231
/ Sequence 231, Application US/10857780
/ Publication No. US20050272043A1
/ GENERAL INFORMATION:
/ APPLICANT: ROTH, RICHARD B.
/ APPLICANT: BRAUN, ANDREAS
/ APPLICANT: KAMMERER, STEFAN M.
/ APPLICANT: NELSON, MATTHEW ROBERTS
/ APPLICANT: RENEKAND, RIKARD HENRY
/ APPLICANT: HOYAL-WRIGHTSON, CAROLYN R.
/ TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF BREAST CANCER AND TREATMENTS
/ FILE REFERENCE: SEQ-4069-CP
/ CURRENT APPLICATION NUMBER: US/10/857,780
/ CURRENT FILING DATE: 2004-05-28
/ PRIOR APPLICATION NUMBER: 10/723,681
/ PRIOR FILING DATE: 2003-11-25
/ PRIOR APPLICATION NUMBER: 60/490,234
/ PRIOR FILING DATE: 2003-07-24
/ PRIOR APPLICATION NUMBER: 60/525,239
/ PRIOR FILING DATE: 2003-11-25
/ NUMBER OF SEQ ID NOS: 4962
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 231
/ LENGTH: 30
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic primer
US-10-857-780-231

Query Match 67.0%; Score 13.4; DB 6; Length 30;
Best Local Similarity 93.3%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCCAGGCGACTCATG 19
DB 16 CCTCGGCGACTCATG 30

RESULT 6
US-11-121-849-29381/c
/ Sequence 29381, Application US/11121849
/ Publication No. US20050272080A1
/ GENERAL INFORMATION:
/ APPLICANT: John Palma
/ TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
/ FILE REFERENCE: 3684.1
/ CURRENT APPLICATION NUMBER: US/11/121,849
/ CURRENT FILING DATE: 2005-05-03
/ PRIOR APPLICATION NUMBER: 60/567,949
/ PRIOR FILING DATE: 2004-05-03
/ NUMBER OF SEQ ID NOS: 673904
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 29381
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-11-121-849-29381

Query Match 66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GACCCCGAGGCACTCAT 18
DB 21 GACTCCAGAGCACCCAT 4

RESULT 7

```
US-11-121-849-242451/C
; Sequence 242451, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 242451
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-242451
Query Match      66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy      2  ACCCCAGGAGCACTCATG 19
Db      20 ACCCAGGAGCACTCATG 3

RESULT 8
US-11-121-849-257893
; Sequence 257893, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 257893
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-257893
Query Match      66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy      3  CCCCCAGGAGCACTCATG 20
Db      5  CCTCAGGAGCACTCATG 22

RESULT 9
US-11-121-849-257894
; Sequence 257894, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 257894
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-322904/C
; Sequence 322904, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 322904
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-322904
Query Match      66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy      1  GACCCAGGAGCACTCAT 18
Db      1  GACCCAGGAGCACTCAT 18

RESULT 10
US-11-121-849-281463/C
; Sequence 281463, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 281463
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-281463
Query Match      66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy      3  CCCCCAGGAGCACTCATG 20
Db      23 CCCCCAGGAGCACTCATG 6

RESULT 11
US-11-121-849-322904/C
; Sequence 322904, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 322904
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-322904
Query Match      66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy      1  GACCCAGGAGCACTCAT 18
Db      1  GACCCAGGAGCACTCAT 18
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Db 18 GACGTCAGGCGACACAT 1

RESULT 12
US-11-121-849-339761/C
; Sequence 339761, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 339761
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-339761

Query Match 66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 CCCCCAGGCGACTCATG 20
DB 25 CCACGAGGCGCATGATG 8

RESULT 13
US-11-121-849-529808/C
; Sequence 529808, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 529808
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-529808

Query Match 66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ACCCCAGGCGACTCATG 19
DB 24 AGCCACAGGCGACTCATG 7

RESULT 14
US-11-121-849-579848/C
; Sequence 579848, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849

; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 579848
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-579848

Query Match 66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GACCCGAGGCGACTCAT 18
DB 18 GACCCGAGGCGTTCAT 1

RESULT 15
US-10-802-796-146
; Sequence 146, Application US/10802796
; Publication No. US20050250104A1
; GENERAL INFORMATION:
; APPLICANT: COLE, STEWART
; APPLICANT: BUCHRIER-BROSCH, ROLAND
; APPLICANT: GORDON, STEPHEN
; APPLICANT: BILLAUT, ALAIN
; TITLE OF INVENTION: A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST
; TITLE OF INVENTION: FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED
; FILE REFERENCE: 05394.0011-00000
; CURRENT APPLICATION NUMBER: US/10/802,796
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/09/673,476
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: PCT/IB99/00740
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 09/060,756
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
; SOFTWARE: Patent In Ver. 2.2
; SEQ ID NO 146
; LENGTH: 75
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-802-796-146

Query Match 66.0%; Score 13.2; DB 6; Length 75;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ACCCCAGGCGACTCATG 19
DB 30 ACCCCAGGCGACTCATG 47

Search completed: December 25, 2005, 04:37:04
Job time : 135.3 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 10:28:41 ; Search time 582 Seconds
(without alignments)
1953.383 Million cell updates/sec

Title: US-09-296-264-12

Perfect score: 20
Sequence: 1 cgacccacagacagaccccc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 1858228

Minimum DB seq length: 20
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ba: *
2: gb_in: *
3: gb_env: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pr: *
9: gb_ro: *
10: gb_scs: *
11: gb_sy: *
12: gb_un: *
13: gb_vi: *
14: gb_htg: *
15: gb_pl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	BD211669	BD211669 Antisense
2	14.4	72.0	60	CQ549205	CQ549205 Sequence
3	14.2	71.0	22	AX663589	AX663589 Sequence
4	14.2	71.0	37	AX527714	AX527714 Sequence
5	14.2	71.0	60	AR035484	AR035484 Sequence
6	13.8	69.0	25	AR003361	AR003361 Sequence
7	13.8	69.0	30	AR261574	AR261574 Sequence
8	13.6	68.0	22	AR643896	AR643896 Sequence
9	13.6	68.0	26	AR168794	AR168794 Sequence
10	13.6	68.0	26	AR168799	AR168799 Sequence
11	13.6	68.0	26	AR168801	AR168801 Sequence
12	13.6	68.0	26	127788	127788 Sequence 20
13	13.6	68.0	26	127793	127793 Sequence 25
14	13.6	68.0	26	127795	127795 Sequence 27
15	13.6	68.0	26	AR200263	AR200263 Sequence
16	13.6	68.0	26	AR200268	AR200268 Sequence
17	13.6	68.0	26	AR200270	AR200270 Sequence
18	13.6	68.0	26	AR262395	AR262395 Sequence

c 19	13.6	68.0	26	6	AR262400	AR262400 Sequence
c 20	13.6	68.0	26	6	AR262402	AR262402 Sequence
c 21	13.6	68.0	45	6	AR168795	AR168795 Sequence
c 22	13.6	68.0	45	6	AR168796	AR168796 Sequence
c 23	13.6	68.0	45	6	BD247106	BD247106 Improved
c 24	13.6	68.0	45	6	127789	127789 Sequence 21
c 25	13.6	68.0	45	6	127790	127790 Sequence 22
c 26	13.6	68.0	45	6	AR200264	AR200264 Sequence
c 27	13.6	68.0	45	6	AR200265	AR200265 Sequence
c 28	13.6	68.0	45	6	AR262396	AR262396 Sequence
c 29	13.6	68.0	45	6	AR262397	AR262397 Sequence
c 30	13.6	68.0	60	8	CQ559333	CQ559333 Sequence
c 31	13.6	68.0	80	8	HSD58347	X64597 H. sapiens D
c 32	13.6	68.0	87	6	BD034159	BD034159 Sequence
c 33	13.6	68.0	87	6	AX282658	AX282658 Sequence
c 34	13.6	68.0	87	6	AX898626	AX898626 Sequence
c 35	13.4	67.0	32	6	AR083991	AR083991 Sequence
c 36	13.4	67.0	60	6	CQ535410	CQ535410 Sequence
c 37	13.2	66.0	27	6	AR063107	AR063107 Sequence
c 38	13.2	66.0	27	6	AR122634	AR122634 Sequence
c 39	13.2	66.0	27	6	AR164262	AR164262 Sequence
c 40	13.2	66.0	27	6	AR208934	AR208934 Sequence
c 41	13.2	66.0	27	6	AR342234	AR342234 Sequence
c 42	13.2	66.0	27	6	AR381255	AR381255 Sequence
c 43	13.2	66.0	27	6	AR383156	AR383156 Sequence
c 44	13.2	66.0	27	6	AR404923	AR404923 Sequence
c 45	13.2	66.0	27	6	AR438591	AR438591 Sequence

ALIGNMENTS

RESULT 1
BD211669
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
ORIGIN

BD211669 20 bp DNA linear PAT 17-JUN-2003
Antisense oligonucleotide sequence of neuropilin and method of
using the same for controlling cell proliferation.
BD211669
BD211669.1 GI:33021439
JP 2002512793-A/12.
Homo sapiens (human)
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 20)
Wright,J.A., Young,A.H. and Lee,Y.S.
Antisense oligonucleotide sequence of neuropilin and method of
using the same for controlling cell proliferation
Patent: JP 2002512793-A 12 08-MAY-2002;
GENENSER TECHNOLOGIES INC
OS Homo sapiens (human)
PN JP 2002512793-A/12
PD 08-MAY-2002
PF 23-APR-1999 JP 2000545999
PR 23-APR-1998 US 60/082791
PI UIM A WRIGHT, AIPING H YOUNG, YOON S LEE
PC C12N15/09,A61K31/711,A61K48/00,A61P35/00,C12N15/00 CC
Antisense oligonucleotide sequence of neuropilin and method of
using the
CC same for controlling cell proliferation
FH key Location/Qualifiers
FT source 1..20 Location/Qualifiers
FT 1..20 Location/Qualifiers
1..20 Location/Qualifiers
/organism="Homo sapiens (human)".
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 76;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGACCCACAGAGCCCC 20
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Db 1 CGACCCACAGAGCCCC 20

RESULT 2
COS49205 60 bp DNA linear PAT 30-JAN-2004
LOCUS Sequence 18840 from Patent WO0210449.
DEFINITION COS49205
ACCESSION COS49205.1 GI:41515632
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.

REFERENCE 1
Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
TITLE Oligonucleotide library for detecting rna transcripts and splice
variants that populate a transcritome
JOURNAL Patent: WO 0210449-A 18840 07-FEB-2002;
Comugen Inc. (US)

FEATURES
source
1..60
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 72.0%; Score 14.4; DB 6; Length 60;
Best Local Similarity 93.8%; Pred. No. 3.6e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGACCCACAGAGCAGC 16
|||||
Db 31 CGACCCACAGAGCTGC 46

RESULT 3
AX663589/c 22 bp DNA linear PAT 22-MAR-2003
LOCUS AX663589
DEFINITION Sequence 19 from Patent WO02092850.
ACCESSION AX663589
VERSION AX663589.1 GI:29163808
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
Algaigha,O.M. and Ralston,S.H.
AUTHORS Diagnostic method for osteoporosis and related disorders
TITLE Patent: WO 02092850-A 19 21-NOV-2002;
JOURNAL The University Court of The University of Aberdeen (GB)

FEATURES
source
1..22
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

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Query Match 71.0%; Score 14.2; DB 6; Length 22;
Best Local Similarity 84.2%; Pred. No. 5e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGACCCACAGAGCCCC 19
|||||
Db 19 CGACCCACTCTCAGCCCC 1

RESULT 4
AX527714/c 37 bp DNA linear PAT 21-NOV-2002
LOCUS AX527714
DEFINITION Sequence 86 from Patent WO0228408.
ACCESSION AX527714
VERSION AX527714.1 GI:25172254
KEYWORDS
SOURCE Murinae gen. sp.
ORGANISM Murinae gen. sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae.

REFERENCE 1
Houston,L.L., Sheridan,P.J., Hawley,S., Glynn,J.M., Chapin,S. and
Baer,A.
TITLE Compositions and methods for the transport of biologically active
agents across cellular barriers
JOURNAL Patent: WO 0228408-A 86 11-APR-2002;
ARIZEKE PHARMACEUTICALS, INC. (US)

FEATURES
source
1..37
/organism="Murinae gen. sp."
/mol_type="unassigned DNA"
/db_xref="taxon:38108"

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Query Match 71.0%; Score 14.2; DB 6; Length 37;
Best Local Similarity 84.2%; Pred. No. 4.8e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GACCCACAGAGCCCC 20
|||||
Db 28 GACGCCACAGAAAGCCCC 10

RESULT 5
AR035484 60 bp DNA linear PAT 29-SEP-1999
LOCUS AR035484
DEFINITION Sequence 56 from patent US 5871902.
ACCESSION AR035484
VERSION AR035484.1 GI:5952152
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 60)
Weininger,S. and Weininger,A.M.
AUTHORS Sequence-specific detection of nucleic acid hybrids using a
TITLE DNA-binding molecule or assembly capable of discriminating perfect
JOURNAL hybrids from non-perfect hybrids
PATENT: US 5871902-A 56 16-FEB-1999;
LOCATION/Qualifiers

FEATURES
source
1..60
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 71.0%; Score 14.2; DB 6; Length 60;
Best Local Similarity 84.2%; Pred. No. 4.5e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GACCCACAGAGCCCC 20
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Db 15 GACACACAGAGAGCCCC 33

RESULT 6
AR003361/c 25 bp DNA linear PAT 04-DEC-1998
LOCUS AR003361
DEFINITION Sequence 8 from patent US 5744303.
ACCESSION AR003361
VERSION AR003361.1 GI:3964620
KEYWORDS

SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Iggo,R., Friend,S.H., Frebourg,T. and Ishioka,C.
TITLE Functional assay for transcriptional regulator genes
JOURNAL Patent: US 5744303-A 8 28-APR-1998;
FEATURES Location/Qualifiers
source 1..25
/organism="unknown"
/mol_type="unassigned DNA"

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Query Match 69.0%; Score 13.8; DB 6; Length 25;
Best Local Similarity 88.2%; Pred. No. 7.8e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CCCCACAGACAGCCCCC 20
| | | | | | | | | | | | | | | | | | | | | |
20 CCCCAGTGCAGCCTCC 4

Db 20 CCCCAGTGCAGCCTCC 4

RESULT 7
LOCUS AR261574 30 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 11 from patent US 6322976.
ACCESSION AR261574
VERSION AR261574.1 GI:28072652
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Altman,T.J., Scott,J. and Stanton,L.N.
TITLE Compositions and methods of disease diagnosis and therapy
JOURNAL Patent: US 6322976-A 11 27-NOV-2001;
Medical Research Council and SCIOS, Inc.; London;
GBX;

FEATURES Location/Qualifiers
source 1..30
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/mol_type="genomic DNA"

ORIGIN
Query Match 69.0%; Score 13.8; DB 6; Length 30;
Best Local Similarity 88.2%; Pred. No. 7.6e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GACCCACAGACAGCCC 18
| | | | | | | | | | | | | | | | | | | | | |
9 GACCCCAAGACAGCAC 25

Db 9 GACCCCAAGACAGCAC 25

RESULT 8
LOCUS AR643896 22 bp DNA linear PAT 20-APR-2005
DEFINITION Sequence 24 from patent US 6867289.
ACCESSION AR643896
VERSION AR643896.1 GI:62782552
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Gorenstein,D.G., Luxon,B.A., Herzog,N. and Aronson,J.
TITLE Thio-modified aptamer synthetic methods and compositions
JOURNAL Patent: US 6867289-A 24 15-MAR-2005;
Board of Regents, The University of Texas Systems; Austin, TX
FEATURES Location/Qualifiers
source 1..22
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/mol_type="genomic DNA"

ORIGIN

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Best Local Similarity 80.0%; Pred. No. 9.8e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGACCCACAGACAGCCCCC 20
| | | | | | | | | | | | | | | | | | | | | |
3 CGCCACACAGACAGCCCCC 22

Db 3 CGCCACACAGACAGCCCCC 22

RESULT 9
LOCUS AR168794 26 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 20 from patent US 6288042.
ACCESSION AR168794
VERSION AR168794.1 GI:17904898
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Rando,R.F., Ojwang,J.O., Hogan,M.E., Wallace,T.L. and Cossum,P.A.
TITLE Anti-viral guanosine-rich tetrad forming oligonucleotides
JOURNAL Patent: US 6288042-A 20 11-SEP-2001;
location/Qualifiers
source 1..26
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 68.0%; Score 13.6; DB 6; Length 26;
Best Local Similarity 80.0%; Pred. No. 9.7e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGACCCACAGACAGCCCCC 20
| | | | | | | | | | | | | | | | | | | | | |
23 CCACCCACCAAGAACCCCC 4

Db 23 CCACCCACCAAGAACCCCC 4

RESULT 10
LOCUS AR168799 26 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 25 from patent US 6288042.
ACCESSION AR168799
VERSION AR168799.1 GI:17904906
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Rando,R.F., Ojwang,J.O., Hogan,M.E., Wallace,T.L. and Cossum,P.A.
TITLE Anti-viral guanosine-rich tetrad forming oligonucleotides
JOURNAL Patent: US 6288042-A 25 11-SEP-2001;
location/Qualifiers
source 1..26
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/mol_type="unassigned DNA"

ORIGIN
Query Match 68.0%; Score 13.6; DB 6; Length 26;
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Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGACCCACAGACAGCCCCC 20
| | | | | | | | | | | | | | | | | | | | | |
23 CCACCCACCAAGAACCCCC 4

Db 23 CCACCCACCAAGAACCCCC 4

RESULT 11
LOCUS AR168801 26 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 27 from patent US 6288042.
ACCESSION AR168801

VERSION AR168801.1 GI:17904909
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

127795/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Query Match 68.0%; Score 13.6; DB 6; Length 26;
Best Local Similarity 80.0%; Pred. No. 9.7e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGACCCACAGACAGCCCCC 20
Db 23 CCACCCACCAACAACCCCC 4

RESULT 12
127788/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

127788
Sequence 20 from patent US 5567604.
127788
127788.1 GI:1818564
Unknown.
Unclassified.
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

1 (bases 1 to 26)
Rando,R.F., Fennewald,S., Zendeñui,J.G. and Ojwang,J.O.
Anti-viral guanosine-rich oligonucleotides
Patent: US 5567604-A 20 22-OCT-1996;
Location/Qualifiers
1..26
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 68.0%; Score 13.6; DB 6; Length 26;
Best Local Similarity 80.0%; Pred. No. 9.7e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGACCCACAGACAGCCCCC 20
Db 23 CCACCCACCAACAACCCCC 4

RESULT 13
127793/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

127793
Sequence 25 from patent US 5567604.
127793
127793.1 GI:1818569
Unknown.
Unclassified.
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

1 (bases 1 to 26)
Rando,R.F., Fennewald,S., Zendeñui,J.G. and Ojwang,J.O.
Anti-viral guanosine-rich oligonucleotides
Patent: US 5567604-A 25 22-OCT-1996;
Location/Qualifiers
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/mol_type="unassigned DNA"

Query Match 68.0%; Score 13.6; DB 6; Length 26;
Best Local Similarity 80.0%; Pred. No. 9.7e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGACCCACAGACAGCCCCC 20
Db 23 CCACCCACCAACAACCCCC 4

RESULT 14
127795/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

127795
Sequence 27 from patent US 5567604.
127795
127795.1 GI:1818571
Unknown.
Unclassified.
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

1 (bases 1 to 26)
Rando,R.F., Fennewald,S., Zendeñui,J.G. and Ojwang,J.O.
Anti-viral guanosine-rich oligonucleotides
Patent: US 5567604-A 27 22-OCT-1996;
Location/Qualifiers
1..26
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 68.0%; Score 13.6; DB 6; Length 26;
Best Local Similarity 80.0%; Pred. No. 9.7e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGACCCACAGACAGCCCCC 20
Db 23 CCACCCACCAACAACCCCC 4

RESULT 15
AR200263/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AR200263
Sequence 20 from patent US 6355785.
AR200263
AR200263.1 GI:20250337
Unknown.
Unclassified.
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

1 (bases 1 to 26)
Rando,R.F., Fennewald,S., Zendeñui,J.G., Ojwang,J.O., Hogan,M.E.,
Pommier,Y. and Mazumder,A.
Guanosine-rich oligonucleotide integrase inhibitors
Patent: US 6355785-A 20 12-MAR-2002;
Location/Qualifiers
1..26
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 68.0%; Score 13.6; DB 6; Length 26;
Best Local Similarity 80.0%; Pred. No. 9.7e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGACCCACAGACAGCCCCC 20
Db 23 CCACCCACCAACAACCCCC 4

Search completed: December 24, 2005, 14:06:19
Job time : 583 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 01:41:40 : Search time 171.4 Seconds
(without alignments)
777.677 Million cell updates/sec

Title: US-09-296-264-12

Perfect score: 20

Sequence: 1 cgacccacagacagcccc 20

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 3390896

Minimum DB seq length: 20

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

N Geneseq_21:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*
- 14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3	AAZ31442
2	20	100.0	20	9	ADN74694
3	15.4	77.0	34	14	ADX83399
4	14.4	72.0	20	14	ADY58545
5	14.4	72.0	60	6	ABN46092
6	14.2	71.0	22	10	AAD52768
7	14.2	71.0	37	6	ABK81254
8	14.2	71.0	37	11	ADL98534
9	14.2	71.0	41	6	ABK60009
10	14.2	71.0	49	2	AAQ33751
11	14.2	71.0	60	2	AAT30628
12	14	70.0	35	7	ADY36854
13	14	70.0	42	6	ABZ50869
14	14	70.0	42	6	ABZ48406
15	14	70.0	42	6	ABZ44642
16	14	70.0	45	4	AAZ82189
17	13.8	69.0	25	2	AAQ61824
18	13.8	69.0	30	3	AAA40611
19	13.8	69.0	30	3	AAA40611

C	20	13.8	69.0	41	6	ABK60008	ABK60008 Human DNA
C	21	13.8	69.0	41	6	ABK60071	ABK60071 Human TAA
C	22	13.8	69.0	42	14	ADY76922	ADY76922 Human TAA
C	23	13.8	69.0	60	3	AAA05788	AAA05788 Streptavi
C	24	13.6	68.0	22	3	AAA53503	AAA53503 NF-KappaB
C	25	13.6	68.0	22	10	ADD43566	ADD43566 Oligonuc
C	26	13.6	68.0	25	9	AC158432	AC158432 Human mic
C	27	13.6	68.0	26	2	AAQ79225	AAQ79225 Guanosine
C	28	13.6	68.0	26	2	AAQ79220	AAQ79220 Guanosine
C	29	13.6	68.0	26	2	AAQ79227	AAQ79227 Guanosine
C	30	13.6	68.0	26	2	AAT51645	AAT51645 Viral int
C	31	13.6	68.0	26	2	AAT51638	AAT51638 Viral int
C	32	13.6	68.0	26	2	AAT51643	AAT51643 Viral int
C	33	13.6	68.0	26	2	AAZ79227	AAZ79227 Oligonuc
C	34	13.6	68.0	26	10	ADG38370	ADG38370 Anti-HIV
C	35	13.6	68.0	32	14	ADY51614	ADY51614 Transcrip
C	36	13.6	68.0	45	2	AAQ79222	AAQ79222 Guanosine
C	37	13.6	68.0	45	2	AAQ79221	AAQ79221 Guanosine
C	38	13.6	68.0	45	2	AAT51639	AAT51639 Viral int
C	39	13.6	68.0	45	2	AAT51640	AAT51640 Viral int
C	40	13.6	68.0	45	2	AAZ79228	AAZ79228 Oligonuc
C	41	13.6	68.0	45	3	AAA05784	AAA05784 Streptavi
C	42	13.6	68.0	45	10	ADG38352	ADG38352 Anti-HIV
C	43	13.6	68.0	65	6	ABN56220	ABN56220 Mouse spl
C	44	13.6	68.0	87	3	AACT0414	AACT0414 Human sec
C	45	13.6	68.0	87	4	AAH43509	AAH43509 C1435G SN

ALIGNMENTS

RESULT 1	AAZ31442	standard; DNA; 20 BP.
ID	AAZ31442	
AC	AAZ31442;	
XX		
DT	07-FEB-2000	(first entry)
XX		
DE	Human neuropilin mRNA specific antisense oligo GTT3612.	
XX		
KW	Neuropilin; human; growth; metastasis; tumor; neovascularisation; cancer;	
KW	papilloma; diabetic retinopathy; antisense; ss.	
XX		
OS	Synthetic.	
OS	Homo sapiens.	
XX		
PN	W0955855-A2.	
XX		
PD	04-NOV-1999.	
XX		
PF	23-APR-1999;	99WO-CA000324.
XX		
PR	23-APR-1998;	98US-0082791P.
XX		
PA	(GENE-) GENESENSE TECHNOLOGIES INC.	
XX		
PI	Wright JA, Young AH, Lee YS;	
XX		
DR	WPI; 2000-023357/02.	
XX		
PT	Antisense oligonucleotides that inhibit neuropilin expression, useful for	
FT	treating cancer.	
XX		
PS	Claim 4; Page 16; 57pp; English.	
CC	Sequences AAZ31431-460 represent antisense oligonucleotides which inhibit	
CC	human neuropilin expression. The antisense oligonucleotides may be used	
CC	to inhibit the growth or metastasis of a mammalian tumor and inhibit	
CC	neovascularisation. The oligonucleotides may be used to treat various	
CC	forms of cancers or tumors, such as sarcomas, melanomas, adenomas,	
CC	carcinomas of solid tissue, hypoxic tumors, squamous cell carcinomas of	
CC	the mouth, throat, larynx and lung, genitourinary cancers such as	

CC cervical and bladder cancer, hematopoietic cancers, colon cancer, breast
 CC cancer, pancreatic cancer, renal cancer, brain cancer, skin cancer, liver
 CC cancer, head and neck cancers, and nervous system cancers, as well as
 CC benign lesions such as papillomas. The methods may be used to treat
 CC neovascularisation disorders such as diabetic retinopathy, and
 CC retinopathy of prematurity and age related macular degeneration
 XX
 SQ Sequence 20 BP; 5 A; 12 C; 3 G; 0 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 3; Length 20;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 CGACCCACAGACAGCCCC 20
 Db 1 CGACCCACAGACAGCCCC 20
 RESULT 2
 ADA74694
 ID ADA74694 standard; DNA; 20 BP.
 AC ADA74694;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE GT1612 antisense oligonucleotide targeted to human neuropilin mRNA.
 XX
 XX neuropilin; VEGF165R; vascular endothelial growth factor receptor;
 KW cytosolic; growth; tumour metastasis; angiogenesis; gene therapy;
 KW GT1612; antisense; human; ss.
 XX
 OS Homo sapiens.
 PN US2003083274-A1.
 XX
 PD 01-MAY-2003.
 XX
 PF 22-APR-1999; 99US-00296264.
 XX
 PR 23-APR-1998; 98US-0082791P.
 XX
 XX (WRIG/) WRIGHT J A.
 PA (YOUNG/) YOUNG A H.
 PA (LEEV/) LEE Y S.
 PI Wright JA, Young AH, Lee YS;
 FI
 DR WPI; 2003-576622/54.
 XX
 PT New antisense oligonucleotide that inhibits neuropilin expression, useful
 PT for inhibiting growth of mammalian tumor or inhibiting metastasis of a
 PT mammalian tumor.
 PS
 XX Claim 1; Page 5; 27pp; English.
 XX
 CC The invention relates to a novel antisense oligonucleotide that inhibits
 CC the expression of neuropilin, also known as VEGF165R (vascular
 CC endothelial growth factor receptor). The oligonucleotide of the invention
 CC demonstrates cytostatic activity and may be useful for inhibiting the
 CC growth or metastasis of a mammalian tumour and to inhibit angiogenesis in
 CC mammals. Furthermore, the oligonucleotide may be utilised during gene
 CC therapy. The current sequence is that of the GT1612 antisense
 CC oligonucleotide of the invention which is targeted to human neuropilin
 CC mRNA.
 CC
 SQ Sequence 20 BP; 5 A; 12 C; 3 G; 0 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 9; Length 20;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 CGACCCACAGACAGCCCC 20

Db 1 CGACCCACAGACAGCCCC 20
 RESULT 3
 ADX83399/c
 ID ADX83399 standard; DNA; 34 BP.
 XX
 AC ADX83399;
 XX
 DT 05-MAY-2005 (first entry)
 XX
 DE Human TEG37 associated primer SEQ ID NO 281.
 XX
 XX cytosolic; protein purification; diagnosis; cancer; cytostatic;
 KW neoplasm; respiratory disease; lung tumor; gastrointestinal disease;
 KW stomach tumor; colon tumor; hepatic tumor; selectable marker; TEG; PCR;
 KW primer; ss.
 XX
 OS Homo sapiens.
 PN WO2005014818-A1.
 XX
 PD 17-FEB-2005.
 XX
 PF 06-AUG-2004; 2004WO-JP011650.
 XX
 PR 08-AUG-2003; 2003JP-00290704.
 XX
 XX (PERS-) PERSBUS PROTEOMICS INC.
 PA (CHUS) CHUGAI SEIYAKU KK.
 PA (ABUR/) ABURATANI H.
 XX
 PI Aburatani H, Hippo Y, Taniguchi H, Chen YX, Ishikawa S;
 PI Fukumoto S, Shimamura T, Kamimura N, Guo YQ, Yamamoto S, Ito Y;
 PI Ito H, Ohtomo T;
 DR WPI; 2005-173106/18.
 XX
 PT Novel protein encoded by any one of TEG1 to TEG64, useful for diagnosing
 PT and treating cancer e.g. lung, hepatic, stomach, colon or pancreatic
 PT cancer.
 PS
 XX Example 11; SEQ ID NO 281; 462pp; Japanese.
 XX
 CC The invention describes a protein (I) encoded by a gene having a
 CC nucleotide sequence chosen from any one of 65 fully defined 418-19341
 CC base pair sequences (SEQ ID No. 1-65) (TEG 1-64) or their fragments. Also
 CC described are: a protein (II) encoded by a gene having a nucleotide
 CC sequence chosen from SEQ ID No. 1, 2, 28, 29, 30, 31, 32, 51, 52, 60 and
 CC 61 or their fragments; a protein (III) encoded by a gene having a
 CC nucleotide sequence chosen from any one of SEQ ID No. 3-13, 22-27 and 33-
 CC 55 or their fragments; protein (IV) encoded by a gene having a nucleotide
 CC sequence chosen from SEQ ID No. 3, 7, 20, 21 and 46-50 or their fragments
 CC ; a protein (V) encoded by a gene having a nucleotide sequence chosen
 CC from SEQ ID No. 14-19, 43-45, 56-59 and 62-65 or their fragments; an
 CC antibody (VI) that specifically recognizes any one of (I)-(V) or their
 CC fragments; a polynucleotide (VII) complementary to the nucleotide
 CC sequence of any one of SEQ ID No. 1-65 or a polynucleotide sequence
 CC capable of hybridizing with SEQ ID No. 1-65; a polynucleotide (VIII)
 CC comprising at least 12 consecutive nucleotides in any one SEQ ID No. 1-65
 CC or a polynucleotide sequence capable of hybridizing with this nucleotide;
 CC a composition (C1) for diagnosing or treating lung cancer; a composition
 CC (C2) for diagnosing or treating stomach cancer; composition (C3) for
 CC diagnosing or treating colon cancer; a composition (C4) for diagnosing or
 CC treating hepatic cancer; a vector (IX) comprising (VII) or (VIII); a cell
 CC (X) comprising (IX); identifying (M1) a compound having anticancer
 CC activity; and diagnosing (M2) cancer. Proteins (I)-(V), an antibody (VI)
 CC that specifically binds the proteins and polynucleotides (VII) and (VIII)
 CC are useful for diagnosing cancer. (M2) comprising measuring the
 CC expression level of (I)-(V) or (VII) or (VIII), or obtaining sample
 CC (blood serum or plasma), and detecting C20orf102 protein in the obtained
 CC sample is also useful for diagnosing cancer such as lung cancer, hepatic

CC cancer or pancreatic cancer, where the C20orf102 protein is a secreted or
CC extracellular C20orf102 protein, which is detected using an antibody
CC which recognizes C20orf102 protein. A composition (C1) comprising protein
CC (II) is useful for diagnosing or treating lung cancer. A composition (C2)
CC comprising protein (III) is useful for diagnosing or treating stomach
CC cancer. A composition (C3) comprising protein (IV) is useful for
CC diagnosing or treating colon cancer. A composition (C4) comprising (V) is
CC useful for diagnosing or treating hepatic cancer. (M1) comprising
CC contacting a cultured human cell with a test compound and identifying a
CC compound that causes a change in expression level of the gene which
CC contains the nucleotide sequence in any one of SEQ ID No. 1-65 is useful
CC for identifying a compound having anticancer activity. A vector (IX) or
CC cell (X) is useful for producing (I) or (VI). An antibody (VI) is useful
CC as a cancer diagnostic marker. This sequence represents a human TEG37
CC associated primer.

XX
XX Sequence 34 BP; 2 A; 9 C; 13 G; 10 T; 0 U; 0 Other;

Query Match 77.0%; Score 15.4; DB 14; Length 34;

Best Local Similarity 94.1%; Pred. No. 2.9e+03;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 GACCCACAGACAGCC 18

Db 25 GACCCACAGACAGCC 9

RESULT 4
ADY58545/c
ID ADY58545 standard; DNA; 20 BP.

AC ADY58545;

DT 19-MAY-2005 (first entry)

DE En1 gene RT-PCR primer.

XX Stem cell; neuron; En1; cell therapy; Parkinsons disease;

KM antiparkinsonian; neurological disease; RT-PCR;

KM reverse transcriptase PCR; primer; ss.

OS Homo sapiens.

PN WO2005021720-A2.

XX 10-MAR-2005.

PF 27-AUG-2004; 2004WO-US027841.

PR 29-AUG-2003; 2003US-0498831P.

PR 02-SEP-2003; 2003US-0499570P.

XX (WISC) WISCONSIN ALUMNI RES FOUND.

XX Zhang S, Thomson VA, Duncan ID, Li X;

XX WPI; 2005-223178/23.

XX
XX
XX Creating synchronous cell populations cultured from embryonic stem cells
XX and have early rosette morphology comprises propagating embryonic stem
XX cells into embryoid bodies and propagating the embryoid bodies into
XX neural stem cells.

XX Example 2; Page 52; 84pp; English.

XX The invention provides a method of creating a synchronous population of
XX cells from primate embryonic stem cells and which are characterized as
XX Sox1-/Pax6+ and or an early rosette morphology. This involves:
XX propagating embryonic stem cells into embryoid bodies; and propagating
XX the embryoid bodies into a synchronous population of neural stem cells in
XX the form of early rosettes, in the presence of FGF2, FGF9 or FGF4.

XX A method of creating a population of synchronized neural stem cells that
XX are Pax6+/Sox1+ comprises culturing Sox1-/Pax6+ cells of early rosette

CC morphology for 4-6 days in the presence of FGF2, FGF4, FGF8 or RA. Cells
CC cultured with FGF8 are En1+ and may be further cultured with SHH to
CC produce a population of midbrain dopamine neurons. Cells cultured with
CC FGF2 are Bfl+ and may be further cultured with SHH to produce a
CC population of forebrain dopamine neurons. Cells cultured with RA are Hox+
CC and may be further cultured to produce a population of spinal motor
CC neurons. Also provided are methods of examining a test compound for the
CC ability to perturb neural cell development. The present sequence is that
CC of a RT-PCR primer for En1. This was used in an example from the
CC invention describing the generation of midbrain dopaminergic (DA) neurons
CC from human embryonic stem cells. The RT-PCR analysis indicated that En1
CC is not expressed at a high level until neuroectodermal cells
CC differentiate into DA neurons. DA dopaminergic neurons may be used for
CC toxicological and pharmaceutical screening and for potential cell therapy
CC in Parkinson's disease.

XX
XX Sequence 20 BP; 2 A; 3 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 72.0%; Score 14.4; DB 14; Length 20;

Best Local Similarity 93.8%; Pred. No. 7.8e+03;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CGACCCACAGACAGC 16

Db 16 CGACCCACAGACAGC 1

RESULT 5
ABN46092
ID ABN46092 standard; DNA; 60 BP.

AC ABN46092;

DT 15-JUL-2002 (first entry)

DE Human spliced transcript detection oligonucleotide SEQ ID NO:18840.

XX Human; mouse; rat; splice transcript; detection; RNA transcript;

KM splice variant; transcriptome; oligonucleotide library; ss.

OS Homo sapiens.

PN WO200210449-A2.

XX 07-FEB-2002.

PF 20-JUL-2001; 2001WO-IB001903.

PR 28-JUL-2000; 2000US-0221607P.

PR 02-MAY-2001; 2001US-0287724P.

XX (COMP-) COMPUGEN INC.

XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

XX WPI; 2002-257383/30.

XX
XX
XX New oligonucleotide libraries comprising oligonucleotides which
XX selectively hybridize to mRNAs transcribed from a transcription unit of a
XX genome, useful for detecting tissue-, pathology-, and developmental-
XX specific genes.

XX Example 1; SEQ ID NO 18840; 47pp; English.

XX The present invention describes oligonucleotide libraries for detecting
XX messenger RNAs that populate a (sub-)transcriptome, where the (sub-
XX)transcriptome comprises messenger RNAs transcribed from multiple
XX transcription units that populate a genome. The library comprises several
XX oligonucleotides, each capable of hybridizing selectively to a set of
XX messenger RNAs transcribed from a given transcription unit of the genome,
XX which encodes one or more messenger RNA splice variants. The

XX oligonucleotide libraries are useful for detecting mRNAs from a
XX biological sample, in expression profiling studies, in qualitatively or

CC	quantitatively characterising the corresponding transcriptome, and in
CC	detecting RNA transcripts and splice variants of human or animal
CC	transcriptomes. The libraries may also be used as specialised mini
CC	libraries to detect transcripts of a sub-transcriptome under a particular
CC	biological or pathological state, and so allowing the detection of tissue
CC	- and pathology-specific genes such as those genes only expressed in
CC	a specific tissue under a specific pathological condition; to detect
CC	developmental specific genes; and to detect RNA transcripts and splice
CC	variants of a transcriptome of a patient suffering from a particular
CC	disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
CC	rats, humans and mice, which are used in the exemplification of the
CC	present invention. N.B. The sequence data for this patent did not form
CC	part of the printed specification, but was obtained in electronic format
CC	directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX	
SQ	Sequence 60 BP; 15 A; 17 C; 14 G; 14 T; 0 U; 0 Other;
Query Match	72.0%; Score 14.4; DB 6; Length 60;
Best Local Similarity	93.8%; Pred. No. 8.1e+03;
Matches 15; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
OY	1 CGACCCACAGCAGC 16
DB	31 CGACCCACAGACTGC 46
RESULT 6	
ID	AAD52768/C
AD	AAD52768 standard; DNA; 22 BP.
XX	
AC	AAD52768;
XX	
DT	14-MAY-2003 (first entry)
XX	
DE	FRA11.1-R PCR primer used to screen mutations in human fra-1 gene.
KW	Bone mineral density; BMD; Fos related antigen-1 gene; osteoporosis;
KM	Fra-1; genetic marker; gene therapy; osteopathic; PCR; primer; ss.
XX	
OS	Unidentified.
XX	
PN	WO200292850-A2.
PD	21-NOV-2002.
PF	17-MAY-2002; 2002WO-CB002263.
PR	17-MAY-2001; 2001GB-00012075.
PA	(UYAB-) UNIV ABERDEEN.
PI	Alagha OME, Ralston SH;
Pt	WPI: 2003-120697/11.
PT	Determining the susceptibility of an individual to a disorder associated
PT	with an abnormal level of bone mineral density, useful for diagnosing
PT	osteoporosis, comprises the use of Fos related antigen-1 gene (Fra-1)
PT	marker.
XX	
PS	Example 2; Page 31; 56pp; English.
XX	
CC	The invention relates to a method for determining the susceptibility of
CC	an individual to a disorder associated with an abnormal level of bone
CC	mineral density (BMD), comprising the use of Fos related antigen-1 gene
CC	(Fra-1) marker. The methods are useful for determining the susceptibility
CC	of an individual to a disorder associated with an abnormal level of BMD
CC	or for diagnosing osteoporosis. The single nucleotide polymorphisms are
CC	useful as genetic markers to identify people with low BMD, so that these
CC	individuals could be targeted for treatment to prevent osteoporosis. The
CC	Fra-1 nucleic acid sequences may be used in gene therapy to treat or
CC	prevent a BMD-associated disorder such as osteoporosis. The present DNA
CC	sequence is a PCR primer used to screen mutations in human fra-1 gene.

CC This sequence is used in the exemplification of the invention
XX
SQ Sequence 22 BP; 3 A; 3 C; 13 G; 3 T; 0 U; 0 Other;
Query Match 71.0%; Score 14.2; DB 10; Length 22;
Best Local Similarity 84.2%; Pred. No. 9.5e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CGACCCACAGACAGCCCC 19
DB 19 CGACCCACTCTCAGCCCC 1
RESULT 7
ABK81254/c
ID ABK81254 standard; DNA; 37 BP.
XX
AC ABK81254;
XX
DT 13-AUG-2002 (first entry)
DE Polymunoglobulin receptor (pIgR) related primer #44.
XX
XX Transcellular transport; transcytotic transport; paracellular transport;
XX respiratory system disorder; lung cancer; tumour; aschma;
KW pathogenic infection; allergy-related disorder;
KW gastrointestinal tract disorder; gastrointestinal hormone disorder;
KW Chron's disease; eating disorder; polymunoglobulin receptor; pIgR;
KW primer; ss.
XX
XX Synthetic.
OS
PN WO200228408-A2.
XX
PD 11-APR-2002.
PF 02-OCT-2001; 2001WO-US030832.
PR 02-OCT-2000; 2000US-0237929P.
PR 13-NOV-2000; 2000US-0248478P.
PR 14-NOV-2000; 2000US-0248819P.
PR 09-FEB-2001; 2001US-0267601P.
XX
PA (ARI2-) ARIZEKE PHARM INC.
XX
PI Houston Lt., Sheridan PJ, Hawley S, Glyn JM, Chaplin S, Baeu A;
XX WPI; 2002-416628/44.
XX
DR Complex useful for transporting active agent through epithelial barrier,
XX PT has biologically active portion and target element directed to ligand
XX PT that confers e.g. transcytotic properties to agent specific to ligand.
XX
PS Example 3; Fig 12B; 379pp; English.
XX
XX The invention described a complex or compound (I) comprising a
CC biologically active portion and a target element (II) directed to a
CC ligand that confers transcellular, transcytotic or paracellular
CC transporting properties to an agent specifically bound to the ligand,
CC where (II) is not an antibody. Alternatively, (I) comprises two or more
CC (II) directed to one or more ligands. (I) is useful for delivering a
CC biologically active agent to an animal, for transporting an active agent
CC through an epithelial or mucosal barrier, and for treating or identifying
CC a disease in an animal e.g. diseases of the respiratory system including
CC lung cancer and tumours, asthma, pathogenic infections, allergy-related
CC disorders, gastrointestinal tract disorders, disorders relating to
CC gastrointestinal hormones, Chron's disease, eating disorders and any
CC disease or disorder involving polymunoglobulin receptor (pIgR)
CC displaying cells. This sequence represents a primer associated with the
CC transport of biologically active agents across cellular barriers
XX
SQ Sequence 37 BP; 3 A; 13 C; 14 G; 7 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 6; Length 37;
Best Local Similarity 84.2%; Pred. No. 9.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GACCCACAGACGCCCC 20
28 GACGCCACAGAACGCCCC 10

Db

RESULT 8
ADL99534/C
ID ADL99534 standard; DNA; 37 BP.
AC ADL99534;
XX 20-MAY-2004 (first entry)
XX Mouse polyimmunoglobulin receptor (pIgR) primer #7.
XX
XX antiapoptotic; antiinflammatory; neuroprotective; ophthalmological;
KW gastrointestinal; osteopathic; nephrotoxic; gene therapy;
KW multicentric molecular complex; transcytotic transport;
KW paracellular transport; calcitonin; osteoporosis; renal failure; colitis;
KW gastroenteritis; inflammatory bowel disease; psoriasis;
KW Alzheimer's disease; optic neuropathy; ophthalmoplegia;
KW polyimmunoglobulin receptor; pIgR; endocytosis; exocytosis; mouse; PCR;
KW primer; ss.
XX
XX Mus sp.
XX
XX US2003166160-A1.
XX
XX 04-SEP-2003.
XX
XX 06-SEP-2001; 2001US-00949039.
XX
XX 06-SEP-2001; 2001US-00949039.
XX
XX (HAWL/) HAWLEY S B.
PA (CHAP/) CHAPIN S.
PA (SHER/) SHERIDAN P L.
PA (HOU/) HOUSTON L L.
PA (GLYN/) GLYNN J M.
XX
PI Hawley SB, Chapin S, Sheridan PL, Houston LL, Glynn JM;
XX WPI; 2003-898076/82.
XX
XX New multimeric molecular complex, useful for preparing a composition for
PT diagnosing or treating e.g. osteoporosis, renal failure, colitis,
PT gastroenteritis, inflammatory bowel disease, psoriasis or Alzheimer's
PT disease.
XX
XX Example 2; Fig 7B; 91pp; English.
XX
XX The invention describes a multimeric molecular complex comprising at
CC least 2 compounds, each of which has at least one targeting element
CC directed to a ligand that confers transcytotic or paracellular
CC transporting properties to a molecular complex specifically bound to the
CC ligand. Also described are: a compound comprising at least 2 targeting
CC elements directed to the ligand; a protein conjugate comprising a
CC biologically active calcitonin polypeptide having a chemical linkage to
CC at least one targeting element directed to the ligand; a pharmaceutical
CC composition comprising the compound, delivering a biologically active
CC agent to an animal; transporting a biologically active agent through an
CC epithelial barrier; treating a disease in an animal; and identifying a
CC disease in an animal. The complex is useful for preparing a composition
CC for diagnosing or treating diseases, e.g., osteoporosis, renal failure,
CC colitis, gastroenteritis, inflammatory bowel disease, psoriasis,
CC Alzheimer's disease, optic neuropathy or ophthalmoplegia. This sequence
CC represents a primer used in the isolation of mouse polyimmunoglobulin
CC receptor (pIgR), a mediator of endocytosis, exocytosis and forward and
CC reverse transcytosis in epithelial cells.

XX
SQ Sequence 37 BP; 3 A; 13 C; 14 G; 7 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 11; Length 37;
Best Local Similarity 84.2%; Pred. No. 9.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GACCCACAGACGCCCC 20
28 GACGCCACAGAACGCCCC 10

Db

RESULT 9
ABS60009/C
ID ABS60009 standard; DNA; 41 BP.
AC ABS60009;
XX 05-NOV-2002 (first entry)
XX
XX Human DNA containing a single nucleotide polymorphism #33.
DE
XX Aminopeptidase P; XNPEP2; bradykinin receptor B1; ds; SNP; BDKRB1;
KW bradykinin receptor B1; TACR1, C1 esterase inhibitor; C1NH; kallikrein 1;
KW KLK1; bradykinin receptor B2; BDKRB2; gene therapy;
KW angiotensin converting enzyme 2; ACE2; protease inhibitor 4; P14;
KW polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma;
KW cardiovascular disease; angina pectoris; hypertension; heart failure;
KW myocardial infarction; ventricular hypertrophy; vascular disease;
KW aneurysm; embolism; thrombosis; coronary artery disease; angioedema;
KW arteriosclerosis; atherosclerosis; hypersensitivity; sepsis;
KW autoimmune disease; inflammatory arthritis; cancer; wound;
KW viral infection; bacterial infection; fungal infection; COPD;
KW Chronic obstructive pulmonary disease; enterocolitis;
KW single-nucleotide polymorphism.
XX
XX Homo sapiens.
XX
XX WO200261131-A2.
XX
XX 08-AUG-2002.
XX
XX 03-DEC-2001; 2001WO-US047235.
XX
XX 04-DEC-2000; 2000US-0251015P.
PR 23-JAN-2001; 2001US-0263678P.
PR 02-MAR-2001; 2001US-0273037P.
XX
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
PA (TSUC/) TSUCHIHASHI Z.
PA (HUI/) HUI L.
XX
XX Tsuchihashi Z, Hui L, Zerba KE, Ma-Edmonds M, Perrone MH;
PI Swanson BN, Powell JR;
XX WPI; 2002-619265/66.
XX
XX New isolated nucleic acid with at least one polymorphic position, useful
PT for detecting, diagnosing and treating disorders such as angioedema,
PT cancer, viral, bacterial or fungal infection, cardiovascular and
PT autoimmune diseases.
XX
XX Claim 3; Page 670; 977pp; English.
XX
XX The invention relates to an isolated nucleic acid from a human gene
CC encoding aminopeptidase P (XNPEP2), bradykinin receptor B1 (BDKRB1),
CC tachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein
CC 1 (KLK1), bradykinin receptor B2 (BDKRB2), angiotensin converting enzyme
CC 2 (ACE2) or protease inhibitor 4 (P14), comprising at least one
CC polymorphic position. Also included are (1) a probe that hybridizes to a
CC nucleotide polymorphisms comprising additional 5' and 3' flanking genomic
CC sequence; (2) analysing (M1) at least one nucleic acid sample comprising

CC obtaining the sample from one or more individuals and determining the
 CC nucleic acid sequence at one or more polymorphic positions in a gene
 CC encoding a protein selected from the group above; (3) constructing (M2)
 CC haplotypes using the genes comprising grouping at least two nucleic acids
 CC ; (4) identifying (M3) an individual at risk of developing a disorder
 CC upon administration of an ACE inhibitor and/or vasopeptidase inhibitor
 CC using the polymorphic data; (5) a library of nucleic acids, each of which
 CC comprises one or more polymorphic positions within a gene encoding a
 CC human protein selected from the group above; and (6) genotyping (M4) an
 CC individual comprising obtaining a nucleic acid sample, determining the
 CC nucleotide present in at least one polymorphic position, and comparing at
 CC least one position with a known data set. The genes, (M1, M2, M3 and M4)
 CC and compositions are useful for detecting, diagnosing, treating,
 CC preventing various disorders such as angioedema and diseases which
 CC involve angiomas, like haemangiomas, tumours, sarcomas, Crohn's
 CC disease, trachomas, and cardiovascular diseases like angina pectoris,
 CC hypertension, heart failure, myocardial infarction, ventricular
 CC hypertrophy, vascular diseases, aneurysm, embolism, thrombosis, coronary
 CC artery disease, arteriosclerosis and/or atherosclerosis, and
 CC hypersensitivity reactions, sepsis, autoimmune diseases, inflammatory
 CC arthritis, cancer, wounds, viral, bacterial or fungal infection, Chronic
 CC obstructive pulmonary disease (COPD) and enterocolitis (many other
 CC diseases and disorders are listed in the specification). The
 CC polynucleotides are also useful for chromosome identification. Antibodies
 CC against the proteins may be utilised for immunophenotyping of cell lines
 CC and biological samples. The present sequence represents or contains the
 CC region surrounding a single-nucleotide polymorphism in one of the genes
 CC encoding one of the proteins listed above

XX Sequence 41 BP; 5 A; 10 C; 17 G; 9 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 6; Length 41;

Best Local Similarity 84.2%; Pred. No. 9.7e+03; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 2 GACCCACAGACAGCCCC 20
 28 GTCCCCACAGCAGCAGCCC 10

RESULT 10

AA033751/c ID AA033751 standard; DNA; 49 BP.

XX AA033751;

AC 25-MAR-2003 (revised)

DT 02-FEB-1993 (first entry)

XX Upstream sequence of microsatellite from clone TGLM162.

KW PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
 KM genetic mapping; traits; amplification; ss.

OS Bos taurus.

XX WO9213102-A1.

XX 06-AUG-1992.

PF 15-JAN-1992; 92WO-US000340.

XX 15-JAN-1991; 91US-00642342.

XX (GENM-) GENMARK.

XX Georges M, Maesey JM;

XX WPI; 1992-284684/34.

XX Polymorphic bovine DNA markers - used in genetic identification, gene
 PT mapping, and selective breeding.
 XX

PS Table 7; Page 229; 517pp; English.

XX The sequence is that upstream of a bovine microsatellite sequence obtd.
 CC by screening a library of bovine MboI DNA fragments of between 250 and
 CC 500 bp with an (AC)₁₅ and a (TC)₁₅ oligonucleotide probe. One out of 50
 CC clones cross-hybridised. Assuming independent distribution of
 CC microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
 CC in the bovine genome is estimated at >100, 000. The sequence information
 CC for ca. 230 such bovine microsatellites is summarised in the
 CC specification and indexed herein (see below). The sequences upstream and
 CC downstream of the microsatellite sequence were used to generate the
 CC required PCR primers for in vitro amplification of the corresp.
 CC microsatellite (using the program OPTIPRIM). The microsatellites may be
 CC used to identify individuals, for parentage testing, and in the genetic
 CC mapping of economic trait loci, or genes involved the determination of
 CC economically important traits esp. in cattle, to allow selective
 CC breeding. See also AA033501-34437. (updated on 25-MAR-2003 to correct PN
 CC field.)

XX Sequence 49 BP; 12 A; 11 C; 16 G; 10 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 2; Length 49;

Best Local Similarity 84.2%; Pred. No. 9.8e+03; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 1 CGACCCACAGACAGCCCC 19
 19 CGACCCCATAGCGGCACC 1

RESULT 11

AAT30628 ID AAT30628 standard; cDNA; 60 BP.

XX AAT30628;

DT 21-FEB-1997 (first entry)

XX Probe nucleic acid #11.

XX Target binding assembly; nucleic acid recognition unit; NF-kappa-B; SPI;
 KM TATA; human papillomavirus; HPV; HPV E2; human immunodeficiency virus;
 KW HIV LTR; Tat binding unit; probe; assembly sequence; asymmetry sequence;
 KM nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria;
 KW virus; ss.

XX Synthetic.

XX WO9617956-A2.

XX 13-JUN-1996.

PF 07-DEC-1995; 95WO-US015944.

XX 09-DEC-1994; 94US-00353476.

XX (GENE-) GENE POOL INC.

XX Weininger S, Weininger AM;

XX WPI; 1996-287199/29.

XX Probe nucleic acids, target binding assemblies, etc - for detection and
 PT localisation of specific nucleic acid sequences, esp. HIV and HPV.

XX Disclosure; Page 82; 172pp; English.

XX AAT30615-T30634 represent probe nucleic acids of the invention. The probe
 CC of the invention contains a target binding region (TBR), a booster
 CC binding region (BBR), and an optional support or attachment (OSA). The
 CC target binding assembly (TBA) recognised by the TBR (see AAT30581-T30614)
 CC of the probe, contains at least one nucleic acid recognition unit (NAR),
 CC and optionally a linker sequence, an assembly sequence (see AAR5994-

CC R95998), an asymmetry sequence (see AAR95999-R96006), a nuclear
CC localisation signal sequence (see AAR96007), and an OSA. The assembly
CC sequence and asymmetry sequences are responsible for the folding and
CC association of the NARs. The NARs (see AAR95965-R95993) are selected from
CC NF-kappa-B, SP1, TATA, human papillomavirus (HPV) E2, HPV LTR, human
CC immunodeficiency virus (HIV) LTR and Tat binding units. The linker
CC sequence is an oligopeptide, which does not interfere with NAR function,
CC but provides stability and control over the spacing of the NAR from the
CC rest of the TNA. The OSA is an attached support or indicator, or other
CC means of localisation of the probe. The probe can be used in a method for
CC detecting or localising a specific target nucleic acid sequence (TNA).
CC The method is highly sensitive, and has a high degree of specificity. The
CC method can be used for detecting specific nucleic acid sequences,
CC including those found in human cells, in HIV, HPV, and other nucleic acid
CC containing systems, including bacteria and viruses

XX SQ Sequence 60 BP; 16 A; 23 C; 13 G; 8 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 2; Length 60;
Best Local Similarity 84.2%; Pred. No. 9.9e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 GACCCACAGACAGCCCC 20
DB 15 GACACACAGACAGCCGCC 33

RESULT 12
ADS31466 71.0%; Score 14.2; DB 2; Length 60;
ID. ADS31466 standard; DNA; 35 BP.

XX AC ADS31466;
XX DT 18-NOV-2004 (first entry)

XX DE Human Turner syndrome repeat-free probe #4 reverse PCR primer.
XX KW Human; in situ hybridisation; Southern blot; chromosome breakpoint;
XX inherited genetic disease; neoplastic disorder; ss; PCR; primer.

XX OS Homo sapiens.
XX PN US200324356-A1.
XX PD 04-DEC-2003.
XX PF 14-MAY-2001; 2001US-00854867.
XX PR 16-MAY-2000; 2000US-00573080.
XX PA (KNOL/) KNOOL J H M.
XX PI (ROGA/) ROGAN P K.
XX PI KNO1 JHM, Rogan PK,
XX DR WPI; 2002-062378/08.

XX PT Single copy genomic hybridization probes for detecting specific nucleic
XX acid sequences in sample by in situ hybridization useful for detection of
XX acquired or inherited genetic diseases.

XX PS Claim 37; SEQ ID NO 499; 30pp; English.

XX CC The invention relates to a nucleic acid hybridisation probe comprising a
XX labelled, single copy nucleic acids of at least 50 nucleotides, which
XX will hybridise to a deduced single copy sequence interval in target
XX nucleic acid (TNA) of known sequence. The single copy sequence is deduced
XX by comparing the target nucleic acid (e.g. a disease causing gene) with a
XX collection of high and low complexity repeat sequences as found in the
XX genome of the organism from containing the target nucleic acid. The probe
XX is generated by PCR on the target sequence. The probe is essentially free
XX of blocking nucleic acid sequences which will hybridise to repeat
XX sequences within the genome of which the TNA is a part, and is labelled

CC with a label selected from fluorochrome-responsive labels, fluorochromes,
CC calorimetric chemical, conjugated proteins, antibodies, antigens and
CC their mixtures. The probe is useful in a hybridisation method, where the
CC hybridisation method is from in situ hybridisation, Southern blot, and
CC other methods in which nucleic acid is immobilised, where the method
CC further comprises selecting a single copy nucleic acid which will
CC hybridise to a duplication or triplicon sequence domain. The probe is useful
CC for determining the existence of previously unknown repeat sequence
CC families in a genome. The method comprises reacting a labelled probe with
CC the genome, causing the probe to hybridise and ascertaining if the probe
CC hybridises to the genome at more than three preferably ten different
CC locations as a determination of new repeat sequence family, where the
CC determining step comprises selecting the single copy sequence from a
CC duplication or triplicon sequence domain. The probe is useful for
CC determining a chromosome breakpoint and is useful in the fields for
CC cytogenetics and molecular genetics for determining the presence of
CC specific nucleic acid sequences in a sample of eukaryotic origin, e.g.
CC the probes may be used to analyse specific chromosomal locations by in
CC situ hybridisation as a detection of acquired or inherited genetic
CC diseases especially for detection of genetic or neoplastic disorders.
CC Unlike prior art techniques, the probe permits more precise chromosomal
CC breakpoint determinations by in situ hybridisation. The present sequence
CC is a PCR primer used to amplify a single copy sequence probe for a human
CC gene associated with an inheritable genetic disorder. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?docid=2003024356.

XX SQ Sequence 35 BP; 8 A; 15 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 70.0%; Score 14; DB 7; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 CCACAGACAGCCCC 19
DB 15 CCACAGACAGCCGCC 28

RESULT 13
ADY36854 70.0%; Score 14; DB 7; Length 35;
ID ADY36854 standard; DNA; 35 BP.

XX AC ADY36854;
XX DT 05-MAY-2005 (first entry)

XX DE Genetic abnormality detection associated primer SEQ ID NO 499.
XX KW hybridization; DNA detection; neoplasm; genetic disorder; cytogenetics;
XX PCR; primer; ss; turners syndrome; endocrine-gen.; endocrine disease;
XX Chromosome aberration; genetic disorder.

XX OS Homo sapiens.
XX PN WO200188089-A2.
XX PD 22-NOV-2001.
XX PF 15-MAY-2001; 2001WO-US015674.
XX PR 16-MAY-2000; 2000US-00573080.
XX PA (CHIL-) CHILDREN'S MERCY HOSPITAL.
XX PI KNO1 JHM, Rogan PK, Cazarro PM;
XX DR WPI; 2002-062378/08.

XX PT Single copy genomic hybridization probes for detecting specific nucleic
XX acid sequences in sample by in situ hybridization useful for detection of
XX acquired or inherited genetic diseases.

XX Claim 36; SEQ ID NO 499; 67pp; English.

PS The invention describes a nucleic acid hybridization probe (I) comprising

XX a labeled, single copy nucleic acids of at least 50 nucleotides, which

CC will hybridize to a deduced single copy sequence interval in target

CC nucleic acid (TNA) of known sequence. (I) is useful in a hybridization

CC method which comprises preparing a reaction mixture comprising TNA and

CC (I) which hybridizes to TNA, and causing (I) to hybridize to TNA, where

CC the hybridization method is from in situ hybridization, Southern blot,

CC and other methods in which nucleic acid is immobilized, where the method

CC further comprises selecting a single copy nucleic acid which will

CC hybridize to a duplication or triplicon sequence domain. (I) is useful for:

CC determining the existence of previously unknown repeat sequence families

CC in a genome; determining a chromosome breakpoint and in the fields of

CC cytogenetics and molecular genetics for determining the presence of

CC specific nucleic acid sequences in a sample of eukaryotic origin, e.g.

CC the probes may be used to analyze specific chromosomal locations by in

CC situ hybridization as a detection of acquired or inherited genetic

CC diseases especially for detection of genetic or neoplastic disorders.

CC Unlike prior art techniques, (I) permits more precise chromosomal

CC breakpoint determinations by in situ hybridization. Hybridization

CC techniques utilizing (I), have made it possible to obtain reliable,

CC easily detectable signals with relatively small probes. A readily

CC detectable signal was obtained with a probe on the order of 2 kb in

CC length, using fluorescent in situ hybridization (FISH) technology. This

CC sensitivity of (I) is improved compared to the prior art, because the

CC probes of (I) are homogeneous single copy sequences. However, smaller

CC amplified segments, each comprising non-repetitive sequences, may also be

CC used in combination as probes to achieve adequate signals for in situ

CC hybridization. Complex single copy probes that hybridize to duplicated or

CC triplicated targets can also increase hybridization signals. This

CC sequence represents a primer used in the isolation of a gene probe for

CC detection of a human cytogenetic abnormality and genetic disorder.

XX

XX Sequence 35 BP; 8 A; 15 C; 6 G; 6 T; 0 U; 0 Other;

XX

XX Query Match 70.0%; Score 14; DB 7; Length 35;

XX Best Local Similarity 100.0%; Pred. No. 1.2e+04;

XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCACAGACAGCCCC 19

DB 15 CCACAGACAGCCCC 28

RESULT 14

ABZ50869/c

ID ABZ50869 standard; DNA; 42 BP.

XX

XX ABZ50869;

XX

XX 26-JUN-2003 (first entry)

XX

XX Human ATP-binding cassette ABCB3/TAP1 gene polymorphic site, #7651.

DE Human ATP-binding cassette ABCB3/TAP1 gene polymorphic site, #7651.

XX

XX Human; drug metabolizing enzyme; gene; drug metabolism; chromosome 6;

KW polymorphic site; drug evaluation; drug screening; genotyping;

KW genetic profiling; therapeutic customisation; adverse reaction;

KW clinical trial; drug approval; ds.

XX

XX Homo sapiens.

OS

XX

XX Key Location/Qualifiers

FT variation replace(20..23,GTGGTGGGTGGAG)

XX

XX /tag= a

XX

XX WO200252044-A2.

XX

XX 04-JUL-2002.

XX

XX 27-DEC-2001; 2001WO-JP011592.

XX

PR 27-DEC-2000; 2000JP-00399443.

PR 02-MAY-2001; 2001JP-00135256.

PR 27-AUG-2001; 2001JP-00256862.

XX

XX (RIKEN) RIKEN KK.

XX

XX Nakamura Y, Sekine A, Iida A, Saito S;

DR WPI; 2002-583571/62.

XX

XX

PT Identifying individuals having a polymorphism, useful for determining the

PT effectiveness or side effect of a drug or treatment protocol, comprises

PT detecting at least one polymorphism in the drug metabolizing enzyme

XX nucleic acid.

XX

PS Claim 23; Page 223; 2785pp; English.

XX

XX Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes

XX encoding enzymes associated with drug metabolism. The invention relates

XX to methods and compositions for identifying individuals who have at least

XX one polymorphism in such drug metabolizing enzyme-encoding genes. The

XX polymorphisms may be identified in a nucleic acid sample using probes or

XX primers specific for a sequence selected from ABZ43217-ABZ50887 using a

XX variety of detection assays, including hybridisation assays, nucleic acid

XX arrays and PCR-based methods. The invention also encompasses methods of

XX evaluating and screening drugs using genetic polymorphism data. Genetic

XX polymorphism data, particularly that relating to single nucleotide

XX polymorphisms (SNPs), may be used in studying the relationship between

XX DNA sequence variations and human diseases, conditions, and responses to

XX drugs. SNPs are also useful as polymorphism markers for discovering genes

XX that cause or exacerbate certain diseases. SNPs are particularly useful

XX in the above respects as they are stable in populations, occur

XX frequently, and have lower mutation rates than other genome variations

XX such as repeating sequences. The detection and analysis of polymorphisms

XX in genes encoding drug metabolizing enzymes allows the customisation of

XX drug therapies based upon the genetic profile of individual patients.

XX This would not only take the guesswork out of selecting the drug with the

XX greatest therapeutic effect for a particular patient, but would also

XX reduce the likelihood of adverse reactions, thereby increasing safety.

XX Methods of the invention are also useful in the drug discovery and

XX approval processes. For example, individuals could be selected for

XX clinical trials only if their genetic profiles indicate that they are

XX capable of responding to a particular drug or drug class, and previously

XX failed drug candidates could be revived if they were matched with more

XX appropriate patient populations. The methods, data and compositions of

XX the invention may therefore lead to an increase in the range of

XX possible drug targets and decreases in the number of adverse drug

XX reactions, failed drug trials, the time taken for a drug to be approved,

XX the length of time patients are on medication and the number of different

XX medications a patient needs to take before finding an effective therapy

XX

XX Sequence 42 BP; 5 A; 4 C; 24 G; 9 T; 0 U; 0 Other;

XX

XX Query Match 70.0%; Score 14; DB 6; Length 42;

XX Best Local Similarity 100.0%; Pred. No. 1.2e+04;

XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CACAGACAGCCCC 20

DB 33 CACAGACAGCCCC 20

RESULT 15

ABZ48406/c

ID ABZ48406 standard; DNA; 42 BP.

XX

XX ABZ48406;

XX

XX 26-JUN-2003 (first entry)

XX

XX Human ATP-binding cassette ABCB2/TAP2 gene polymorphic site, #5189.

DE Human ATP-binding cassette ABCB2/TAP2 gene polymorphic site, #5189.

XX

XX Human; drug metabolizing enzyme; gene; drug metabolism; chromosome 6;

XX

KM polymorphic site; drug evaluation; drug screening; genotyping;
 KM genetic profiling; therapeutic customisation; adverse reaction;
 KM clinical trial; drug approval; ds.

OS Homo sapiens.

Key Location/Qualifiers
 FT replacement(20..23,GTGCTGGGTGGAG)
 FT /+tag= a

PN WO200252044-A2.

PD 04-JUL-2002.

PF 27-DEC-2001; 2001WO-UP011592.

PR 27-DEC-2000; 2000JP-00399443.

PR 02-MAY-2001; 2001JP-00135256.

PR 27-AUG-2001; 2001JP-00256862.

PA (RIKE) RIKEN KK.

PI Nakamura Y, Sekine A, Iida A, Saito S;

DR WPI; 2002-583571/62.

PT Identifying individuals having a polymorphism, useful for determining the
 PT effectiveness or side effect of a drug or treatment protocol, comprises
 PT detecting at least one polymorphism in the drug metabolizing enzyme
 PT nucleic acid.

PS Claim 23; Page 165; 27855p; English.

CC Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes
 CC encoding enzymes associated with drug metabolism. The invention relates
 CC to methods and compositions for identifying individuals who have at least
 CC one polymorphism in such drug metabolising enzyme-encoding genes. The
 CC polymorphisms may be identified in a nucleic acid sample using probes or
 CC primers specific for a sequence selected from ABZ43217-ABZ50887 using a
 CC variety of detection assays, including hybridisation assays, nucleic acid
 CC arrays and PCR-based methods. The invention also encompasses methods of
 CC evaluating and screening drugs using genetic polymorphism data. Genetic
 CC polymorphisms (SNPs), particularly that relating to single nucleotide
 CC polymorphisms (SNPs), may be used in studying the relationship between
 CC DNA sequence variations and human diseases, conditions, and responses to
 CC drugs. SNPs are also useful as polymorphism markers for discovering genes
 CC that cause or exacerbate certain diseases. SNPs are particularly useful
 CC in the above respects as they are stable in populations, occur
 CC frequently, and have lower mutation rates than other genome variations
 CC such as repeating sequences. The detection and analysis of polymorphisms
 CC in genes encoding drug metabolising enzymes allows the customisation of
 CC drug therapies based upon the genetic profile of individual patients.
 CC This would not only take the guesswork out of selecting the drug with the
 CC greatest therapeutic effect for a particular patient, but would also
 CC reduce the likelihood of adverse reactions, thereby increasing safety.
 CC Methods of the invention are also useful in the drug discovery and
 CC approval processes. For example, individuals could be selected for
 CC clinical trials only if their genetic profiles indicate that they are
 CC capable of responding to a particular drug or drug class, and previously
 CC failed drug candidates could be revived if they were matched with more
 CC appropriate patient populations. The methods, data and compositions of
 CC the invention may therefore lead to an increase in the range of
 CC possible drug targets and decreases in the number of adverse drug
 CC reactions, failed drug trials, the time taken for a drug to be approved,
 CC the length of time patients are on medication and the number of different
 CC medications a patient needs to take before finding an effective therapy

SC Sequence 42 BP; 5 A; 4 C; 24 G; 9 T; 0 U; 0 Other;

Query Match 70.0%; Score 14; DB 6; Length 42;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 CACAGACAGCCCCC 20
 |||||
 Db 33 CACAGACAGCCCCC 20

Search completed: December 24, 2005, 12:29:08
 Job time : 173.4 secs

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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 10:37:31 ; Search time 1572 Seconds
(without alignments)
595.256 Million cell updates/sec

Title: US-09-296-264-12

Perfect score: 20
Sequence: 1 cgaccacacagacagaccccc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 768474

Minimum DB seq length: 20
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.8	74.0	41	2	BG616493
2	14.8	74.0	58	11	CR187505
3	14.2	71.0	53	7	CV604285
4	14.2	71.0	85	9	AZ428622
5	13.8	69.0	40	1	AA877262
6	13.8	69.0	49	1	AI815199
7	13.8	69.0	50	1	AUI04946
8	13.8	69.0	72	10	CL267582
9	13.8	69.0	76	1	AI601162
10	13.8	69.0	79	8	HA2857
11	13.8	69.0	83	11	CR828745
12	13.8	69.0	90	10	EX218915
13	13.8	69.0	93	9	AZ949869
14	13.8	69.0	100	2	BG213902
15	13.6	68.0	61	1	AI015169
16	13.6	68.0	64	1	AI061438
17	13.6	68.0	66	9	AQ254888
18	13.6	68.0	66	9	CC536588
19	13.6	68.0	66	11	DME547169
20	13.6	68.0	70	1	AI856414
21	13.6	68.0	73	9	AQ254591
22	13.6	68.0	82	8	T25069

23	13.6	68.0	91	11	DME546741	AJ546741 Drosophila
24	13.6	68.0	92	1	AA866273	AA866273 o338f06.s
25	13.6	68.0	94	10	CZ071607	CZ071607 TRGA SSRO
26	13.4	67.0	49	7	CN601471	CN601471 EG-MOI_00
27	13.4	67.0	53	11	CR095894	CR095894 Reverse B
28	13.4	67.0	88	1	AA270168	AA270168 va58h01.r
29	13.4	67.0	97	5	B0614622	B0614622 IK99e01.y
30	13.2	66.0	44	10	AJ596054	AJ596054 Arabidops
31	13.2	66.0	45	9	AZ954608	AZ954608 2M0220524
32	13.2	66.0	61	1	AI612903	AI612903 cy33d04.x
33	13.2	66.0	61	8	H39535	H39535 y168a08.r1
34	13.2	66.0	66	9	AF219041	AF219041 AF219041
35	13.2	66.0	69	7	CR559334	CR559334 DKF204680
36	13.2	66.0	72	3	B0271752	B0271752 ik17h10.x
37	13.2	66.0	73	3	BM128826	BM128826 if17b08.x
38	13.2	66.0	81	1	AI828860	AI828860 t681g12.x
39	13.2	66.0	82	10	AL943582	AL943582 Arabidops
40	13.2	66.0	84	2	BE566379	BE566379 601339975
41	13.2	66.0	84	8	W21701	W21701 ZEST00787 M
42	13.2	66.0	86	3	BM312177	BM312177 ig41b10.x
43	13.2	66.0	87	10	CL302042	CL302042 P009E08 G
44	13.2	66.0	90	3	BM353195	BM353195 ig76h05.x
45	13.2	66.0	97	2	BE463686	BE463686 hx79b04.x

ALIGNMENTS

RESULT 1
LOCUS BG616493 41 bp mRNA linear EST 18-APR-2001
DEFINITION 602616656P1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:4733796 5',
RNA sequence.
BG616493
VERSION BG616493.1 GI:13667864
ACCESSION
KEYWORDS
SOURCE
ORGANISM

Homo sapiens (human)
Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 41)

REFERENCE NIH-MGC http://mgc.nci.nih.gov/.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.llnl.gov
Plate: LNCM595 row: 0 column: 13.

FEATURES

source

Location/Qualifiers
1..41
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4733796"
/lab_host="DH10B (TI phage-resistant)"
/clone_id="NIH_MGC_76"
/note="Organ: liver; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggccgctggcgc); Site 2: SfiI (ggccatcagcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTAATGCGC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGAGCGCGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.85 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

[illegible]

FEATURES	source	1. .53	/organism="Atellomycetes capsulatus"	
			/mol_type="mRNA"	
			/strain="G217B"	
			/db_xref="taxon:5037"	
			/dev_stage="mycelia"	
			/lab_host="GC10"	
			/clone_1lb="Hc7B_M"	
			/notes="Vector: PCR4-TOPO; Site 1: EcoRI flanks TA cloning site; Site 2: EcoRI flanks TA cloning site; polyA mRNA was captured with oligo d(T) magnetic beads and eluted. for AACGAGGGTAAACAGCAGAGTACTTTTATTTTATTTTAA was used for priming reverse transcription in the presence of Superscript II Rase. The 5' primer (5' GCCGGCGGCTTAATACGATCCTATATAGGG) annealed to cytosine nucleosides added by terminal transferase to the 5' end of the transcript. Amplification during the PCR used primers 5' AACGAGGGTAAACAGCAGCAGA and 5' GCCGGCTTAATACGATCCTATAGGG and Clone-TOECH Tag DNA polymerase. PCR products between 500 and 2,000 bp were size-fractionated from 0.7% LE/TAE agarose and cloned into the TOPO TA site of Invitrogen plasmid vector PCR4-TOPO."	
ORIGIN				
Query Match		71.0%;	Score 14.2;	DB 7;
Best Local Similarity		84.2%;	Pred. No. 9.6e+04;	
Matches	16;	Conservative	0;	Mismatches 3; Indels 0; Gaps 0;
Qy	2	GACCCCAAGACAGCCCCC	20	
Db	50	GACCCCAAAATGGCCCCC	32	
RESULT 4				
AZ428622				
LOCUS				
DEFINITION				
ACCESSION				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
COMMENT				
FEATURES				
source				

`/organism="Mus musculus"`
`/mol_type="genomic DNA"`
`/strain="C57BL/6J"`
`/db_xref="taxon:10090"`
`/clone="U061CM0212N10"`
`/sex="Male"`
`/lab_host="E. Coli strain XL10-gold, T1-resistant, F-"`
`/clone_libs="Mouse 10kb plasmid U061CM library"`
`/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD2 (G11473211[g]AF12972.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-gold (Stratagene) cells and selected for ampicillin resistance."`

ORIGIN

Query Match	71.0%;	Score 14.2;	DB 9;	Length 85;
Best Local Similarity	84.2%;	Pred. No. 1e+05;		
Matches 16;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;

Qy	2	GACCCACAGACGCCCC	20
Db	15	GACTCAGACACCCCCC	33

RESULT 5	AA877262/c	LOCUS	DEFINITION
	AA877262	40 bp	mRNA
	ng94d06.01	NCI CGAP Co10 Homo sapiens	linear
	similar to gb:U6038	TYROSINE-PROTEIN KINASE LYN (HUMAN);	EST 31-MAR-1998
	sequence.		IMAGE:115979 3'

ACCESSION	AA877262
VERSION	AA877262.1
KEYWORDS	EST.

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

REFERENCE	1 (bases 1 to 40)
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL	Tumor Gene Index
COMMENT	Unpublished (1997)
	Contact: Robert Strausberg, Ph.D.

Email: CGabbs-rc@mail.nih.gov
Tissue Procurement: Ian Kirsch, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/MLML at: www-bio.lml.gov/bdip/image/image.html

Trace considered overall poor quality
Insert Length: 1388 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.

FEATURES

Source

```

1..40
/organism="Homo sapiens"
/mol_type="mrna"
/db_xref="taxon:9606"
/clone="IMAGE:1159979"
/tissue_type="colon tumor RER+"
/lab_host="DH10B"
/clone_1fb="Not CGAP Col10"
name="Organ.colon.Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
RER+ colon tumor, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adapters (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT73
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo (N-Soares)". "

```

ORIGIN

Query Match	69.0%	Score 13.8	DB 1	Length 40;
Best Local Similarity	88.2%	Pred. No. 1.4e+05;		
Matches 15; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

Qy	1	CGACCCACAGACAGCC	17
Db	38	CGAGCCAGAGACAGCC	22

LOCUS	DEFINITION	LOCUS	DEFINITION
AI815199	w772c04.x1 NCI CGAP Pan1 Homo sapiens CDNA IMAGE:2420934 3'	AI815199	49 bp mRNA linear EST 07-MAR-2000
AI815199	similar to SW:PRP4 HUMAN P10163 SALIVARY PROLINE-RICH PROTEIN PO	AI815199	49 bp mRNA linear EST 07-MAR-2000
AI815199	PRECURSOR ;, mRNA Sequence.	AI815199	49 bp mRNA linear EST 07-MAR-2000

ACCESSION	AI815199
VERSION	AI815199.1
KEYWORDS	EST.
SOURCE	Homo sapiens (human)

REFERENCE
AUTHORS NCBI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

JOURNAL COMMENT **Unpublished (1997)**
Contact: Robert Strausberg, Ph.D.

Email: cgaps-remail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www-bio.linn.gov/bdtp/image/image.html

Trace considered overall poor quality
Insert Length: 300 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.

FEATURES
SOURCE

```

1..49
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2420934"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/clone_1b="NCI CGAP Pan1"
/note="Organ: pancreas; Vector: pCMV-Sport6; Site 1: SalI;
Site 2: NotI. Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.72 kb. Life Technologies catalog #:
11548-013"

```

ORIGIN

Query Match 69.0%; Score 13.8; DB 1; Length 49;
 Best Local Similarity 88.2%; Pred. No. 1.4e+05;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 CCCACAGACAGCCCC 20
 |||||
 26 CCCCAAGAGAGCCCC 42

Db

RESULT 7
 AUI04946/c 50 bp mRNA linear EST 28-JAN-2004
 LOCUS AUI04946 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 DEFINITION HRC05670, mRNA sequence.
 ACCESSION AUI04946
 VERSION AUI04946.1 GI:13554467
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 50)
 Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
 Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
 Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
 Diverse transcriptional initiation revealed by fine, large-scale
 mapping of mRNA start sites
 EMBO Rep. 2 (5), 388-393 (2001)
 11375929

JOURNAL PUBMED
 COMMENT Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
 Sugano, S. Construction and characterization of a full
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
 149-156 (1997).

FEATURES
 Location/Qualifiers
 1..50
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="HRC05670"
 /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 69.0%; Score 13.8; DB 1; Length 50;
 Best Local Similarity 88.2%; Pred. No. 1.4e+05;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 CCCACAGACAGCCCC 20
 |||||
 38 CCCCGACAGACCCCC 22

Db

RESULT 8
 CL267582 72 bp DNA linear GSS 08-FEB-2005
 LOCUS Ggal_128d_LR_D05 Ggal LR-1 Gallus gallus genomic clone
 DEFINITION Ggal_128d_LR_D05, genomic survey sequence.
 ACCESSION CL267582
 VERSION CL267582.1 GI:58744924
 KEYWORDS GSS.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 1 (bases 1 to 72)
 Wicker, T., Robertson, J.S., Schulze, S.R., Feltus, F.A., Magrini, V.,
 Morrison, J.A., Mardis, E.R., Wilson, R.K., Peterson, D.G.,

TITLE Paterson, A.H. and Ivarie, R.
 JOURNAL The repetitive landscape of the chicken genome
 PUBMED Genome Res. 15 (1), 126-136 (2005)
 15256510

COMMENT Contact: Paterson AH
 Plant Genome Mapping Laboratory
 University of Georgia, Center for Applied Genetic Technologies
 Riverbend Research Laboratory, Room 162, 110 Riverbend Road,
 Athens, GA 30602 USA
 Tel: 7065830169
 Fax: 7065830160
 Email: paterson@uga.edu
 Sequence from single/low-copy (SL) Cot fraction, Cot >100
 Class: Hydroxyapatite-fractionated DNA.

FEATURES
 Location/Qualifiers
 1..72
 /organism="Gallus gallus"
 /mol_type="genomic DNA"
 /db_xref="taxon:9031"
 /clone="Ggal_128d_LR_D05"
 /sex="female"
 /clone_lib="Ggal_LR-1"
 /note="Produced by Cot-based cloning and sequencing
 (CBCS)"

ORIGIN

Query Match 69.0%; Score 13.8; DB 10; Length 72;
 Best Local Similarity 88.2%; Pred. No. 1.5e+05;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 GACCCACAGACAGCCC 18
 |||||
 58 GACCCCATAGAGAGCCC 42

Db

RESULT 9
 A1601162 76 bp mRNA linear EST 21-APR-1999
 LOCUS a1601162.1
 DEFINITION a1601162.1 Bartshead colon HPLRB7 Homo sapiens cDNA clone
 IMAGE:2152442.3, similar to TR:Q62901 Q62901 ATROHIN-1 RELATED
 PROTEIN, mRNA sequence.

ACCESSION A1601162
 VERSION A1601162.1 GI:4610368
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 76)
 Hillier, L., Allen, M., Bowles, J., Dubuque, T., Geisel, G., Jost, S.,
 Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,
 Martin, J., Moore, B., Scheinberg, K., Seepoe, M., Tan, F.,
 Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
 WashU-NCI human EST Project
 Unpublished (1997)

JOURNAL
 COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Trace considered overall poor quality
 Possible reversed clone; similarity on wrong strand
 Seq primer: -40UP from Gibco
 High quality sequence stop: 1.

FEATURES
 Location/Qualifiers
 1..76
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"

```

/c/clone="IMAGE:2152442"
/dev_stage="adult, age 25"
/lab_host="DH10B (phage resistant)"
/clone_1ib="Barcode colon HPLRB7"
/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: EcoRI; Site 2: NotI; 1st strand cDNA was primed with a Not I - oligo(dT) primer (5' TGTTGCAATCTGAAGTGACGGCCGCCCTTTTTTTTTTTTTTTTTTTT 3'); double-stranded cDNA was ligated to Eco RI adaptors [5' ATTACTAGTAAT 3' and 5' ATTACTAGTG 3'], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library constructed by Bob Barcode."

ORIGIN

Query Match      69.0%; Score 13.8; DB 1; Length 76;
Best Local Similarity 88.2%; Pred. No. 1.5e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4   CCCACAGACGCCCC 20
          ||||| | | | | |
Db       27  CCCACAGATAGACCCC 43

RESULT 10
LOCUS     H42857              79 bp    mRNA    linear    EST J1-JUL-1995
DEFINITION yo10e01.a1 Soares adult brain N2b5H55Y Homo sapiens cDNA clone IMAGE:177528 3' similar to gb:M64241 QM PROTEIN (HUMAN);, mRNA sequence.
ACCESSION H42857
VERSION   H42857.1 GI:918909
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 79)
AUTHORS  Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Holtman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,U., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Tiveakskis,E., Waterston,R., Williamson,A., Woldmann,P. and Wilson,R.
TITLE     The Mashu-Merck EST Project
JOURNAL   Unpublished (1995)
COMMENT   Contact: Wilson RK
           Washington University School of Medicine
           444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
           Tel: 314 286 1800
           Fax: 314 286 1810
           Email: est@watson.wustl.edu
           Insert Size: 1472
           High quality sequence starts: 1
           High quality sequence stops: 1
           Source: IMAGE Consortium, LNLN
           This clone is available royalty-free through LNLN; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
           Trace considered overall poor quality
           Insert Length: 1472 Std Error: 0.00
           Seq primer: Promega -2im13
           High quality sequence stop: 1.
           Location/Qualifiers
             1..79
               /organism="Homo sapiens"
               /mol_type="mRNA"
               /db_xref="GDB:3839724"
               /db_xref="taxon:9606"
               /clone="IMAGE:177528"
               /sex="Male"
               /dev_stage="55-year old"
               /lab_host="DH10B (ampicillin resistant)"

```

```

/clone_lib="Soares adult brain N25SHB5Y"
/note="Organ: brain; Vector: pT73D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTCGCGAGCGCGCGCTTTTTTTTTTTT 3'] double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 53. Library constructed by Bento Soares and M.Patima Ronaldo. The adult brain RNA was provided by Dr. Donald H. Gilden. Tissue was acquired 17-18 hours after death which occurred in consequence of ruptured aortic aneurysm. RNA was prepared from a pool of tissues representing the following areas of the brain: frontal, parietal, temporal and occipital cortex from the left and right hemispheres, subcortical white matter, basal ganglia, thalamus, cerebellum, midbrain, pons and medulla."

ORIGIN

Query Match          69.0%; Score 13.8; DB 8; Length 79;
Best Local Similarity 88.2%; Pred. No. 1.5e+05;
Matches    15; Conservative      0; Mismatches   2; Indels     0; Gaps     0.

Oy      2  GACCCGACAGACGCC 18
         |||||
Db       28  GACCCGACAGCATTCCC 44

RESULT 11
CR828745/c      83 bp DNA linear GSS 27-sep-2004
LOCUS           GR0AAA60A08PM1 INRA BAC Bos taurus genomic clone INRab_19A05, DNA
DEFINITION     sequence, genomic survey sequence.
ACCESSION      CR828745
VERSION        CR828745.1 GI:52764834
KEYWORDS       GSS.
SOURCE         Bos taurus (cow)
ORGANISM       Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 83)
Bovine BAC End Sequences from the INRA bovine BAC library
Unpublished
2 (bases 1 to 83)
Genoscope.
Direct Submission
Submitted (20-SEP-2004) Genoscope - Centre National de Sequençage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segr@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
Contact: Andre Eggen
Department of Animal Genetics - LGDC
INRA
78350 Jouy-en-Josas, France
Tel: 33 1 34 65 24 24
Fax: 33 1 34 65 24 78
Email: eggen@jouy.inra.fr
Clones are derived from the INRA bovine BAC library
(http://locus.jouy.inra.fr/fpc/cattle_bac_map.htm). For BAC library
availability, please contact Andre Eggen (eggen@jouy.inra.fr). This
work was undertaken as part of the International Bovine BAC
Mapping Consortium (IBMC) by INRA (Jouy-en-Josas) and Genoscope
(Evry) Plate: 19 row: A column: 05
Seq primer: M13 Forward
Class: BAC ends.
Location/Qualifiers
1..83
organism="Bos taurus"
mol_type="genomic DNA"
strain="Bred: Holstein"
```

/db_xref="taxon:9913"
 /clone="INRAB_19A05"
 /sex="Male"
 /cell_type="fibroblast"
 /clone_lib="INRA Bovine BAC"
 /note="Vector: pBelBAC11; Site: 1: HindIII; Holstein bull;
 INRA Bovine BAC library (Male) produced by Andre Esgen
 Genoscope sequence ID : GR0AAA60AG08FM1"

ORIGIN

Query Match 69.0%; Score 13.8; DB 11; Length 83;
 Best Local Similarity 88.2%; Pred. No. 1.5e+05;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CCCCACAGACAGCCCC 20
 43 CCCCACAGACTCCCCC 27

Db

RESULT 12
 BX218915 90 bp DNA linear GSS 29-JAN-2003
 DEFINITION Danio rerio genomic clone DKEX-270H12, genomic survey sequence.
 ACCESSION BX218915
 VERSION BX218915.1 GI:28050801
 KEYWORDS GSS.
 SOURCE Danio rerio (zebrafish)

ORIGIN

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Danio.
 1 (bases 1 to 90)
 Humphray, S.J., Huckle, E. and Durham, J.L.
 Direct Submission
 Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome
 Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
 humphray@sanger.ac.uk Unpublished

REFERENCE

AUTHORS
 TITLE
 JOURNAL
 COMMENT
 This sequence was generated from the T7 end of BAC 270H12. 270H12
 is part of the Danio rerio BAC library created by R. Plasterk and N.V.
 Keygene. Further details:
 http://www.sanger.ac.uk/Projects/D_rerio/
 Location/Qualifiers

FEATURES

source
 1..90
 /organism="Danio rerio"
 /mol_type="genomic DNA"
 /db_xref="taxon:7955"
 /clone="DKEX-270H12"
 /issue_type="Testis"
 /note="Vector pIndigoBAC-536"

ORIGIN

Query Match 69.0%; Score 13.8; DB 10; Length 90;
 Best Local Similarity 88.2%; Pred. No. 1.5e+05;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGACCCACAGACGCC 17
 72 CGACCCACAGACGAC 88

Db

RESULT 13
 AZ949869 93 bp DNA linear GSS 27-APR-2001
 LOCUS 2M0213107R Mouse 10kb plasmid UGCGM library Mus musculus genomic
 DEFINITION Clone UGCGM0213107 R, genomic survey sequence.
 ACCESSION AZ949869
 VERSION AZ949869.1 GI:13821096
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM
 Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 1 (bases 1 to 93)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausen, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plates: 0213 row: 1 column: 07
 Seq primer: CACACGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 93.
 Location/Qualifiers

FEATURES

source
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCG2M0213107"
 /sex="Female"
 /lab_host="E. coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCGM library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (female) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (g14732114[gbl]AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 69.0%; Score 13.8; DB 9; Length 93;
 Best Local Similarity 88.2%; Pred. No. 1.5e+05;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ACCCAGACAGACGCC 19
 71 ACCCAGATACAGCCCC 55

Db

RESULT 14
 BG213902 100 bp mRNA linear EST 21-APR-2001
 LOCUS R3733525 Atherya RAGE library Homo sapiens cDNA, mRNA sequence.
 DEFINITION BG213902
 ACCESSION BG213902
 VERSION BG213902.1 GI:13735589
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominae; Homo.


```

REFERENCE 1 (bases 1 to 100)
AUTHORS Harrington,J.J., Sherf, B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramchandran,R.,
Whittington,J., Lerner,J., Costanzo,D., McElligott,K., Booser,S.,
Mays,R., Smith,E., Veloso,N., Kliska,A., Hesse,J., Cothren,K., Lo,K.,
Offenbacher,J., Danzig,J., and Ducar,M.
TITLE Creation of genome-wide protein expression libraries using random
activation of gene expression
JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
PUBMED 11329013
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com.
FEATURES
source
1..100
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="HT1080"
/clone_lib="Athersys RAGE library"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology' in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
ORIGIN
Query Match 69.0%; Score 13.8; DB 2; Length 100;
Best Local Similarity 88.2%; Pred. No. 1.5e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 ACCCCACAGACGCCCC 19
DB 46 ACCCCAAAGAGAGCCCC 62
RESULT 15
LOCUS A1015169 61 bp mRNA linear EST 16-JUN-1998
DEFINITION ot74905.81 Soares fetal_fetus_Nb2HP8 9w Homo sapiens cDNA clone
IMAGE:1622552.3' similar to TR:P94915 P94915
GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE HOMOLOG. ; mRNA sequence.
ACCESSION A1015169
VERSION A1015169.1 GI:32295505
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 61)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-rcmail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: -40m3 fwd. ET from Amersham
High quality sequence stop: 1.
location/Qualifiers
1..61
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1622552"
/dev_stage="8-9 weeks"
FEATURES
source

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/lab host="DH108"
/clone_lib="Soares fetal_fetus_Nb2HP8 9w"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from pooled 8-9 week
(fetal) fetus material with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAAGGAGGAGCGCGCTTAATTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo. "
ORIGIN
Query Match 68.0%; Score 13.6; DB 1; Length 61;
Best Local Similarity 80.0%; Pred. No. 1.8e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CGACCCACAGACGCCCC 20
DB 3 CGGCACACAGACCGCCCC 22
Search completed: December 24, 2005, 18:28:47
Job time : 1575 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 11:34:25 ; Search time 48.1 Seconds

(without alignments)
739.111 Million cell updates/sec

Title: US-09-296-264-12

Perfect score: 20
Sequence: 1 cgaccccccagacagcccc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1134872

Minimum DB seq length: 20
Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents NA:*

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- 2: /cgn2_6/ptodata/1/ina/5 COMB.seq:*
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- 5: /cgn2_6/ptodata/1/ina/H COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/PTUS COMB.seq:*
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- 8: /cgn2_6/ptodata/1/ina/RE COMB.seq:*
- 9: /cgn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15.8	79.0	25	3	US-09-396-196G-106480
2	14.2	71.0	60	2	US-08-353-476-56
3	13.8	69.0	25	2	US-08-447-179-8
4	13.8	69.0	30	3	US-09-270-542-11
5	13.6	68.0	22	3	US-09-425-804-24
6	13.6	68.0	26	2	US-08-145-704-20
7	13.6	68.0	26	2	US-08-145-704-25
8	13.6	68.0	26	2	US-08-145-704-27
9	13.6	68.0	26	3	US-08-987-574-20
10	13.6	68.0	26	3	US-08-987-574-25
11	13.6	68.0	26	3	US-08-987-574-27
12	13.6	68.0	26	3	US-08-535-168-20
13	13.6	68.0	26	3	US-08-535-168-25
14	13.6	68.0	26	3	US-08-535-168-27
15	13.6	68.0	26	3	US-09-017-974-20
16	13.6	68.0	26	3	US-09-017-974-25
17	13.6	68.0	26	3	US-09-017-974-27
18	13.6	68.0	26	3	US-08-682-255A-20
19	13.6	68.0	26	3	US-08-682-255A-25
20	13.6	68.0	26	3	US-08-682-255A-27
21	13.6	68.0	26	3	US-09-429-130-20
22	13.6	68.0	26	3	US-09-429-130-25
23	13.6	68.0	26	3	US-09-429-130-27
24	13.6	68.0	26	6	PCT-US96-11786-20

c	25	13.6	68.0	26	6	PCT-US96-11786-25	Sequence 25, Appl
c	26	13.6	68.0	26	6	PCT-US96-11786-27	Sequence 27, Appl
c	27	13.6	68.0	45	2	US-08-145-704-21	Sequence 21, Appl
c	28	13.6	68.0	45	2	US-08-145-704-22	Sequence 22, Appl
c	29	13.6	68.0	45	3	US-08-987-574-21	Sequence 21, Appl
c	30	13.6	68.0	45	3	US-08-987-574-22	Sequence 22, Appl
c	31	13.6	68.0	45	3	US-08-535-168-21	Sequence 21, Appl
c	32	13.6	68.0	45	3	US-08-535-168-22	Sequence 22, Appl
c	33	13.6	68.0	45	3	US-09-017-974-21	Sequence 21, Appl
c	34	13.6	68.0	45	3	US-09-017-974-22	Sequence 22, Appl
c	35	13.6	68.0	45	3	US-08-682-255A-21	Sequence 21, Appl
c	36	13.6	68.0	45	3	US-08-682-255A-22	Sequence 22, Appl
c	37	13.6	68.0	45	3	US-09-429-130-21	Sequence 21, Appl
c	38	13.6	68.0	45	3	US-09-429-130-22	Sequence 22, Appl
c	39	13.6	68.0	45	6	PCT-US96-11786-21	Sequence 21, Appl
c	40	13.6	68.0	45	6	PCT-US96-11786-22	Sequence 22, Appl
c	41	13.6	68.0	87	3	US-09-513-999C-14489	Sequence 14489, A
c	42	13.4	67.0	25	3	US-09-396-196G-43777	Sequence 43777, A
c	43	13.4	67.0	25	3	US-09-396-196G-77695	Sequence 77695, A
c	44	13.4	67.0	25	3	US-09-396-196G-77696	Sequence 77696, A
c	45	13.4	67.0	32	2	US-08-867-941-60	Sequence 60, Appl

ALIGNMENTS

```
RESULT 1
US-09-396-196G-106480
; Sequence 106480, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: PasteSeq for Windows Version 4.0
; SEQ ID NO 106480
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-106480

Query Match      79.0%; Score 15.8; DB 3; Length 25;
Best Local Similarity 89.5%; Pred. No. 5.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      1 CGACCCACGACGACGACCC 19
Db      6 CGACCCGACGACGACGAC 24

RESULT 2
US-08-353-476-56
; Sequence 56, Application US/08353476
; Patent No. 5871802
; GENERAL INFORMATION:
; APPLICANT: Weininger, Susan
; APPLICANT: Weininger, Arthur M
; TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A
; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
; NUMBER OF SEQUENCES: 117
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st St., Suite A-1
; CITY: Gainesville
; STATE: Florida
```

```

; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/353,476
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Bencen, Gerard H
; REGISTRATION NUMBER: 35,746
; REFERENCE/DOCKET NUMBER: GP-100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 372-5800
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 60 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; US-08-353-476-56

Query Match          71.0%; Score 14.2; DB 2; Length 60;
Best Local Similarity 84.2%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 GACCCACAGACAGCCCC 20
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DB      15 GACACCACAGACAGCCCC 33

RESULT 3
US-08-447-179-8/c
; Sequence 8, Application US/08447179
; Patent No. 5744303
; GENERAL INFORMATION:
; APPLICANT: Iggo, Richard
; APPLICANT: Friend, Stephen H.
; APPLICANT: Feboury, Thierry
; APPLICANT: Ishioka, Chikashi
; TITLE OF INVENTION: FUNCTIONAL ASSAY FOR TUMOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 558X
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,179
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/046,033
; FILING DATE: 12 APRIL 1993
; APPLICATION NUMBER: 07/956,696
; FILING DATE: 10 OCTOBER 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
```

```

; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/159002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-447-179-8

Query Match          69.0%; Score 13.8; DB 2; Length 25;
Best Local Similarity 88.2%; Pred. No. 3.8e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4 CCCCACAGACAGCCCC 20
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DB      20 CCCCACAGACAGCCTCC 4

RESULT 4
US-09-270-542-11
; Sequence 11, Application US/09270542
; Patent No. 6322976
; GENERAL INFORMATION:
; APPLICANT: Altman, Timothy
; APPLICANT: Scott, James
; APPLICANT: Stanton, Lawrence
; TITLE OF INVENTION: Compositions and Methods of Disease Diagnosis and
; TITLE OF INVENTION: Therapy
; FILE REFERENCE: 4198/78179
; CURRENT APPLICATION NUMBER: US/09/270,542
; CURRENT FILING DATE: 1999-03-17
; EARLIER APPLICATION NUMBER: 09/221,222
; EARLIER FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-09-270-542-11

Query Match          69.0%; Score 13.8; DB 3; Length 30;
Best Local Similarity 88.2%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GACCCACAGACAGCCC 18
        ||| ||| ||| ||| |||
DB      9 GACCCCAAGACAGCAC 25

RESULT 5
US-09-425-804-24
; Sequence 24, Application US/09425804
; Patent No. 6867289
; GENERAL INFORMATION:
; APPLICANT: Gorenstein, David G.
; APPLICANT: King, David U.
; APPLICANT: Ventura, Daniel A.
; APPLICANT: Brasier, Allan R.
; TITLE OF INVENTION: Thio-Modified Aptamer Synthetic Methods and
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: 122144-00200
; CURRENT APPLICATION NUMBER: US/09/425,804
; CURRENT FILING DATE: 1999-10-25
; PRIOR APPLICATION NUMBER: 60/105,600
; PRIOR FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
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SEQ ID NO 24
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: aptamer
US-09-425-804-24

Query Match 68.0%; Score 13.6; DB 3; Length 22;
Best Local Similarity 80.0%; Pred. No. 4.7e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGACCCACAGACGCCCC 20
Db 3 CCCCCACACACGCCCC 22

RESULT 6

US-08-145-704-20/c
Sequence 20, Application US/08145704
Patent No. 5567604

GENERAL INFORMATION:
APPLICANT: Rando, Robert F.
APPLICANT: Fennwald, Susan
APPLICANT: Zendegeu, Joseph G.
APPLICANT: Joshua O. Ojwang
TITLE OF INVENTION: Anti-viral Guanosine-Rich
TITLE OF INVENTION: Oligonucleotides
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESSES:
ADDRESS: Fulbright & Jaworski
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/145,704
FILING DATE: 28-OCT-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,027
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5574-CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5151
TELEFAX: 713/651-5246
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 26
OTHER INFORMATION: /note= "Amine moiety attached to 3'
OTHER INFORMATION: end"
US-08-145-704-20

Query Match 68.0%; Score 13.6; DB 2; Length 26;
Best Local Similarity 80.0%; Pred. No. 4.7e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGACCCACAGACGCCCC 20
Db 23 CCCCCACACACGCCCC 4

RESULT 7

US-08-145-704-25/c
Sequence 25, Application US/08145704
Patent No. 5567604

GENERAL INFORMATION:
APPLICANT: Rando, Robert F.
APPLICANT: Fennwald, Susan
APPLICANT: Zendegeu, Joseph G.
APPLICANT: Joshua O. Ojwang
TITLE OF INVENTION: Anti-viral Guanosine-Rich
TITLE OF INVENTION: Oligonucleotides
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESSES:
ADDRESS: Fulbright & Jaworski
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/145,704
FILING DATE: 28-OCT-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,027
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5574-CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5151
TELEFAX: 713/651-5246
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 26
OTHER INFORMATION: /note= "cholesterol moiety attached
OTHER INFORMATION: to 3' end"
US-08-145-704-25

Query Match 68.0%; Score 13.6; DB 2; Length 26;
Best Local Similarity 80.0%; Pred. No. 4.7e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGACCCACAGACGCCCC 20
Db 23 CCCCCACACACGCCCC 4

RESULT 8

US-08-145-704-27/c
Sequence 27, Application US/08145704
Patent No. 5567604

GENERAL INFORMATION:

APPLICANT: Rando, Robert F.
APPLICANT: Fennewald, Susan
APPLICANT: Zendegui, Joseph G.
APPLICANT: Joshua O. Ojwang
TITLE OF INVENTION: Anti-Viral Guanosine-Rich
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fulbright & Jaworski
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/145,704
FILING DATE: 28-OCT-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,027
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5574-CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5151
TELEFAX: 713/651-5246
TELEX: 762829
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 26
OTHER INFORMATION: /note="phosphorothioate backbone"
OTHER INFORMATION: and amine moiety attached to backbone"
US-08-145-704-27

Query Match 68.0%; Score 13.6; DB 2; Length 26;
Best Local Similarity 80.0%; Pred. No. 4.7e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGACCCCAAGACAGCCCC 20
DB 23 CCACCCCAAGACAGCCCC 4

RESULT 9
US-08-987-574-20/c
Sequence 20, Application US/08987574
Patent No. 6150339
GENERAL INFORMATION:
APPLICANT: Rando, Robert F.
APPLICANT: Fennewald, Susan
APPLICANT: Zendegui, Joseph G.
APPLICANT: Ojwang, Joshua O.
APPLICANT: Hogan, Michael E.
TITLE OF INVENTION: Anti-Viral Guanosine-Rich
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fulbright & Jaworski
STREET: 1301 McKinney, Suite 5100

CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/987,574
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04529
FILING DATE: 28-OCT-1993
APPLICATION NUMBER: US 08/053,027
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5574-CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5151
TELEFAX: 713/651-5246
TELEX: 762829
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 26
OTHER INFORMATION: /note="Amine moiety
OTHER INFORMATION: attached to 3' end"
US-08-987-574-20

Query Match 68.0%; Score 13.6; DB 3; Length 26;
Best Local Similarity 80.0%; Pred. No. 4.7e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGACCCCAAGACAGCCCC 20
DB 23 CCACCCCAAGACAGCCCC 4

RESULT 10
US-08-987-574-25/c
Sequence 25, Application US/08987574
Patent No. 6150339
GENERAL INFORMATION:
APPLICANT: Rando, Robert F.
APPLICANT: Fennewald, Susan
APPLICANT: Zendegui, Joseph G.
APPLICANT: Ojwang, Joshua O.
APPLICANT: Hogan, Michael E.
TITLE OF INVENTION: Anti-Viral Guanosine-Rich
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fulbright & Jaworski
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/987,574
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04529
FILING DATE: 28-OCT-1993
APPLICATION NUMBER: US 08/053,027
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5574-CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5151
TELEFAX: 713/651-5246
TELEX: 762829
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 26
OTHER INFORMATION: /note="cholesterol moiety"
OTHER INFORMATION: attached to 3' end"
US-08-987-574-25

Query Match 68.0%; Score 13.6; DB 3; Length 26;
Best Local Similarity 80.0%; Pred. No. 4.7e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGACCCCAAGACAGCCGCC 20
Db 23 CCACCCCAAGACAGCCGCC 4

RESULT 11
US-08-987-574-27/c
Sequence 27, Application US/08987574
Patent No. 6150339
GENERAL INFORMATION:
APPLICANT: Rando, Robert F.
APPLICANT: Fennwald, Susan
APPLICANT: Zendequi, Joseph G.
APPLICANT: Ojwang, Joshua O.
APPLICANT: Hogan, Michael E.
TITLE OF INVENTION: Anti-Viral Guanosine-Rich
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/987,574
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04529
FILING DATE: 28-OCT-1993

APPLICATION NUMBER: US 08/053,027
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5574-CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5151
TELEFAX: 713/651-5246
TELEX: 762829
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 26
OTHER INFORMATION: /note="phosphorothioate
OTHER INFORMATION: backbone and amine moiety attached to
OTHER INFORMATION: backbone"
US-08-987-574-27

Query Match 68.0%; Score 13.6; DB 3; Length 26;
Best Local Similarity 80.0%; Pred. No. 4.7e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGACCCCAAGACAGCCGCC 20
Db 23 CCACCCCAAGACAGCCGCC 4

RESULT 12
US-08-535-168-20/c
Sequence 20, Application US/08535168
Patent No. 6184369
GENERAL INFORMATION:
APPLICANT: Rando, Robert F.
APPLICANT: Fennwald, Susan
APPLICANT: Zendequi, Joseph G.
APPLICANT: Ojwang, Joshua O.
APPLICANT: Hogan, Michael E.
TITLE OF INVENTION: Anti-Viral Guanosine-Rich
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,168
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04529
FILING DATE: 28-OCT-1993
APPLICATION NUMBER: US 08/053,027
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5574-CIP
TELECOMMUNICATION INFORMATION:

TELEPHONE: 713/651-5151
TELEFAX: 713/651-5246
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 26
OTHER INFORMATION: /note="Amine moiety"
OTHER INFORMATION: attached to 3' end"
US-08-535-168-20

Query Match 68.0%; Score 13.6; DB 3; Length 26;
Best Local Similarity 80.0%; Pred. No. 4.7e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CGACCCACAGACAGCCCC 20
Db 23 CCACCCACAGCAACACCCC 4

RESULT 13
US-08-535-168-25/C
Sequence 25, Application US/08535168
Patent No. 6184369
GENERAL INFORMATION:
APPLICANT: Rando, Robert F.
APPLICANT: Zennwald, Susan
APPLICANT: Zendegei, Joseph G.
APPLICANT: Ojwang, Joshua O.
APPLICANT: Hogan, Michael E.
TITLE OF INVENTION: Anti-Viral Guanosine-Rich
TITLE OF INVENTION: Oligonucleotides
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSER: Fulbright & Jaworski
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,168
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04529
FILING DATE: 28-OCT-1993
APPLICATION NUMBER: US 08/053,027
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5574-CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5151
TELEFAX: 713/651-5246
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 26
OTHER INFORMATION: /note="cholesterol moiety"
OTHER INFORMATION: attached to 3' end"
US-08-535-168-25

Query Match 68.0%; Score 13.6; DB 3; Length 26;
Best Local Similarity 80.0%; Pred. No. 4.7e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CGACCCACAGACAGCCCC 20
Db 23 CCACCCACAGCAACACCCC 4

RESULT 14
US-08-535-168-27/C
Sequence 27, Application US/08535168
Patent No. 6184369
GENERAL INFORMATION:
APPLICANT: Rando, Robert F.
APPLICANT: Zennwald, Susan
APPLICANT: Zendegei, Joseph G.
APPLICANT: Ojwang, Joshua O.
APPLICANT: Hogan, Michael E.
TITLE OF INVENTION: Anti-Viral Guanosine-Rich
TITLE OF INVENTION: Oligonucleotides
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSER: Fulbright & Jaworski
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,168
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04529
FILING DATE: 28-OCT-1993
APPLICATION NUMBER: US 08/053,027
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5574-CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5151
TELEFAX: 713/651-5246
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 26
OTHER INFORMATION: /note="phosphorothioate
OTHER INFORMATION: backbone and amine moiety attached to
OTHER INFORMATION: backbone"

US-08-535-168-27

Query Match 68.0%; Score 13.6; DB 3; Length 26;
Best Local Similarity 80.0%; Pred. No. 4.7e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Search completed: December 24, 2005, 18:36:31
Job time : 49.1 secs

QY 1 CGACCCGACGACGACCC 20
DB 23 CCACCCGACGACGACCC 4

RESULT 15

US-09-017-974-20/C
; Sequence 20, Application US/09017974
; Patent No. 6288042
; GENERAL INFORMATION:
; APPLICANT: Rando, Robert F.
; APPLICANT: Ojwang, Joshua O.
; APPLICANT: Hogan, Michael E.
; APPLICANT: Wallace, Thomas L.
; APPLICANT: Cossum, Paul A.
; TITLE OF INVENTION: Anti-Viral Guanosine-Rich
; TITLE OF INVENTION: Tetrad Forming Oligonucleotides
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Conley, Rose & Tayon, P.C.
; STREET: 600 Travis, Suite 1800
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77002-2912
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word 97 (saved as .txt file)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/017,974
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/037,374
; FILING DATE: 04-FEB-97
; APPLICATION NUMBER:
; FILING DATE: 09-DEC-97
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniel, C. Steven
; REGISTRATION NUMBER: 33,962
; REFERENCE/DOCKET NUMBER: 1472-06223
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/238-8010
; TELEFAX: 713/238-8008
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 26
; OTHER INFORMATION: /note="Amine moiety
; OTHER INFORMATION: attached to 3' end"
; US-09-017-974-20

Query Match 68.0%; Score 13.6; DB 3; Length 26;
Best Local Similarity 80.0%; Pred. No. 4.7e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGACCCGACGACGACCC 20
DB 23 CCACCCGACGACGACCC 4

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2	15.8	79.0	25	8	US-10-719-900-326337	Sequence 226337,
3	15.8	79.0	25	9	US-10-809-189-106480	Sequence 106480,
4	14.8	74.0	25	10	US-11-036-317-1296812	Sequence 196612,
5	14.8	74.0	25	10	US-11-036-317-866280	Sequence 866280
6	14.8	74.0	25	10	US-11-036-317-875037	Sequence 875037
7	14.8	74.0	25	10	US-11-036-317-904609	Sequence 904609
8	14.8	74.0	25	10	US-11-036-317-925089	Sequence 925089
9	14.8	74.0	25	10	US-11-036-317-945122	Sequence 945122
10	14.8	74.0	59	9	US-10-708-204-6770	Sequence 6770, App
11	14.4	72.0	20	9	US-10-928-805-10	Sequence 10, App
12	14.4	72.0	25	10	US-11-036-317-229142	Sequence 229142
13	14.4	72.0	25	10	US-11-036-317-238794	Sequence 238794
14	14.4	72.0	25	10	US-11-036-317-289773	Sequence 289773
15	14.4	72.0	25	10	US-11-036-317-321991	Sequence 321991
16	14.4	72.0	25	10	US-11-036-317-902096	Sequence 902096
17	14.4	72.0	60	3	US-09-908-975-18840	Sequence 18840, <i>f</i>
18	14.2	71.0	25	8	US-10-719-900-226338	Sequence 226338,
19	14.2	71.0	25	10	US-11-036-317-412186	Sequence 412186
20	14.2	71.0	25	10	US-11-036-317-559047	Sequence 559047
21	14.2	71.0	37	3	US-09-969-748C-86	Sequence 86, App
22	14.2	71.0	37	3	US-09-969-039-90	Sequence 90, App
23	14.2	71.0	41	5	US-10-005-956-195	Sequence 195, App

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	US-08-860-844-56	US-10-407-543-55	US-09-854-867-499	US-10-719-900-397010	US-10-005-956-194		US-10-005-956-194		US-10-005-956-257	US-10-794-514-615	US-10-214-417-10	US-10-756-247-10	US-10-756-247-51		US-10-098-2638-58423	US-11-036-317-118236	US-11-036-317-247083	US-11-036-317-256002	US-09-808-995-28968	US-10-261-494-5	US-10-681-773-42267	US-10-681-773-47694	US-10-681-773-71920	US-10-681-773-81753	US-10-681-773-98087		US-10-719-956-668216
	Sequence 56, App	Sequence 56, App	Sequence 499, App	Sequence 197010, App	Sequence 194, App		Sequence 194, App		Sequence 257, App	Sequence 615, App	Sequence 10, App	Sequence 22, App	Sequence 51, App		Sequence 58423, App	Sequence 178236, App	Sequence 247083, App	Sequence 256002, App	Sequence 28968, App	Sequence 5, App	Sequence 42267, App	Sequence 47694, App	Sequence 71920, App	Sequence 81753, App	Sequence 98087, App		Sequence 668216, App

ALIGNMENTS

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? RESULT 1
? US-09-296-264-12
? Sequence 12, Application US/09296264
? Publication No. US20030083274A1
? GENERAL INFORMATION:
? APPLICANT: WRIGHT, Jim A.
? APPLICANT: YOUNG, Aiping H.
? APPLICANT: LEE, Yoon S.
? TITLE OF INVENTION: NEUROFILIN ANTISENSE OLIGONUCLEOTIDE SEQUENCES AND
? TITLE OF INVENTION: METHODS OF USING SAME TO MODULATE CELL GROWTH
? FILE REFERENCE: 032396-043
? CURRENT APPLICATION NUMBER: US/09/296,264
? CURRENT FILING DATE: 1999-04-22
? EARLIER APPLICATION NUMBER: US 60/082,791
? EARLIER FILING DATE: 1998-04-23
? NUMBER OF SEQ ID NOS: 35
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 12
? LENGTH: 20
? TYPE: DNA
? ORGANISM: Human
? US-09-296-264-12

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Query Match      100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 29;
Matches      20; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

Cy          1 CGACCCCGACAGACGCCCCC 20
            |||||
Db          1 CGACCCCGACAGACGCCCCC 20
            |||||

RESULT 2
US-10-719-900-226337
Sequence 226337, Application US/10719900
Publication No. US2005026164A1
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 962914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

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; SEQ ID NO 226337
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-226337

Query Match          79.0%; Score 15.8; DB 8; Length 25;
Best Local Similarity 89.5%; Pred. No. 2e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      2 GACCCACAGACAGCCCC 20
DB      7 GACCCGACAGACAGCCCC 25

RESULT 3
US-10-809-189-106480
; Sequence 106480, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltman
; APPLICANT: David Mack
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 106480
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-809-189-106480

Query Match          79.0%; Score 15.8; DB 9; Length 25;
Best Local Similarity 89.5%; Pred. No. 2e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      1 CGACCCACAGACAGCCCC 19
DB      6 CGACCCCAAGACAGCCAC 24

RESULT 4
US-11-036-317-196812/c
; Sequence 196812, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 196812
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-196812

Query Match          74.0%; Score 14.8; DB 10; Length 25;
Best Local Similarity 88.9%; Pred. No. 5.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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OY      3 ACCCCACAGACAGCCCC 20
DB      25 AGCCACAGACAGCCCC 8

RESULT 5
US-11-036-317-866280/c
; Sequence 866280, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 866280
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-866280

Query Match          74.0%; Score 14.8; DB 10; Length 25;
Best Local Similarity 88.9%; Pred. No. 5.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      2 GACCCACAGACAGCCCC 19
DB      20 GACTCCATGACAGCCCC 3

RESULT 6
US-11-036-317-875037/c
; Sequence 875037, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 875037
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-875037

Query Match          74.0%; Score 14.8; DB 10; Length 25;
Best Local Similarity 88.9%; Pred. No. 5.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      3 ACCCCACAGACAGCCCC 20
DB      25 AGCCACAGACAGCCCC 8

RESULT 7
US-11-036-317-904609/c
; Sequence 904609, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
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; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 904609
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-904609

Query Match
Best Local Similarity 74.0%; Score 14.8; DB 10; Length 25;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 GACCCACAGACAGCCCC 19
Db 25 GACTCCATGACAGCCCC 8

RESULT 8
US-11-036-317-925089/c
; Sequence 925089, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 925089
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-925089

Query Match
Best Local Similarity 74.0%; Score 14.8; DB 10; Length 25;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 GACCCACAGACAGCCCC 19
Db 22 GACTCCATGACAGCCCC 5

RESULT 9
US-11-036-317-946122/c
; Sequence 946122, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 946122
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-946122

Query Match
Best Local Similarity 74.0%; Score 14.8; DB 10; Length 25;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 GACCCACAGACAGCCCC 19
Db 22 GACTCCATGACAGCCCC 5

RESULT 10
US-10-708-204-6770
; Sequence 6770, Application US/10708204
; Publication No. US20050222399A1
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES
; FILE REFERENCE: 55033
; CURRENT APPLICATION NUMBER: US/10/708,204
; CURRENT FILING DATE: 2004-02-16
; NUMBER OF SEQ ID NOS: 7351
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6770
; LENGTH: 59
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-708-204-6770

Query Match
Best Local Similarity 74.0%; Score 14.8; DB 9; Length 59;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 CGACCCACAGACAGCCCC 18
Db 10 CGACCCACAGACAGCCCC 27

RESULT 11
US-10-928-805-10/c
; Sequence 10, Application US/10928805
; Publication No. US20050095706A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Su-Chun
; APPLICANT: Thomson, James A.
; APPLICANT: Duncan, Ian D.
; APPLICANT: Li, Xue-Jun
; TITLE OF INVENTION: METHOD OF IN VITRO DIFFERENTIATION OF TRANSPLANTABLE NEURAL
; TITLE OF INVENTION: PRECURSOR CELLS FROM PRIMATE EMBRYONIC STEM CELLS
; FILE REFERENCE: 960296.00170
; CURRENT APPLICATION NUMBER: US/10/928,805
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: 09/970,382
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/498,831
; PRIOR FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: 60/499,570
; PRIOR FILING DATE: 2003-09-02
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic PCR primer
US-10-928-805-10

Query Match
Best Local Similarity 72.0%; Score 14.4; DB 9; Length 20;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 1 CGACCCACAGACG 16
|||
Db 16 CGACCCACAGACTGC 1

RESULT 12

US-11-036-317-229142/c
; Sequence 229142, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 229142
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-229142

Query Match 72.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%; Pred. No. 8.4e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CCCACAGACGCCCC 20
|||
Db 24 CCCACAGCCAGCCCC 9

RESULT 13

US-11-036-317-239794/c
; Sequence 239794, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 239794
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-239794

Query Match 72.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%; Pred. No. 8.4e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CCCACAGACGCCCC 20
|||
Db 25 CCCACAGCCAGCCCC 10

RESULT 14

US-11-036-317-289773
; Sequence 289773, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 289773
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-289773

Query Match 72.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%; Pred. No. 8.4e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GACCCACAGACGCC 17
|||
Db 1 GACCCACAGTCAGCC 16

RESULT 15

US-11-036-317-321191
; Sequence 321191, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 321191
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-321191

Query Match 72.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%; Pred. No. 8.4e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GACCCACAGACGCC 17
|||
Db 2 GACCCACAGTCAGCC 17

Search completed: December 25, 2005, 04:14:26
Job time : 338.6 secs

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OM nucleic - nucleic search, using sw model

Run on: December 24, 2005, 18:29:07 ; Search time 135.3 Seconds
(without alignments)
76.712 Million cell updates/sec

Title: US-09-296-264-12

Perfect score: 20
Sequence: 1 CGACCCACAGACAGCCCC 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 416828 seqs, 259477437 residues

Total number of hits satisfying chosen parameters: 1608458

Minimum DB seq length: 20
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA New:*

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10: /cgn2_6/ptodata/2/pubpna/US15_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	15.2	76.0	32	US-10-939-294A-17540, A Sequence 17540, A
2	15.2	76.0	32	US-10-939-294A-18605, A Sequence 18605, A
3	14.4	72.0	25	US-11-121-849-198397, A Sequence 198397, A
4	13.8	69.0	25	US-11-121-849-406866, A Sequence 406866, A
5	13.8	69.0	25	US-11-121-849-591761, A Sequence 591761, A
6	13.6	68.0	25	US-11-121-849-72822, A Sequence 72822, A
7	13.6	68.0	32	US-10-939-294A-16100, A Sequence 16100, A
8	13.4	67.0	25	US-11-121-849-614035, A Sequence 614035, A
9	13.2	66.0	25	US-11-121-849-5889, A Sequence 5889, A
10	13.2	66.0	25	US-11-121-849-43866, A Sequence 43866, A
11	13.2	66.0	25	US-11-121-849-150364, A Sequence 150364, A
12	13.2	66.0	25	US-11-121-849-184358, A Sequence 184358, A
13	13.2	66.0	25	US-11-121-849-195942, A Sequence 195942, A
14	13.2	66.0	25	US-11-121-849-255530, A Sequence 255530, A
15	13.2	66.0	25	US-11-121-849-625612, A Sequence 625612, A
16	13.2	66.0	25	US-11-121-849-635163, A Sequence 635163, A
17	13.2	66.0	32	US-11-121-849-635163, A Sequence 635163, A
18	13.2	66.0	25	US-11-121-849-635163, A Sequence 635163, A
19	12.8	64.0	25	US-11-121-849-28089, A Sequence 28089, A
20	12.8	64.0	25	US-11-121-849-37194, A Sequence 37194, A
21	12.8	64.0	25	US-11-121-849-127013, A Sequence 127013, A
22	12.8	64.0	25	US-11-121-849-152795, A Sequence 152795, A
23	12.8	64.0	25	US-11-121-849-240973, A Sequence 240973, A

24	12.8	64.0	25	US-11-121-849-240974, A Sequence 240974, A
25	12.6	63.0	25	US-10-750-185-24051, A Sequence 24051, A
26	12.6	63.0	25	US-11-121-849-61546, A Sequence 61546, A
27	12.6	63.0	25	US-11-121-849-62184, A Sequence 62184, A
28	12.6	63.0	25	US-11-121-849-197255, A Sequence 197255, A
29	12.6	63.0	25	US-11-121-849-224392, A Sequence 224392, A
30	12.6	63.0	25	US-11-121-849-332017, A Sequence 332017, A
31	12.6	63.0	25	US-11-121-849-359878, A Sequence 359878, A
32	12.6	63.0	54	US-10-842-206-25, A Sequence 206-25, A
33	12.6	63.0	54	US-10-980-459-11, A Sequence 459-11, A
34	12.4	62.0	21	US-10-831-997-1494, A Sequence 1494, A
35	12.4	62.0	25	US-11-121-849-22396, A Sequence 22396, A
36	12.4	62.0	25	US-11-121-849-40888, A Sequence 40888, A
37	12.4	62.0	25	US-11-121-849-151988, A Sequence 151988, A
38	12.4	62.0	25	US-11-121-849-180868, A Sequence 180868, A
39	12.4	62.0	25	US-11-121-849-514223, A Sequence 514223, A
40	12.4	62.0	25	US-11-121-849-539671, A Sequence 539671, A
41	12.2	61.0	25	US-11-121-849-789, A Sequence 789, A
42	12.2	61.0	25	US-11-121-849-23384, A Sequence 23384, A
43	12.2	61.0	25	US-11-121-849-116914, A Sequence 116914, A
44	12.2	61.0	25	US-11-121-849-119578, A Sequence 119578, A
45	12.2	61.0	25	US-11-121-849-157056, A Sequence 157056, A

ALIGNMENTS:

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RESULT 1
US-10-939-294A-17540/c
; Sequence 17540, Application US/10939294A
; Publication No. US20050266417A1
; GENERAL INFORMATION:
; APPLICANT: Barany, Francis
; APPLICANT: Turner, Daniel
; APPLICANT: Pincas, Manesh
; APPLICANT: Pincas, Hanna
; TITLE OF INVENTION: Methods for identifying target nucleic acid molecules
; FILE REFERENCE: 19603/4121 (CRF D-2995-02)
; CURRENT APPLICATION NUMBER: US/10/939,294A
; PRIOR FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: US 60/502/731
; PRIOR FILING DATE: 2003-09-12
; NUMBER OF SEQ ID NOS: 38895
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17540
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: oligonucleotide probe
US-10-939-294A-17540
Query Match
Best Local Similarity 85.0%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CGACCCACAGACAGCCCC 20
Db 21 CGACCCACAGACAGCCCC 2
;
RESULT 2
US-10-939-294A-18605/c
; Sequence 18605, Application US/10939294A
; Publication No. US20050266417A1
; GENERAL INFORMATION:
; APPLICANT: Barany, Francis
; APPLICANT: Turner, Daniel
; APPLICANT: Pincas, Manesh
; APPLICANT: Pincas, Hanna
; TITLE OF INVENTION: Methods for identifying target nucleic acid molecules
; FILE REFERENCE: 19603/4121 (CRF D-2995-02)
; CURRENT APPLICATION NUMBER: US/10/939,294A

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/ CURRENT FILING DATE: 2004-09-10
/ PRIOR APPLICATION NUMBER: US 60/502/731
/ PRIOR FILING DATE: 2003-09-12
/ NUMBER OF SEQ ID NOS: 3895
/ SOFTWARE: Patentin version 3.3
/ SEQ ID NO 18605
/ LENGTH: 32
/ TYPE: DNA
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: oligonucleotide probe
US-10-939-294A-18605

Query Match
Best Local Similarity 76.0%; Score 15.2; DB 6; Length 32;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGACCCCAAGACAGCCGCC 20
DB 21 CGACCCCAAGACAGCCGCC 2

RESULT 3
US-11-121-849-198397
/ Sequence 198397, Application US/11121849
/ Publication No. US20050272080A1
/ GENERAL INFORMATION:
/ APPLICANT: John Palma
/ TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
/ FILE REFERENCE: 3684.1
/ CURRENT APPLICATION NUMBER: US/11/121,849
/ CURRENT FILING DATE: 2005-05-03
/ PRIOR APPLICATION NUMBER: 60/567,949
/ PRIOR FILING DATE: 2004-05-03
/ NUMBER OF SEQ ID NOS: 673904
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 198397
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-11-121-849-198397

Query Match
Best Local Similarity 72.0%; Score 14.4; DB 7; Length 25;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGACCCCAAGACAGCCGCC 16
DB 7 CGACCCCAAGACAGCCGCC 22

RESULT 4
US-11-121-849-406866/c
/ Sequence 406866, Application US/11121849
/ Publication No. US20050272080A1
/ GENERAL INFORMATION:
/ APPLICANT: John Palma
/ TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
/ FILE REFERENCE: 3684.1
/ CURRENT APPLICATION NUMBER: US/11/121,849
/ CURRENT FILING DATE: 2005-05-03
/ PRIOR APPLICATION NUMBER: 60/567,949
/ PRIOR FILING DATE: 2004-05-03
/ NUMBER OF SEQ ID NOS: 673904
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 406866
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-11-121-849-406866
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Query Match
Best Local Similarity 69.0%; Score 13.8; DB 7; Length 25;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ACCCCCAAGACAGCCGCC 19
DB 22 ACACCCCAAGACAGCCGCC 6

RESULT 5
US-11-121-849-591761
/ Sequence 591761, Application US/11121849
/ Publication No. US20050272080A1
/ GENERAL INFORMATION:
/ APPLICANT: John Palma
/ TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
/ FILE REFERENCE: 3684.1
/ CURRENT APPLICATION NUMBER: US/11/121,849
/ CURRENT FILING DATE: 2005-05-03
/ PRIOR APPLICATION NUMBER: 60/567,949
/ PRIOR FILING DATE: 2004-05-03
/ NUMBER OF SEQ ID NOS: 673904
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 591761
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-11-121-849-591761

Query Match
Best Local Similarity 69.0%; Score 13.8; DB 7; Length 25;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GACCCCAAGACAGCCGCC 18
DB 6 GACTCTCAAGACAGCCGCC 22

RESULT 6
US-11-121-849-77282/c
/ Sequence 77282, Application US/11121849
/ Publication No. US20050272080A1
/ GENERAL INFORMATION:
/ APPLICANT: John Palma
/ TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
/ FILE REFERENCE: 3684.1
/ CURRENT APPLICATION NUMBER: US/11/121,849
/ CURRENT FILING DATE: 2005-05-03
/ PRIOR APPLICATION NUMBER: 60/567,949
/ PRIOR FILING DATE: 2004-05-03
/ NUMBER OF SEQ ID NOS: 673904
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 77282
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-11-121-849-77282

Query Match
Best Local Similarity 68.0%; Score 13.6; DB 7; Length 25;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGACCCCAAGACAGCCGCC 20
DB 22 CGACCCCAAGACAGCCGCC 3

RESULT 7
US-10-939-294A-16100/c
/ Sequence 16100, Application US/10939294A
/ Publication No. US20050266417A1
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; GENERAL INFORMATION:
; APPLICANT: Barany, Francis
; APPLICANT: Turner, Daniel
; APPLICANT: Pingel, Maneesh
; APPLICANT: Pincas, Hanna
; TITLE OF INVENTION: Methods for identifying target nucleic acid molecules
; FILE REFERENCE: 19603/4121 (CRF D-2995-02)
; CURRENT APPLICATION NUMBER: US/10/939,294A
; PRIOR FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: US 60/502/731
; PRIOR FILING DATE: 2003-09-12
; NUMBER OF SEQ ID NOS: 38895
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16100
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: oligonucleotide probe
US-10-939-294A-16100

Query Match      68.0%; Score 13.6; DB 6; Length 32;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy      1 CGACCCACAGACAGCCCC 20
Db      21 CGACCCACAGCTACCCGCC 2

RESULT 8
US-11-121-849-614035
; Sequence 614035, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 614035
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-614035

Query Match      67.0%; Score 13.4; DB 7; Length 25;
Best Local Similarity 93.3%; Pred. No. 1.5e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      2 GACCCACAGACAGC 16
Db      3 GACCCACAGACAGC 17

RESULT 9
US-11-121-849-5889
; Sequence 5889, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
```

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; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 5889
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-5889

Query Match      66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy      2 GACCCACAGACAGCCCC 19
Db      4 GACCCACAGACAGCCCC 21

RESULT 10
US-11-121-849-43866/C
; Sequence 43866, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 43866
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-43866

Query Match      66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy      1 CGACCCACAGACAGCCCC 18
Db      19 CCATCCACAGTACGCC 2

RESULT 11
US-11-121-849-150364
; Sequence 150364, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 150364
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-150364

Query Match      66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy      3 ACCCCACAGACAGCCCC 20
```

Db 2 ATCCCACTACAGAGCCCC 19

RESULT 12

US-11-121-849-184358
; Sequence 184358, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Method of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 184358
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-184358

Query Match 66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GACCCACAGACAGCCCC 19
Db 4 GACCAACAGACCTCCCC 21

RESULT 13

US-11-121-849-195942
; Sequence 195942, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Method of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 195942
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-195942

Query Match 66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CGACCCACAGACAGCCCC 18
Db 2 CGACTCCACGAGAGCCCC 19

RESULT 14

US-11-121-849-255530
; Sequence 255530, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Method of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1

; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 255530
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-255530

Query Match 66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GACCCACAGACAGCCCC 19
Db 3 GACCCCAAGATAGCCAC 20

RESULT 15

US-11-121-849-625612
; Sequence 625612, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Method of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 625612
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-625612

Query Match 66.0%; Score 13.2; DB 7; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GACCCACAGACAGCCCC 19
Db 2 GACGACAGACATCCCC 19

Search completed: December 25, 2005, 04:37:04
Job time : 135.3 secs